

**Table 1.** Current gene targets and status

| GENE                                          | FUNCTION                                                        | NOTES                                                                                                                                                                                                                                                                                                             | PURPOSE                                                                                                                                                                                                                                                                        | SPECIFICITY                                                                                        | RELEVANCE                                                                                                                                                                                                                                                                                                                                                                                                                                                                  | WHERE ARE WE?                                                                                                                                     |
|-----------------------------------------------|-----------------------------------------------------------------|-------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------|--------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------|----------------------------------------------------------------------------------------------------|----------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------|---------------------------------------------------------------------------------------------------------------------------------------------------|
| <b>PHOSPHORUS</b>                             |                                                                 |                                                                                                                                                                                                                                                                                                                   |                                                                                                                                                                                                                                                                                |                                                                                                    |                                                                                                                                                                                                                                                                                                                                                                                                                                                                            |                                                                                                                                                   |
| pstS                                          | phosphate transport: high-affinity phosphate binding protein    | prokaryotic; often is present in several copies per genome; not all copies are induced by P limitation                                                                                                                                                                                                            | <b>qPCR</b> : presence or absence of a genetic potential to scavenge low concentrations of Pi; <b>qRT-PCR</b> : activation of pstS expression indicates P limitation;                                                                                                          | Cyanobacterial group specific: N2-fixing vs non-fixing or genus specific; Syn groups               | Indicate Pi limitation                                                                                                                                                                                                                                                                                                                                                                                                                                                     | Have to start by sequencing genes from MB, ALOHA                                                                                                  |
| phoA                                          | utilization of various organic phosphates: alkaline phosphatase | Eukaryotic and prokaryotic; activity is observed under P limitation: eukaryotic - response to external P; cyanobacteria - response to internal P status (phoR is soluble, but an unknown mechanism of activation may exist); single or multicopy gene                                                             | <b>qPCR</b> : presence or absence of a genetic potential to utilize alternative source of P from DOP; <b>qRT-PCR</b> : activation of phoA expression indicates P limitation;                                                                                                   | Group-specific (phylum): to differentiate the responses between cya, bacteria, and eukaryotes      | Indicates Pi limitation.                                                                                                                                                                                                                                                                                                                                                                                                                                                   | Have to start by sequencing genes from MB, ALOHA                                                                                                  |
| phoX                                          | alkaline phosphatase                                            | More abundant than phoA in the marine environment. Four clusters (based on metagenomic surveys and env PCRs): Proteobacteria-only, Roseo-only, 'other' gammas and Bacteriodesetes, Cyanos                                                                                                                         | <b>qPCR</b> : presence or absence of a genetic potential to utilize alternative source of P from DOP; <b>qRT-PCR</b> : activation of phoX expression indicates P limitation;                                                                                                   | gamma-specific, alpha-specific, Syn and Pro-specific                                               | Indicates Pi limitation.                                                                                                                                                                                                                                                                                                                                                                                                                                                   | Have to start by sequencing genes from MB, ALOHA                                                                                                  |
| phnD                                          | phosphonate transport: phosphonate-binding protein              | in Syn, expression is activated when DIP is low; in Pro HLII clade, expression is constitutive; Syn and Pro phn genes do not belong to the pho regulon; in other cya that have C-P lyase pathway, expression of phnD is regulated by phoBR; in eubacteria, regulation is P dependent or activation by PN presence | <b>qPCR</b> : presence or absence of a genetic potential to utilize phosphonates (2-AEP); <b>qRT-PCR</b> : activation of phnD expression (in Syn) indicates P limitation or P starvation, but may be a different profile from pstS and phoA expression;                        | genera specific                                                                                    | Low DIP, utilization of phosphonates                                                                                                                                                                                                                                                                                                                                                                                                                                       | Have to start by sequencing genes from MB, ALOHA;                                                                                                 |
| phnJ (or another conserved gene from phnG-M ) | phosphonate utilization by C-P lyase pathway                    | some cyanobacteria (other than Syn and Pro) and bacteria; single copy                                                                                                                                                                                                                                             | <b>qPCR</b> : presence or absence of a genetic potential to utilize (and synthesize?) various phosphonates and produce methane; <b>qRT-PCR</b> : activation of phnJ expression indicates P limitation and potential assimilation of phosphonate pool and production of methane | Two groups (if possible): cyanobacterial and bacterial                                             | Low DIP, utilization of phosphonates, CH4 release                                                                                                                                                                                                                                                                                                                                                                                                                          | Have to start by sequencing genes from MB, ALOHA                                                                                                  |
| <b>IRON</b>                                   |                                                                 |                                                                                                                                                                                                                                                                                                                   |                                                                                                                                                                                                                                                                                |                                                                                                    |                                                                                                                                                                                                                                                                                                                                                                                                                                                                            |                                                                                                                                                   |
| idiA                                          | iron transport in some bacteria and cyanobacteria               | cyanobacterial and bacterial; srl0513=idiA is a periplasmic iron binding protein in Syn PCC 6803 (other names: futA, sfuA, hitA, mapA?); consider also genes: isiA, dpsA, isiB, fur                                                                                                                               | <b>qPCR</b> : presence or absence of a genetic potential to scavenge Fe; <b>qRT-PCR</b> : Fe limitation                                                                                                                                                                        | cyanobacterial groups: N2-fixing, non-fixing or genera specific; diatoms, SAR11 and other bacteria | <b>Fe limitation. MB</b> : Johnson et al. (2001) observe high Fe flux at first Spring upwelling event, followed by [Fe] decrease while upwelling continues. Monitoring <i>idiA</i> expression will reveal the time scale of the biological response and whether the decrease is due to increased biological uptake after an adaptation period (could also be abiotic). (Up June to Aug, then decreases through to Oct '99) Relevant at all stations C1, M0, M1 (and ALOHA) | Have to start by sequencing genes from MB, ALOHA                                                                                                  |
| <b>NITROGEN</b>                               |                                                                 |                                                                                                                                                                                                                                                                                                                   |                                                                                                                                                                                                                                                                                |                                                                                                    |                                                                                                                                                                                                                                                                                                                                                                                                                                                                            |                                                                                                                                                   |
|                                               |                                                                 | more important in oligotrophic areas; diel periodicity (grp A more active in day, grpB at night) depending on O2 production (PS II) or localization (heterocysts)                                                                                                                                                 | <b>qPCR</b> : presence of N-fixers; <b>qRT-PCR</b> : degree to which N is fixed (which in turn influences primary productivity)                                                                                                                                                | gamma proteobacteria, grp A, B, C, tricho and heterocyst-cluster 1, 2, and 3                       | <b>MB</b> : Johnson attempted to measure N2 fixation and it was negligible, even at his "oligotrophic" station off shore along CalCOFI transect line 67. <b>ALOHA</b> : relevant and changes over time (Church et al., 2005)                                                                                                                                                                                                                                               | Probes for gammas, grp A, B, C, tricho and heterocyst-cluster 1, 2, and 3 already developed and ordered, just need to optimize with ESP reagents. |
| nifH                                          | N fixation                                                      |                                                                                                                                                                                                                                                                                                                   |                                                                                                                                                                                                                                                                                |                                                                                                    |                                                                                                                                                                                                                                                                                                                                                                                                                                                                            |                                                                                                                                                   |
|                                               |                                                                 | all 3 genes necessary to make the permease; regulated by ntcA; expressed in response to N-limitation                                                                                                                                                                                                              | <b>qPCR</b> : ability of community to transport urea; <b>qRT-PCR</b> : active urea transport (N-stressed population)                                                                                                                                                           | Cyanobacteria, diatoms, Proteobacteria                                                             | <b>MB</b> : Johnson et al. observe uncoupling of primary production max (using O2 as a proxy) and NO3 max, in verticle profiles. Has never looked at organic N sources. Likely to be most significant nearshore (and change with extent of ag runoff. Kudela's group (2007) show increased domoic acid production with urea vs. other N sources.                                                                                                                           | Have to start by sequencing ureases from MB, ALOHA                                                                                                |
| urtABE                                        | urea transport                                                  |                                                                                                                                                                                                                                                                                                                   |                                                                                                                                                                                                                                                                                |                                                                                                    |                                                                                                                                                                                                                                                                                                                                                                                                                                                                            |                                                                                                                                                   |
|                                               |                                                                 | production of NH4, CO2; constitutively expressed in some organisms and may not be a good indicator of urea utilization                                                                                                                                                                                            | <b>qPCR</b> : ability of community to use urea (if transported); <b>qRT-PCR</b> : constitutively expressed so maybe doesn't mean much                                                                                                                                          | Syn and Pro, diatoms?, Proteobacteria?                                                             | same as urtA                                                                                                                                                                                                                                                                                                                                                                                                                                                               | Have to start by sequencing ureases from MB, ALOHA                                                                                                |
| ureC                                          | urease                                                          |                                                                                                                                                                                                                                                                                                                   |                                                                                                                                                                                                                                                                                |                                                                                                    |                                                                                                                                                                                                                                                                                                                                                                                                                                                                            |                                                                                                                                                   |
|                                               |                                                                 | regulates expression of several operons involved in utilization of alternate N sources                                                                                                                                                                                                                            | <b>qPCR</b> : Ability to respond to ammonium limitation (and likely use other sources of N); <b>qRT-PCR</b> : Ammonium limitation                                                                                                                                              | Syn and Pro                                                                                        | N limitation                                                                                                                                                                                                                                                                                                                                                                                                                                                               | Have to start by sequencing ntcA from MB, ALOHA                                                                                                   |
| ntcA                                          | global N regulator                                              |                                                                                                                                                                                                                                                                                                                   |                                                                                                                                                                                                                                                                                |                                                                                                    |                                                                                                                                                                                                                                                                                                                                                                                                                                                                            |                                                                                                                                                   |
|                                               |                                                                 | ammonia oxidation to NO2 by Crenarchaeota, Bacteria                                                                                                                                                                                                                                                               | <b>qPCR</b> : presence of ammonia oxidizers; <b>qRT-PCR</b> : active oxidation of ammonia                                                                                                                                                                                      | Archaeal, Bacterial                                                                                | Already done in <b>MB</b> and <b>ALOHA</b> (Mincer et al., 2007)- Archaeal amoA abundance higher at ALOHA                                                                                                                                                                                                                                                                                                                                                                  | Primers, probes developed for MB, ALOHA                                                                                                           |
| amoA                                          | ammonia oxidation                                               |                                                                                                                                                                                                                                                                                                                   |                                                                                                                                                                                                                                                                                |                                                                                                    |                                                                                                                                                                                                                                                                                                                                                                                                                                                                            |                                                                                                                                                   |
| <b>METHANE</b>                                |                                                                 |                                                                                                                                                                                                                                                                                                                   |                                                                                                                                                                                                                                                                                |                                                                                                    |                                                                                                                                                                                                                                                                                                                                                                                                                                                                            |                                                                                                                                                   |
|                                               |                                                                 | water column supersaturated with methane (w/respect to the atm)                                                                                                                                                                                                                                                   | aerobic methanotrophy in the water column                                                                                                                                                                                                                                      | gamma proteobacterial                                                                              | AOA amoA transcript profiles in Monterey Bay (Santoro in press) might look more like CH4 profiles than NH3 profiles (Tillbrook and Karl, 1999; not the case for AOB). pmoA and amoA are homologues and both can usually act on both methane and ammonia*                                                                                                                                                                                                                   | Have to start by sequencing genes from MB, ALOHA                                                                                                  |
| pmoA??                                        | aerobic methanotrophy                                           |                                                                                                                                                                                                                                                                                                                   |                                                                                                                                                                                                                                                                                |                                                                                                    |                                                                                                                                                                                                                                                                                                                                                                                                                                                                            |                                                                                                                                                   |

**Table 2.** Current status of biogeochemical cycling probe implementation on ESP

| Gene                                        | Organism/group               | Assay type | Reference                | Location     | Has been run on ESP? | Has been deployed? | Benefits | Science                                                                                                                                                         |
|---------------------------------------------|------------------------------|------------|--------------------------|--------------|----------------------|--------------------|----------|-----------------------------------------------------------------------------------------------------------------------------------------------------------------|
| 16S rRNA                                    | Crenarchaea                  | TaqMan     | Preston et al., unpubl.  | Monterey Bay | Y                    | Y                  | ABC      | Big players in N cycling in Monterey Bay. Correlation between Cren numbers and [NO <sub>3</sub> ]? Will also let us know which wcrs to target for furth         |
| 16S rRNA                                    | SAR11                        | TaqMan     | "                        | Monterey Bay | Y                    | Y                  | ABC      | Become more abundant with upwelling                                                                                                                             |
| ammonia monooxygenase, grp A                | Crenarchaea                  | TaqMan     | Mosier et al., unpubl.   | Monterey Bay | Y                    | Y                  | D        | Subclades of Crens vary in abundances over depth. Might give us another indication of stratification or upwelling..                                             |
| ammonia monooxygenase, grp B                | Crenarchaea                  | TaqMan     | "                        | Monterey Bay | Y                    | Y                  | D        | "                                                                                                                                                               |
| ammonium transporters, amt                  | Synechococcus                | TaqMan     | Turk et al., unpubl.     | Monterey Bay |                      |                    | A        | Big players in C, N cycling in Monterey Bay. Will help to characterize what dictates their blooms                                                               |
| assim. nitrate reductase, grp A             | Synechococcus                | TaqMan     | Paerl et al., 2009       | Monterey Bay |                      |                    | D        | N stress and utilization of NO <sub>3</sub> . Will help to characterize the conditions under which various subclades dominate                                   |
| assim. nitrate reductase, grp B             | Synechococcus                | TaqMan     | "                        | Monterey Bay | Y                    | Y                  | D        | "                                                                                                                                                               |
| assim. nitrate reductase, grp C             | Synechococcus                | TaqMan     | "                        | Monterey Bay |                      |                    | D        | "                                                                                                                                                               |
| assim. nitrate reductase, grp D             | Synechococcus                | TaqMan     | "                        | Monterey Bay | Y                    |                    | D        | "                                                                                                                                                               |
| assim. nitrate reductase, grp E             | Synechococcus                | TaqMan     | "                        | Monterey Bay | Y                    | Y                  | D        | "                                                                                                                                                               |
| dimethylsulfoniopropionate demethylase      | Roseobacter sp.              | TaqMan     | Varaljay et al., unpubl. | Monterey Bay |                      |                    | ABC      | DMS from release and subsequent cloud nucleation                                                                                                                |
| dimethylsulfoniopropionate demethylase, D/1 | SAR11                        | SYBR Green | Varaljay et al., unpubl. | Monterey Bay | Y                    |                    | ABC      | Can tell whether blooms of dmdA-containing SAR11 subclades coincide with phytoplankton blooms                                                                   |
| dimethylsulfoniopropionate demethylase, D/1 | SAR11                        | TaqMan     | "                        | Monterey Bay | Y                    |                    | ABC      | "                                                                                                                                                               |
| dimethylsulfoniopropionate demethylase, D/1 | SAR11                        | TaqMan+    | "                        | Monterey Bay | Y                    |                    | ABC      | "                                                                                                                                                               |
| dimethylsulfoniopropionate demethylase, D/3 | SAR11                        | SYBR Green | "                        | Monterey Bay | Y                    |                    | ABC      | "                                                                                                                                                               |
| dimethylsulfoniopropionate demethylase, D/3 | SAR11                        | TaqMan     | "                        | Monterey Bay | Y                    |                    | ABC      | "                                                                                                                                                               |
| dimethylsulfoniopropionate demethylase, D/3 | SAR11                        | TaqMan+    | "                        | Monterey Bay | Y                    |                    | ABC      | "                                                                                                                                                               |
| DMSP lyase                                  | Roseobacter sp.              | TaqMan     | "                        | Monterey Bay |                      |                    | ABC      | Production of DMS                                                                                                                                               |
| nitrogenase                                 | gamma proteobacteria         | TaqMan     | Church et al., 2005      | Hawaii       |                      |                    | A        | Nitrogen fixation by diferent diazotroph groups                                                                                                                 |
| nitrogenase                                 | heterocystous cyano          | TaqMan     | "                        | Hawaii       |                      |                    | A        | "                                                                                                                                                               |
| nitrogenase                                 | unicellular cyano, grp A     | TaqMan     | "                        | Hawaii       |                      |                    | A        | "                                                                                                                                                               |
| nitrogenase                                 | unicellular cyano, grp B     | TaqMan     | "                        | Hawaii       |                      |                    | A        | "                                                                                                                                                               |
| phosphatase, phoX                           | Synechococcus                | TaqMan     | Padilla et al., unpubl.  | Monterey Bay |                      |                    | A        | P limitation, utilization of organic P source                                                                                                                   |
| phosphonate lyase, phnJ                     | "other cyano" (not Syn, Pro) | TaqMan     | Cote et al., unpubl.     | Hawaii       |                      |                    | A        | Low DIP, phosphonate utilization and CH <sub>4</sub> release                                                                                                    |
| phosphonate transport, phnD                 | Synechococcus                | TaqMan     | "                        | Monterey Bay |                      |                    | A        | Low DIP, utilization of phosphonates                                                                                                                            |
| RuBisCO                                     | Deep clades                  | SYBR Green | Preston et al., unpubl.  | deep sea     | Y                    | Y                  |          | Abundances                                                                                                                                                      |
| RuBisCO                                     | Synechococcus                | TaqMan     | Turk et al., unpubl.     | Monterey Bay | Y                    | Y                  | A        | Big players in C, N cycling in Monterey Bay. Will help to characterize what dictates their blooms, etc. Also lets us know what groups to target for other genes |
| urease, cluster B                           | gamma proteobacteria         | TaqMan     | "                        | Monterey Bay |                      |                    | ABC      | Urea utilization                                                                                                                                                |
| urease, cluster C                           | Roseo-like (alpha)           | TaqMan     | "                        | Monterey Bay |                      |                    | C        | "                                                                                                                                                               |
| urease, cluster E                           | Roseo-like (alpha)           | TaqMan     | "                        | Monterey Bay |                      |                    | C        | "                                                                                                                                                               |
| urease, grp A                               | Synechococcus                | TaqMan     | "                        | Monterey Bay |                      |                    | A        | "                                                                                                                                                               |
| urease, grp B                               | Synechococcus                | TaqMan     | "                        | Monterey Bay |                      |                    | A        | "                                                                                                                                                               |

**Notes:****A:** temporal**B:** robust assay**C:** Target is always abundant and can be as positive control**D:** Paerl et al., submitted; Santoro and Francis

**Table 3.** Cyanobacterial probes that have been successfully applied to environmental samples

| CATEGORY     | TARGET      | FUNCTION                                                                                | METHOD                      | RELEVANCE                                                                                                                                  | SPECIFICITY                                                                                                                     | REFERENCE                                                                                      | NOTES                                                                                       |
|--------------|-------------|-----------------------------------------------------------------------------------------|-----------------------------|--------------------------------------------------------------------------------------------------------------------------------------------|---------------------------------------------------------------------------------------------------------------------------------|------------------------------------------------------------------------------------------------|---------------------------------------------------------------------------------------------|
| CELL CYCLE   | ftsZ        | cell cycle protein                                                                      | qRT-PCR                     | High expression indicates beginning of cell division                                                                                       | Prochlorococcus                                                                                                                 | Holtzendorff et al., 2002                                                                      | Diel expression                                                                             |
| DIVERSITY    | rbcl        | ribulose-1,5-bisphosphate carboxylase/oxygenase                                         | PCR/RT-PCR                  | Diversity and activity of phytoplankton                                                                                                    | All phytoplankton                                                                                                               | Pichard et al., 1997                                                                           | Diel expression                                                                             |
| DIVERSITY    | psbA        | Photosystem II core protein D1                                                          | PCR                         | PCR: diversity/abundance of photosynthetic organisms                                                                                       | Photosynthetic organisms (eukaryotes and cyanobacteria)                                                                         | Zeidner et al., 2003                                                                           | Diel expression                                                                             |
| DIVERSITY    | 16S-23S ITS | intergenic spacer between 16S and 23S genes                                             | PCR                         | PCR: diversity/abundance of cyanobacteria                                                                                                  | Cyanobacteria                                                                                                                   | Rocap et al., 2002                                                                             |                                                                                             |
| DIVERSITY    | rpoC1       | DNA-dependent RNA Polymerase                                                            | PCR                         | PCR: diversity/abundance of cyanobacteria                                                                                                  | Cyanobacteria and Prochlorophytes                                                                                               | Palenik and Hazelkorn, 1992                                                                    |                                                                                             |
| DIVERSITY    | cpcBA-IGS   | region of cpc (phycocyanin) including intergenic spacer and cpcA, cpcB flanking regions | PCR                         | PCR: Synechococcus diversity and phycobillin content                                                                                       | Synechococcus spp.                                                                                                              | Robertson et al., 2001                                                                         |                                                                                             |
| DIVERSITY    | cpeB        | phycoerythrin                                                                           | PCR                         | PCR: Prochlorococcus HL and LL diversity/abundance                                                                                         | Prochlorococcus HL and LL                                                                                                       | Steglich et al., 2003                                                                          |                                                                                             |
| DIVERSITY    | 16S rRNA    | 16S ribosomal RNA gene                                                                  | PCR                         | diversity                                                                                                                                  | 1. bacteria and archaea; 2. Groups: cyanobacteria, alpha, beta, gamma-proteobacteria, bacteroidetes, planctomycetes, firmicutes | 1. Weisburg et al., 1991; 2. Ashelford et al., 2002; Muhling et al., 2008                      | For group-specific, used DGGE PCR                                                           |
| IRON         | isiB        | flavodoxin                                                                              | qRT-PCR                     | Expression indicates iron limitation                                                                                                       | two Trichodesmium clades                                                                                                        | Chappell and Webb, 2009                                                                        |                                                                                             |
| IRON         | isiA        | iron stress induced protein                                                             | qRT-PCR (TaqMan)            | Iron and/or oxidative stress.                                                                                                              | Crocospaera                                                                                                                     | Hewson et al., 2009                                                                            |                                                                                             |
| NITROGEN     | nifH        | dinitrogen reductase                                                                    | PCR, qPCR, qRT-PCR (TaqMan) | 1. qPCR: diversity and abundance of nitrogen fixing organisms; 2. qRT-PCR: their participation in nitrogen fixation                        | 1. Degenerate for all; 2. Cyanobacterial; 3. Group-specific: Gr. A, B, III, Trichodesmium                                       | 1. Zehr and McReynolds, 1989; Zani et al., 2000; 2. Olson et al., 1999; 3. Church et al., 2005 | Diel expression                                                                             |
| NITROGEN     | ntcA        | nitrogen global control transcription regulator                                         | PCR/RT-PCR                  | 1. PCR: diversity/ abundance; 2) RT-PCR: Expression shows nitrogen (NH <sub>4</sub> <sup>+</sup> ) limitation                              | 1. Picocyanobacteria 2. Synechococcus-specific                                                                                  | Lindell and Post, 2001; Penno et al., 2006                                                     | Expression shows nitrogen (NH <sub>4</sub> <sup>+</sup> ) limitation (Lindell et al., 2005) |
| NITROGEN     | cynA        | cyanate-binding protein, ABC transporter subunit                                        | PCR                         | PCR: a genetic ability to acquire cyanate from outside                                                                                     | 1. Cyanobacteria; 2. Synechococcus; 3. Prochlorococcus                                                                          | Kamennaya et al., 2008                                                                         | Expression in N-limited cultures (Tolonene et al., 2006)                                    |
| NITROGEN     | urtA        | urea-binding protein, ABC transporter subunit                                           | PCR                         | PCR: urea acquisition                                                                                                                      | 1. Cyanobacteria; 2. Synechococcus                                                                                              | Kamennaya et al., 2008                                                                         |                                                                                             |
| NITROGEN     | nifD        | dinitrogenase                                                                           | PCR                         | diversity                                                                                                                                  | cyanobacteria                                                                                                                   | Roeselers et al., 2007                                                                         |                                                                                             |
| NITROGEN     | narB        | nitrate reductase                                                                       | PCR                         | PCR: an ability to assimilate nitrate                                                                                                      | Cyanobacteria                                                                                                                   | Jenkins et al., 2006                                                                           |                                                                                             |
| PHOSPHORUS   | pstS (sphX) | high affinity phosphate binding protein, ABC transporter                                | qRT-PCR                     | Expression indicates Pi limitation                                                                                                         | Trichodesmium                                                                                                                   | Orchard et al., 2009                                                                           | multiply diverse copies                                                                     |
| PHOSPHORUS   | phoA        | phosphatase (Zn <sup>2+</sup> )                                                         | qRT-PCR                     | Expression indicates Pi limitation                                                                                                         | Trichodesmium                                                                                                                   | Orchard et al., 2009                                                                           |                                                                                             |
| PHOSPHORUS   | phoX        | phosphatase (Ca <sup>2+</sup> )                                                         | 1. PCR; 2. qRT-PCR          | 1. PCR: Presence of PhoX type (Ca <sup>2+</sup> ) phosphatase; 2. Expression indicates Pi limitation and utilization of organic phosphates | 1. Bacteria; 2. Trichodesmium                                                                                                   | 1. Sebastian and Amermman, 2009; 2. Orchard et al., 2009                                       |                                                                                             |
| PHOSPHORUS   | phnD        | phosphonate-binding protein; ABC transporter                                            | RT-PCR                      | Expression indicates Pi limitation and potential utilization (transport) of phosphonates                                                   | 1. Trichodesmium; 2. Synechococcus-specific, Prochlorococcus-specific                                                           | 1. Dyhrman et al., 2006; 2. Ilikchyan et al., 2009                                             | In some cya (e.g. Trichodesmium), multiply diverse copies of phnD                           |
| PHOSPHORUS   | phnJ        | C-P lyase protein                                                                       | PCR/RT-PCR                  | 1. Presence of C-P lyase pathway for phosphonate utilization; 2. Expression indicates Pi limitation and potential phosphonate utilization  | Trichodesmium                                                                                                                   | Dyhrman et al., 2006                                                                           |                                                                                             |
| TOXIN        | ndaF        | nodularin synthetase gene subunit F                                                     | qPCR                        | Quantification of toxin-producing Nodularia                                                                                                | Nodularia                                                                                                                       | Koskenniemi et al., 2007                                                                       | Specificity: 30 copies per L                                                                |
| BIOSYNTHESIS | nrps        | nonribosomal peptide synthetases                                                        | PCR                         | A genetic ability to synthesize natural products                                                                                           | Cyanobacteria                                                                                                                   | Ehrenreich et al., 2005                                                                        |                                                                                             |
| BIOSYNTHESIS | mps         | modular polyketide synthases                                                            | PCR                         | A genetic ability to synthesize natural products                                                                                           | Cyanobacteria                                                                                                                   | Ehrenreich et al., 2005                                                                        |                                                                                             |