

Supporting information

Table 3. Genes involved in structure or major metabolic processes which are absent or in lower copy numbers in *P. marinus* SS120 (Pma) than in the freshwater cyanobacteria *Thermosynechococcus elongatus* (Tel), *Synechocystis* sp. PCC6803 (Syn) and *Anabaena* sp. PCC7120 (Ana).

Functional system, protein	Gene name	COG no.	Number of genes per genome			
			Pma	Tel	Syn	Ana
PHOTOSYNTHESIS						
Allophycocyanin	<i>apcA</i>	-	0	2	1	2
	<i>apcBCDE</i>		0	1	1	1
	<i>apcF</i>		0	2	1	1
Phycocyanin	<i>cpcABDE</i>	-	0	1	1	1
	<i>F</i>		0	1	2	1
	<i>cpcC</i>		0	3	2	4
	<i>cpcG</i>					
PSII reaction center D1	<i>psbA</i>	-	1	3	3	5
PSII reaction center D2	<i>psbD</i>	-	1	2	2	2
PSII 12 kDa extrinsic protein	<i>psbU</i>	-	0	1	1	1
Cytochrome <i>c550</i>	<i>psbV</i>	-	0	1	1	1
Oxygen-independent coproporphyrinogen III oxidase	<i>hemN</i>	0635	1	2	2	2
Mg-protoporphyrin IX monomethylester aerobic cyclization system	<i>acsF, crdI</i>	-	1	2	2	3
Heme oxygenase	<i>ho</i>	5398	1	2	2	2
INFORMATIONAL SYSTEMS						
Translation factor SUA5	<i>SUA5</i>	0009	1	2	3	2
Asparaginyl-tRNA synthetase	<i>asnS</i>	0017	0	1	1	1
Ribosomal protein L25	<i>rplY</i>	1825	0	1	1	1
DNA polymerase III alpha subunit	<i>dnaE</i>	0587	1	2*	2*	2*
DNA repair ATPase	<i>sbcC</i>	0419	1	2	3	4
Superfamily I DNA helicase	<i>uvrD</i>	0210	1	2	2	3
DNA mismatch repair protein	<i>mutL</i>	0323	0	1	1	1
Deoxyribodipyrimidine photolyase/cryptochrome	<i>phrA</i>	0415	0	2	2	2
Ribonuclease HI/HII	<i>rnhA</i>	0328	1	2	2	2
DNA-binding protein HupA	<i>hupA</i>	0783	0	2	1	4
16.6 kDa heat shock protein	<i>ipbA</i>		0	1	1	2
ATPases involved in chromosome partitioning	<i>soj</i>	1192	0	3	4	9
DnaJ class chaperone	<i>dnaJ</i>	2214	2	5	5	11
Zn-dependent protease with chaperone function	<i>htpX</i>	501	0	2	3	6
Site-specific recombinases	<i>pin</i>	1961	0	2	1	2
Circadian clock protein KaiA	<i>kaiA</i>	-	0	1	1	1
Circadian clock protein KaiB	<i>kaiB</i>	0526	1	3	2	2
TRANSPORT SYSTEMS						
CO ₂ uptake protein CupA/CupB	<i>cupA</i>	-	0	2	2	2
NAD(P)H-quinone oxidoreductase, NdhF subunit	<i>ndhF</i>	1009	1	3	3	3
NAD(P)H-quinone oxidoreductase, NdhD subunit	<i>ndhD</i>	1008	2	4	4	5
Ammonia permease	<i>amt</i>	0004	1	2	3	3
ABC-type urea transporter	<i>urtABCDE</i>	-	0	1	1	1
Oxyanion-transporting ATPase	<i>arsA</i>	0003	0	2	2	3
Cu/Zn-transport ATPase	<i>zntA</i>	2217	1	3	5	11
Permeases of the major facilitator superfamily	<i>proP</i>	0477	4	12	9	20
Ferrous iron transport protein B	<i>feoB</i>	0370	0	2	1	1

METABOLISM						
Nitrate reductase	<i>narB</i>	0243	0	1	1	1
Nitrite reductase	<i>nirA</i>	0155	0	1	1	1
6-Phosphofructokinase	<i>pfkA</i>	0205	0	1	2	1
Glycerol-3-phosphate dehydrogenase	<i>gpsA</i>	0240	0	1	1	1
Acetate kinase	<i>ackA</i>	0282	0	1	1	1
Fructose-2,6-bisphosphatase	<i>gpmB</i>	0406	1	4	3	6
Malic enzyme	<i>sfcA</i>	0281	0	1	1	1
Phosphoenolpyruvate synthase/ pyruvate phosphate dikinase	<i>ppsA</i>	0574	0	2	1	5
Xylulose 5-phosphate phosphoketolase	<i>xpkA</i>	3957	0	2	2	3
ADP-ribose pyrophosphatase	<i>nudF</i>	1051	0	2	3	5
Urease subunits and accessory proteins	<i>ureABC</i>	-	0	1	1	1
	<i>ureDEFG</i>	-	0	1	1	1
Cytochrome bd oxidase subunit I	<i>cydA</i>	1271	0	1	1	1
Cytochrome bd oxidase subunit II	<i>cydB</i>	1294	0	1	1	1
Cyanophycin synthetase	<i>cphA</i>	-	0	1	1	3
Cyanophycinase	<i>cphB</i>	-	0	1	1	3
Cell wall amidohydrolases	<i>nlpD</i>	0739	0	4	4	8
PILUS BIOGENESIS**						
Pilin	<i>pilA</i>	2165	0	2	1	1
Membrane protein with Walker box motif	<i>pilB</i>	2804	0	1	1	1
Inner membrane protein	<i>pilC</i>	1459	0	2	1	1
ABC transporter ATP-binding protein	<i>pilH</i>	1131	0	1	1	1
Pilus assembly protein PilM	<i>pilM</i>	4972	0	1	1	1
Pilus assembly protein PilN	<i>pilN</i>	3166	0	1	1	1
Pilus assembly protein PilO	<i>pilO</i>	3167	0	1	1	1
Secretin	<i>pilQ</i>	4786	0	1	1	1
Membrane protein with Walker box motif	<i>pilT</i>	2805	0	2	2	2
OTHER MOTILITY-RELATED PROTEINS**						
Motility-related protein kinase	<i>spkA</i>	0515	0	1	2	3
Pentapeptide repeats-containing protein	<i>ppr1</i>	1357	0	2	1	1
	<i>ppr2</i>	1357	0	6	9	17

*2 separate *dnaE* genes give rise to N and C terminal part of DNA polymerase III alpha subunit that are joined posttranslationally by trans-splicing.

Taken from Bhaya, D., Takahashi, A., Shahi, P. & Grossman, A. R. (2001) *J. Bacteriol.* **183, 6140-6143 and D. Bhaya (pers. comm.)