

Supplementary material

Table S1. Primers used for qRT-PCR in this work.

Inorganic pyrophosphatase (<i>ppa</i> ; all3570)	ppaRT fwd	GCTACGCTCACGTAAAATCTTTG
	ppaRT rev	TTTGTAACCTACGGAAAACTCAGC
P _i transporter (<i>pstS1</i> ; all4575)	pstS1RT fwd	ACTAGCTTACAACCTGCCTGG
	pstS1RT rev	AGGTTGACATTAGGGTTAGCAG
P _i transporter (<i>pstS2</i> ; all0911)	pstS2RT fwd	GATGACGGATGCTGAAATTGC
	pstS2RT rev	TGTTGCACGGGATAATCTGAG
Phosphatase/kinase 2 (<i>ppk2</i> ; all2088)	ppk2RT_fwd	GTAAATGATGTGCGTGAAAGGG
	ppk2RT_rev	GTGTAAACCATTTGCGATCGG
Polyphosphate kinase 1 (<i>ppk1</i> ; alr3593)	ppk1RT_fwd	TCGTCTATGGTTTAGTGGGTCT
	ppk1RT_rev	CTGTATAGAGTCGTGCCGTTT
Polyphosphate-dependent glucokinase (<i>ppgk</i> ; all1371)	PPGKRT_fwd	AAAGGTAAGGGTGTAGAGTTGG
	PPGKRT_rev	CTTCGTAAGTTTCCCCTTTGC
Exo-polyphosphatase (<i>ppx</i> ; all3552)	ppxRT_fwd	GAGAATGACAAATGCCGAAAGAG
	ppxRT_rev	AATGACTCCACACCCAACAG
Inositol monophosphatase (all2917)	vtcRT_fwd	TTTGGGTAAGTTAGAGGACGC
	vtcRT_rev	TGGAGTGTTGAGGAAAGTGAC
Ribonuclease (<i>rnpA</i>) — endogenous control	rnpART_fwd	GCGAGCATTAATAACCGTCATC
	rnpART_rev	ACCGCCCTCTTACTAACTTTG

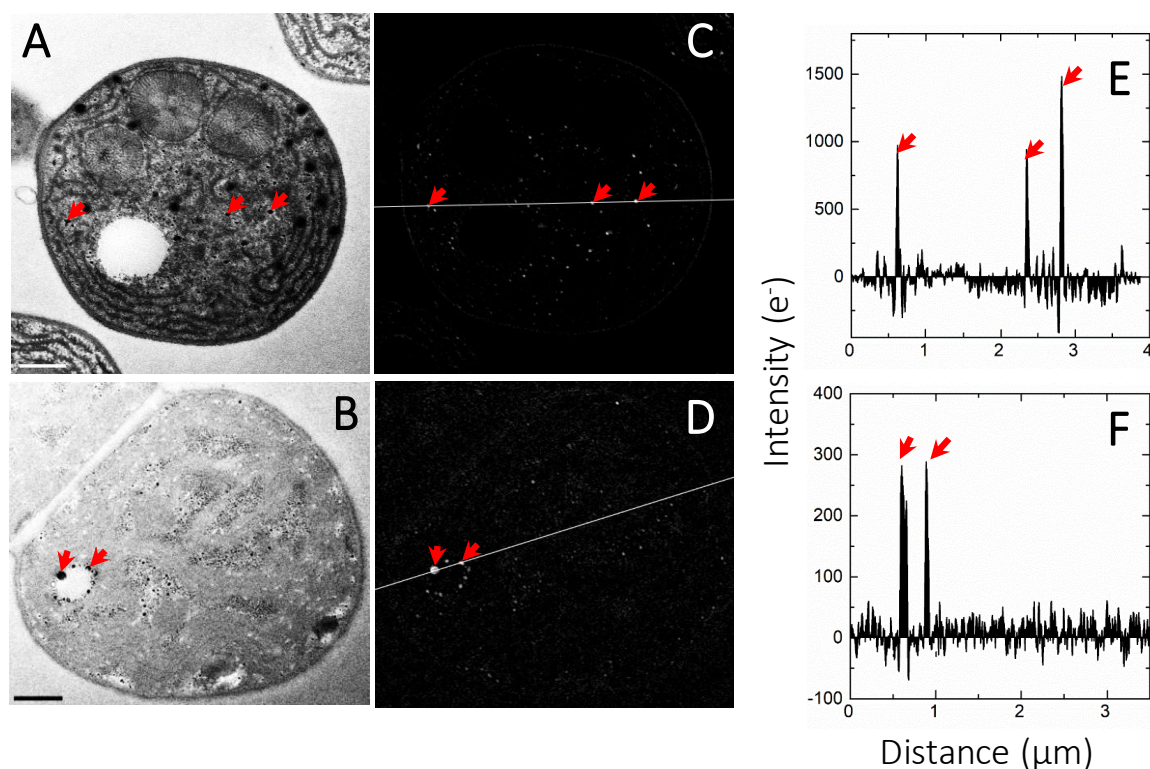


Fig. S1. Accumulation of polyphosphate in the cells of *Nostoc* sp. PCC 7118 visualized energy-filtered transmission electron microscopy (EFTEM). Transient polyphosphate accumulation during lag-phase (4 h after re-feeding of P-starved cells with P_i; A, C, E) and re-accumulation of polyphosphate at early stationary phase (7 d after re-feeding of P-starved cells with P_i; B, D, F; see also Figs. 6, 7). TEM images (A, B) along with the corresponding EFTEM P-maps (C, D), and P signal intensity profiles (E, F, see the white lines in C, D) are shown. Scale bar = 0.5 μm .

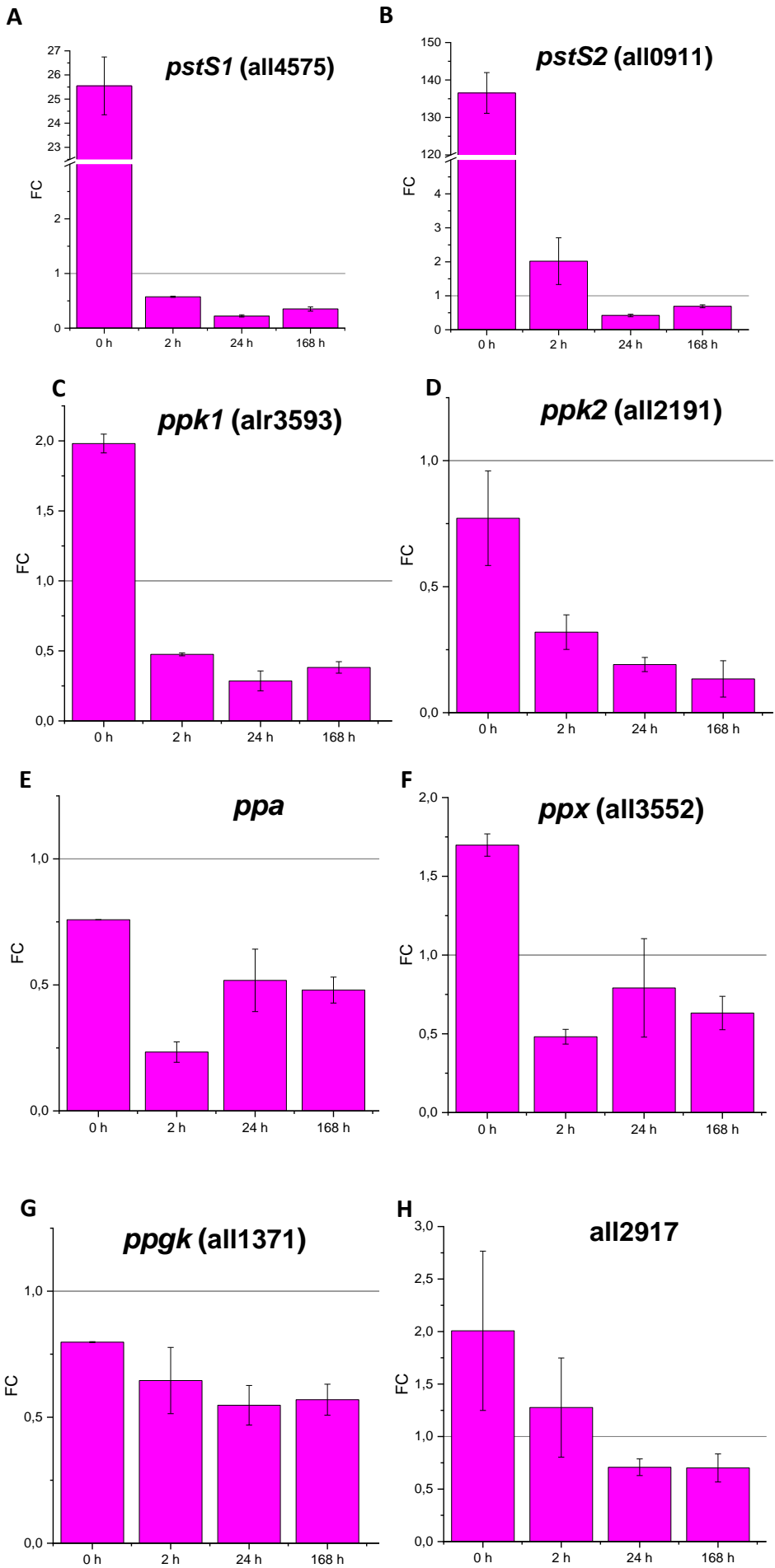


Fig. S2. Changes in the expression of the genes coding for the (A, B) P_i transporters; (C, D) putative polyphosphate kinases; (E) inorganic pyrophosphatase; (F) endonuclease; (G) polyP-dependent glucokinase; and (H) an inositol monophosphatase in the P-starved cells *Nostoc* sp. PCC 7118 at different times after P_i re-feeding (indicated on the graphs) estimated with qRT-PCR (see Methods). The transcript levels of the target genes vs. ribonuclease rnpA (endogenous control) were calculated on fold-change scale relative to those at P-sufficient logarithmic growth.

Table S2. Changes in the expression level (log₂FC FPKM calculated relative to the P-sufficient exponentially growing preculture) of the genes involved in response to shortage of P and, potentially, in its luxury uptake in *Nostoc* sp. PCC 7118. The tentative functional annotation was given according to the published genome of its parent strain *Nostoc* sp. PCC 7120 [1-4].

ORF	Name (description)	Conditions			
		Preculture (+P)	P-starved (-P)	Recovery (+P)	
				1 day	7 days
all4502	<i>sphS</i> (P-starvation response regulator, sensory histidine kinase)	0.28	-0.97	-0.47	-0.62
all4503	<i>sphR</i> (P-starvation response regulator)	0.53	-1.39	-0.82	-0.81
all4501	<i>phoU</i> (P-starvation response regulator, repressor of <i>Pho</i> regulon)	-0.14	-0.6	-0.52	0.46
all4573	<i>pstA1</i> (ABC-type P _i transporter/binding protein)*	-1.92	-0.43	-0.47	-0.1
all4572	<i>pstB1</i> (ABC-type P _i transporter/binding protein)	-1.56	-0.28	-0.1	-0.58
all4574	<i>pstC1</i> (ABC-type P _i transporter/binding protein)*	-2.76	-0.13	-0.29	-0.09
all4575	<i>pstS1</i> (ABC-type P _i transporter/binding protein)*	-3.74	-0.18	-0.37	-0.69
alr1094	<i>sphX</i> (putative periplasmic P _i transporter – P _i -binding protein, ABC-type)	-0.46	-0.56	-0.65	0.06
all0917	putative periplasmic transporter, ABC-type	-5.43	1.8	0.96	0.75
all0907	<i>pstX</i> (an ABC-type P _i transporter/binding protein)*	-1.01	0.03	-1.09	-0.59
all0909	<i>pstA2</i> (ABC-type P _i transporter/binding protein)*	-2.76	0.88	-0.16	-1.92
all0908	<i>pstB2</i> (ABC-type P _i transporter/binding protein)*	-0.94	-0.4	-0.9	-0.45
all0910	<i>pstC2</i> (ABC-type P _i transporter/binding protein)*	-3.62	-0.37	-0.58	-0.79
all0911	<i>pstS2</i> (ABC-type P _i transporter/binding protein)*	-6.09	0.95	-0.03	-0.78

*High-affinity P_i transporters residing in the cytoplasmic membrane.

Table S3. Changes in the expression level (log₂FC FPKM calculated relative to the P-sufficient exponentially growing preculture) of the genes involved in phosphonate uptake and assimilation in *Nostoc* sp. PCC 7118. The tentative functional annotation ois given according to the published genome of its parent strain *Nostoc* sp. PCC 7120 [1-3].

ORF	Name	Conditions			
		Preculture (+P)	P-starved (-P)	Recovery (+P)	
				1 day	7 days
all2230	<i>phnC</i>	-4.74	0.38	-1	-1
all2228	<i>phnD</i>	-2.53	-1.38	-1.8	-1
alr2226	<i>phnE</i>	-2.85	0.25	0.11	0.77
alll2225	<i>phnG</i>	-0.39	-0.99	-5.38	-1.25
all2224	<i>phnH</i>	-0.66	0.48	-1.38	-1.38

Table S4. Changes in the expression level (\log_2 FC FPKM calculated relative to the P-sufficient exponentially growing preculture) of the genes encoding the components of the light-harvesting antenna and RuBisCo in *Nostoc* sp. PCC 7118. The tentative functional annotation ois given according to the published genome of its parent strain *Nostoc* sp. PCC 7120 [4].

Name (description)	Conditions			
	Preculture	P-starved	Recovery (+P)	
	(+P)	(-P)	1 day	7 days
<i>pecA</i> (phycoerythrocyanin alpha chain)	4.26	-9.41	-5.21	-0.99
<i>pecB</i> (phycoerythrocyanin beta chain)	4.23	-10.61	-4.79	-1.09
<i>pecC</i> (phycoerythrocyanin-associated rod linker protein)	4.54	-7.71	-4.77	-1.67
<i>pecE</i> (bilin biosynthesis protein)	4.62	-6.25	-4.76	-2.52
<i>pecF</i> (bilin biosynthesis protein)	3.25	-4.69	-3.4	-2.61
<i>cpcA</i> (phycocyanin alpha chain)	2.48	-5.2	-0.57	0.73
<i>cpcB</i> (phycocyanin beta chain)	2.49	-5.35	-0.58	0.7
<i>cpcC</i> (phycocyanin-associated rod linker protein)	3.53	-5.38	-1.61	0.27
<i>cpcD</i> (rod-capping linker polypeptide)	3.87	-7.34	-1.44	0.54
<i>cpcE</i> (phycocyanobilin lyase alpha subunit)	4.26	-7.84	-1.67	0.62
<i>cpcF</i> (phycocyanobilin lyase beta subunit)	3.86	-6.56	-1.52	-0.02
<i>cpcG1</i> (phycobilisome rod-core linker protein)	3.37	-5.61	-1.17	0.1
<i>cpcG2</i> (phycobilisome rod-core linker protein)	3.24	-4.01	-1.14	0.22
<i>cpcG3</i> (phycobilisome rod-core linker protein)	3.24	-4.35	-1	0.07
<i>cpcG4</i> (phycobilisome rod-core linker protein)	0.79	-1.41	0.21	0.69
<i>rbcL</i> (RuBisCo large subunit)	1.35	-1.25	-0.08	-0.53
<i>rbcS</i> (RuBisCo small subunit)	1.34	-1.33	0.07	-0.46
<i>rca</i> (RuBisCo activase)	-0.35	-0.79	0.41	-0.69

Table S5. Changes in the expression level (\log_2 FC FPKM calculated relative to the P-sufficient exponentially growing preculture) of the genes encoding the enzymes of cyanophycin turnover in *Nostoc* sp. PCC 7118. The tentative functional annotation ois given according to the published genome of its parent strain *Nostoc* sp. PCC 7120 [4].

ORF	Name (description)	Conditions			
		Preculture	P-starved	Recovery (+P)	
		(+P)	(-P)	1 day	7 days
–	<i>cphA1</i> (cyanophycin synthase)	-1.82	1.09	0.53	0.85
–	<i>cphA2</i> (cyanophycin synthase)	0.24	-0.19	0.08	0.08
–	<i>cphB2</i> (cyanophycin synthase)	1.11	-1.03	-0.34	-0.11
all3922	– (isoaspartyl dipeptidase)	-0.43	1.27	0.75	0.13

References

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