

Supplemental Material to:

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Translational control of small heat shock genes in mesophilic and thermophilic cyanobacteria by RNA thermometers

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Translational control of small heat shock genes in mesophilic and thermophilic cyanobacteria by RNA thermometers

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Supplementary Information

Fig. S1 Sequence alignment of *hspA*-5'UTR from *Thermosynechococci*.

Table S1 Strains, plasmids, and oligonucleotides used in this study

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Fig. S1

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                                -35                                -10                                *
T. vulcanus hspA      GATCGTTAAACCCACTTGTATCAAGACTTGCATCCTCTATAGTGAAGGTGGGTAGAGGG
T. elongatus hspA   GATCGTTAAACCCACTTGTATCAAGACTTGCATCCTCTATAGTGAAGGTGGGTAGAGGG
                        *****
                                IR
T. vulcanus hspA      AATCAGCCCAAGTCACGAGCAAAGGCAATACAAGCAAATTTAGTTGTTGGTGCTGTTCTC
T. elongatus hspA   AATCAGCCCAAGTCACGAGCAAAGGCAATACAAGCAAATTTAGTTGTTGGTGCTGTTCTC
                        *****
                                SD
T. vulcanus hspA      TCTGTCAACCATCCCGCGGGCAATCTAAAACATA-----TACAGGAGGATAAGCGTATGGCA
T. elongatus hspA   TCTGTCAACCATCCCGCGGGCAATCTAAAACATAAACGATACAGGAGGATAAGCGTATGGCA
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Fig. S1 Sequence alignment of *hspA* upstream region from *Thermosynechococci*.

The sequence alignment was performed using ClustalW2^{1, 2}, asterisks mark similar positions. Promoter sequence, transcriptional start site (-), Shine-Dalgarno sequence (SD), and ATG are depicted in bold. The *hspA* nucleotide sequence from *T. vulcanus* was retrieved from³, as well as the highlighted inverted repeat, a putative DNA protein binding site. The transcriptional start site was mapped before.⁴ The *hspA* upstream region from both *Thermosynechococci* is highly similar, the 5'UTR just being elongated by 6 nt. Therefore, the same transcriptional start site as for *T. vulcanus hspA* was assumed for *T. elongatus hspA*.

Strain, plasmid, or oligonucleotide	Relevant characteristic or Sequence	Source or Reference
Strains		
<i>Escherichia coli</i> DH5 α	<i>supE44</i> , Δ <i>lacU169</i> (Φ 80d <i>lacZ</i> Δ M15), <i>hsdR17</i> , <i>recA1</i> , <i>endA1</i> , <i>gyrA96</i> , <i>thi-1</i> , <i>relA1</i>	5, 6 7 8 9
<i>Thermosynechococcus elongatus</i> BP-1	Wild type	
<i>Anabaena variabilis</i> ATCC 29413	Wild type	
<i>Nostoc</i> sp. PCC 7120 (<i>Anabaena</i> sp. PCC 7120)	Wild type	
Plasmids		
pUC18	Cloning vector, Ap ^r	10
pBAD2- <i>bgaB</i>	Arabinose inducible; reporter gene system for translational fusions to <i>bgaB</i> ; Ap ^r	11
pBAD2- <i>hsp17</i> (pBO1836)	pBAD2- <i>bgaB</i> based, <i>Synechocystis hsp17</i> -5'UTR plus 2 codons fused to <i>bgaB</i>	11
pT7 <i>hspA</i> -cdr (pBO1858)	pUC18 based, contains T7 promoter, <i>hspA</i> -5'UTR plus 20 codons, HpyCH4v	This study
pUC18- <i>avashort</i> (pBO2154)	pUC18 cloning vector harboring <i>ava3076</i> -5'UTR plus 2 codons (NheI, EcoRI)	This study
pUC18- <i>avalong</i> (pBO2155)	pUC18 cloning vector harboring <i>ava4812</i> -5'UTR plus 2 codons (NheI, EcoRI)	This study
pUC18- <i>alrshort</i> (pBO2761)	pUC18 cloning vector harboring <i>alr0286</i> -5'UTR plus 2 codons (NheI, EcoRI)	This study
pUC18- <i>alrlong</i> (pBO2762)	pUC18 cloning vector harboring <i>alr1809</i> -5'UTR plus 2 codons (NheI, EcoRI)	This study
pBAD2- <i>avashort</i> (pBO2161)	pBAD2- <i>bgaB</i> based, insert cloned from pUC18- <i>avashort</i> via NheI, EcoRI	This study
pBAD2- <i>avalong</i> (pBO2162)	pBAD2- <i>bgaB</i> based, insert cloned from pUC18- <i>avalong</i> via NheI, EcoRI	This study
pBAD2- <i>alrshort</i> (pBO2795)	pBAD2- <i>bgaB</i> based, insert cloned from pUC18- <i>alrshort</i> via NheI, EcoRI	This study
pBAD2- <i>alrlong</i> (pBO2796)	pBAD2- <i>bgaB</i> based, insert cloned from pUC18- <i>alrlong</i> via NheI, EcoRI	This study
pT7 <i>avalong</i> (pBO2772)	pUC18 based, contains T7 promoter, <i>avalong</i> -5'UTR plus ATG, EcoRV	This study
pT7 <i>avashort</i> -cdr (pBO2775)	pUC18 based, contains T7 promoter, <i>avashort</i> -5'UTR plus 24 codons, EcoRV	This study
pBAD2- <i>avalong</i> Δ loop1 (pBO2799)	pBAD2- <i>avalong</i> -based, site directed mutagenesis with primers 712, 713	This study
pBAD2- <i>avalong</i> Δ T90 (pBO3051)	pBAD2- <i>avalong</i> -based, site directed mutagenesis with primers 716, 717	This study
pBAD2- <i>avalong</i> CC88/91AA (pBO2816)	pBAD2- <i>avalong</i> -based, site directed mutagenesis with primers 1278, 1279	This study
pBAD2- <i>avalong</i> 2A (pBO2793)	pBAD2- <i>avalong</i> -based, site directed mutagenesis with primers 980, 981	This study

pBAD2- <i>avalong4A</i> (pBO2794)	pBAD2- <i>avalong</i> -based, site directed mutagenesis with primers 1003, 1004	This study
pBAD2- <i>avashort</i> -antiSD1 (pBO2751)	pBAD2- <i>avashort</i> -based, randomized substitution of C34, C35 by T34, A35	This study
pBAD2- <i>avashort</i> -antiSD2 (pBO2752)	pBAD2- <i>avashort</i> -based, randomized substitution of C34, C35 by T34, T35	This study
pBAD2- <i>avashort</i> -antiSD3 (pBO2753)	pBAD2- <i>avashort</i> -based, randomized substitution of C34, C35 by G34, A35	This study
pBAD2- <i>avashort</i> -antiSD4 (pBO2754)	pBAD2- <i>avashort</i> -based, randomized substitution of C34, C35 by G34, G35	This study
pBAD2- <i>avashort</i> C46A (pBO2798)	pBAD2- <i>avashort</i> -based, site directed mutagenesis with primers 734, 735	This study

Oligonucleotides

371 T7 <i>hspA</i> for	GAAATTAATACGACTCACTATAGGGGGGTAGAGGGAATCAGCCCAAG (pBO1858)
372 <i>hspA</i> _cdrev	<u>TGCAGTTCATTTGGCGTTGAATTGC</u> (pBO1858)
552 for- <i>bgaB3076</i>	<u>TTGCTAGCAAGATTAAGCCTGGAAGCG</u> (pBO2154, RNA probe forward primer)
553 rev- <i>bgaB3076</i>	<u>TTGAATTCTGTCATATCTTTGACTCCTC</u> (pBO2154)
550 for- <i>bgaB4812</i>	<u>TTGCTAGCGAAGGAGCTAGAGATTAAGC</u> (pBO2155, RNA probe forward primer)
551 rev- <i>bgaB4812</i>	<u>TTGAATTCTGCCATAATATCACCTCTAA</u> (pBO2155, pBO2762)
1002 for- <i>bgaB0286</i>	<u>TTGCTAGCAAATGAAAGATTAAGCCTG</u> (pBO2761)
668 Revalr0286	<u>TTGAATTCTGTCATAGTTTTGACTCCTC</u> (pBO2761)
526 for- <i>bgaB1809</i>	<u>TTGCTAGCGAAGGAGCTAGAAATTAAGC</u> (pBO2762)
862 T73076for	TTGAAATTAATACGACTCACTATAGGAAGATTAAGCCTGGAAGCG (pBO2775)
857 3076_72cdrev	<u>TTGATATCCTCAAACAAATGATTTAA</u> (pBO2775)
859 T74812for	TTGAAATTAATACGACTCACTATAGGGAAGGAGCTAGAGATTAAGC (pBO2772)
860 4812bluntrev	<u>TTGATATCCATAATATCACCTCTAAAATGC</u> (pBO2772)
712 4812dloop_for	GATTAAGCTTTTCCACAAAAAAGCTTAATAATAGC (pBO2799)
713 4812dloop_rev	GCTATTATTAAGCTTTTTTGTGGAAAAGCTTAATC (pBO2799)
716 4812dT90_for	GCTTAATAATAGCCTCTGATAAGCAAATGTTG (pBO3051)
717 4812dT90_rev	CAACATTTGCTTATCAGAGGCTATTATTAAGC (pBO3051)
1278 QCC88/91Afw	GCTTAATAATAGCATTATGATAAGCAAATGTTGC (pBO2816)
1279 QCC88/91Arv	GCAACATTTGCTTATCATAATGCTATTATTAAGC (pBO2816)
710 3076QC_for	GCGATTTCGCAGGAAAA DD TTAGAGGAGTCAAAG (pBO2751-2754)
711 3076QC_rev	CTTTGACTCCTCTAA HH TTTTTCTGCGAATCGC (pBO2751-2754)
734 3076_C46A_for	GGAAAACCTTAGAGGAGTAAAAGATATGACAGAATTC (pBO2798)
735 3076_C46A_rev	GAATTCTGTCATATCTTTTACTCCTCTAAGGTTTTCC (pBO2798)

529 RACE_3076	TCTTGCCAAGGGTTCCAACG
461 RACE_4812	TCTTCAAGTTCAGCAGCAGG
Adapter for 5'RACE	GTCAGCAATCCCTAACGAG (<i>GAG ribonucleotides</i>)
Adapter primer for 5'RACE	GTCAGCAATCCCTAACGAG
1028 avashort_RNAprobe_rev	GAAATTAATACGACTCACTATAGGGAGGTAATGTCAAATTC AAG
1029 avalong_RNAprobe_rev	GAAATTAATACGACTCACTATAGGGAGCCAGCAGCAGATTCAATG
980 Qc_c53-4af	CAAATTAATTC AACAATATAAATCTTATTTAATTAGTAAAAAGC (pBO2793)
981 Qc_c53-4ar	GCTTTTTACTAATTAATAAGATTTATATTGTTGAATTAATTTG (pBO2793)
1003 Qc4812_53-6A	AAATTAATTC AACAATATAAAAATTATTTAATTAGTAAAAAG (pBO2794)
1004 Qc4812_53-6A	CTTTTTACTAATTAATAATTTTTTATATTGTTGAATTAATTT (pBO2794)

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