

**Table S1.** Primers used in this study.

Name	Sequence (5' to 3')	Purpose of primer	Expected size (bp)	Cycles/Tm	Reference
Sll0180_F	AGACAATCTAGAATGGTTAGAAA ACGCTCC	PCR for <i>sll0180</i> ( <i>acrA</i> )	1,506	30 /59.0 °C	This study
Sll0180_R	AGACAAACTAGTTTACAGGGAAG ACTCGAG	PCR for <i>sll0180</i> ( <i>acrA</i> )			This study
Slr2131_F	AGACAATCTAGAGAGTCGGCTGG AGATTGAGCC	PCR for <i>slr2131</i> ( <i>acrB</i> )	3,300	30 /59.0 °C	This study
Slr2131_R	AGACAAACTAGTCTAGCTATTCTT TTGGGA	PCR for <i>slr2131</i> ( <i>acrB</i> )			
Slr2170_F	AGACAAACTAGTGGTTGGAGATC CCCGCGCAT	PCR for <i>slr1270</i> ( <i>tolC</i> )	1,751	30 /56.0 °C	This study
Slr2170_R	AGACAACTGCAGCCCATCGTCTC AGAC	PCR for <i>slr1270</i> ( <i>tolC</i> )			This study
UUSpsbA2_F	CACTCAGATAGGAGCCATCTTGC	Colony PCR			Eungrasamee et al. 2020
DDSpsbA2_R	CACTCAGATAGGAGCCATCTTGC	Colony PCR			Eungrasamee et al. 2020
Cm_R	CAGCTCGAGGCTTGGATTCT	Colony PCR			Eungrasamee et al. 2020
RTacrA_F360	CAACCTAGTGGCTACCAACT	RT-PCR for <i>sll0180</i>	360	28 /54.0 °C (BG <sub>11</sub> )	This study
RTacrA_R360	GCCAAGTTAAGATTGGCCTG	RT-PCR for <i>sll0180</i>		32 /54.0 °C (BG <sub>11</sub> -N)	
				28 /54.0 °C (BG <sub>11</sub> + 1.5%NaCl)	
RTacrB_F380	CAATGCGGAAGTGGTGGAAA	RT-PCR for <i>slr2131</i>	380	28 /54.0 °C (BG <sub>11</sub> )	This study
RTacrB_R380	CAAAAATCCGTACATCCCCC	RT-PCR for <i>slr2131</i>		32 /54.0 °C (BG <sub>11</sub> -N)	
				28 /54.0 °C (BG <sub>11</sub> + 1.5%NaCl)	
RTtolC_F480	CTGAGAAATAATGAACAACTCCA GC	RT-PCR for <i>slr1270</i>	480	30 /56.0 °C (BG <sub>11</sub> )	This study
RTtolC_R480	CCAACCCGGCCTGTTCTAAC	RT-PCR for <i>slr1270</i>		33 /56.0 °C (BG <sub>11</sub> -N)	
				30 /56.0 °C (BG <sub>11</sub> + 1.5%NaCl)	
RTlipA_F379	TTGGCGGAGCAAGTGAAGCAAT	RT-PCR for <i>lipA</i>	379	30 /56.0 °C (BG <sub>11</sub> )	Eungrasamee et al. 2019
RTlipA_R379	CATGGACCAGCACAGGCAAAAT	RT-PCR for <i>lipA</i>		33 /56.0 °C (BG <sub>11</sub> -N)	
				30 /56.0 °C (BG <sub>11</sub> + 1.5%NaCl)	
RTplsX_F488	AAGGGGTGGTGGAAATGGAA	RT-PCR for <i>plsX</i>	488	33 /52.0 °C (BG <sub>11</sub> )	Towijit et al. 2018
RTplsX_R488	AAGTAGGTCCCTTCCTTCGG	RT-PCR for <i>plsX</i>		39 /52.0 °C (BG <sub>11</sub> -N)	
				32 /52.0 °C (BG <sub>11</sub> + 1.5%NaCl)	

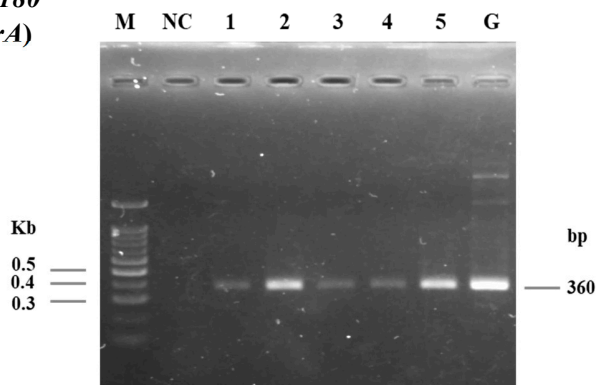
Name	Sequence (5' to 3')	Purpose of primer	Expected size	Cycles/Tm	Reference
RTaas_F307	GTGGTTTATCGCCGATCAAG	RT-PCR for <i>aas</i>	307	33 /55.0 °C (BG <sub>11</sub> )	Eungrasamee et al. 2019
RTaas_R307	TTCCTGGCGGGGAACGGGAG	RT-PCR for <i>aas</i>		32 /55.0 °C (BG <sub>11</sub> -N)	
				32 /55.0 °C (BG <sub>11</sub> +1.5%NaCl)	
RTertB_F462	TGACCAATATTCTGCGGGACGTT	RT-PCR for <i>crtB</i>	462	33 /56.0 °C (BG <sub>11</sub> )	Natesungnoen et al. 2023
RTertB_R462	TAGAGACTGCAGAGTGAGTCCTT AGC	RT-PCR for <i>crtB</i>		30 /56.0 °C (BG <sub>11</sub> -N)	
				29 /56.0 °C (BG <sub>11</sub> +1.5%NaCl)	
RTchlG_F435	TACATTGCCCTACCGTGGTGG	RT-PCR for <i>chlG</i>	435	30 /59.0 °C (BG <sub>11</sub> )	Natesungnoen et al. 2023
RTchlG_R435	TCAAATCCCCGCATGGCCTA	RT-PCR for <i>chlG</i>		32 /59.0 °C (BG <sub>11</sub> -N)	
				30 /59.0 °C (BG <sub>11</sub> +1.5%NaCl)	
RT16SrRNA_F521	AGTTCTGACGGTACCTGATGA	RT-PCR for <i>16S</i>	521	15 /56.0 °C (BG <sub>11</sub> )	Natesungnoen et al. 2023
RT16SrRNA_R521	GTCAAGCCTTGGTAAGGTTAT	RT-PCR for <i>16S</i>		19 /56.0 °C (BG <sub>11</sub> -N)	
				15 /56.0 °C (BG <sub>11</sub> +1.5%NaCl)	

**Table S2 PCR conditions for checking transformants**

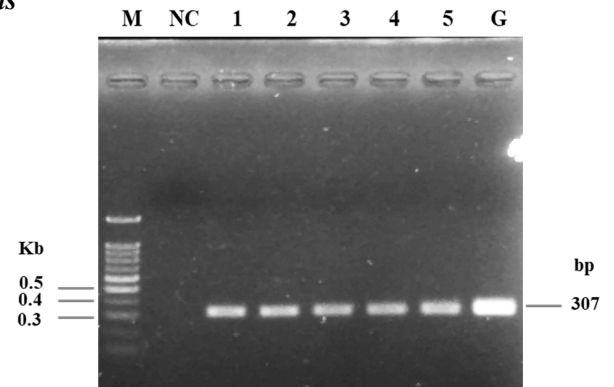
Strains	Pair of primers	Cycles/Tm	Expected size (bp)
OA	UUSpsbA2/ DDSpsbA2	30 /56.0 °C	3966
	SlI0180_F /Cm_R	30 /59.0 °C	2506
OB	UUSpsbA2/ DDSpsbA2	30 /56.0 °C	5760
	Slr2131_F /Cm_R	30 /57.0 °C	4,300
OC	UUSpsbA2/ DDSpsbA2	30 /56.0 °C	4211
	Slr2170_F /Cm_R	30 /58.0 °C	2751
OABC	SlI0180_F / RTacrB_R380	30 /59.0 °C	2158
	SlI0180_F / RTolC_R480	30 /56.0 °C	5766
	UUSpsbA2/ SlI0180_R	30 /57.0 °C	2176
	Slr2131_F /Cm_R	30 /57.0 °C	6051

**Figure S1:** The expression of genes in each strain cultured under normal BG<sub>11</sub> medium analyzed by RT-PCR analysis

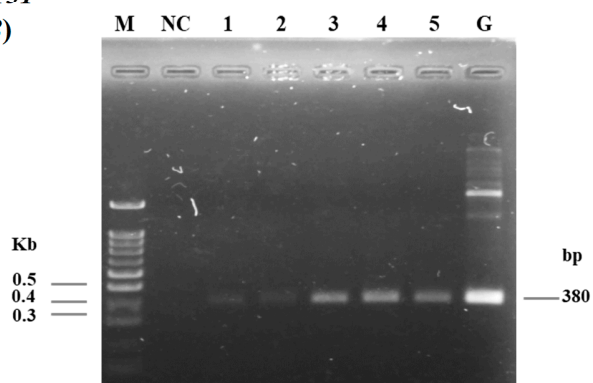
**A. *slr0180*  
(*acrA*)**



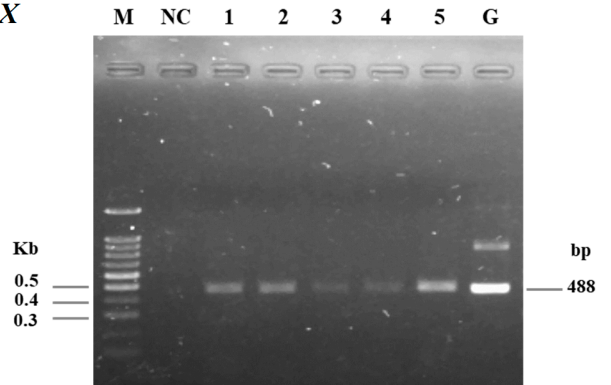
**E. *aas***



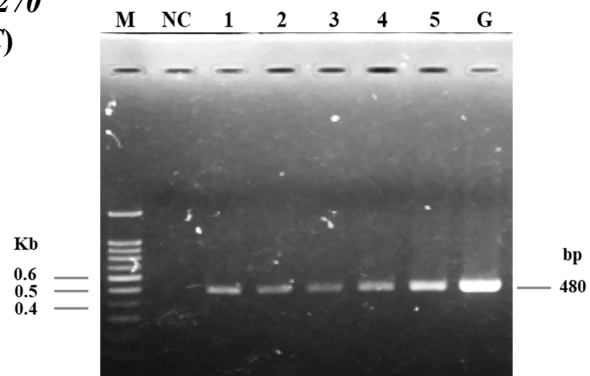
**B. *slr2131*  
(*acrB*)**



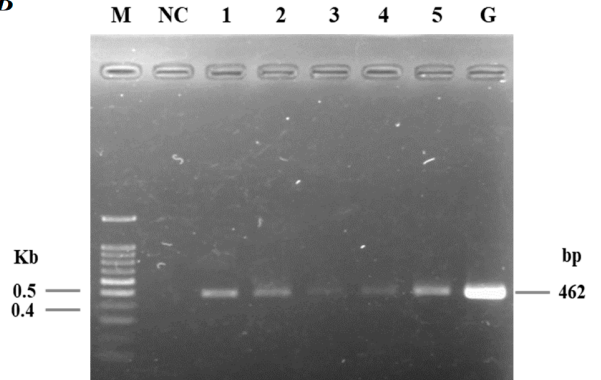
**F. *plsX***



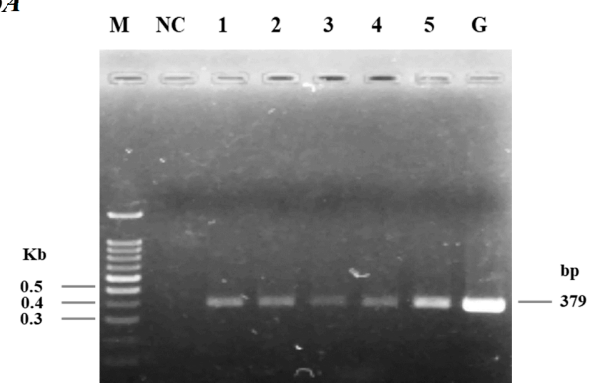
**C. *slr1270*  
(*tolC*)**



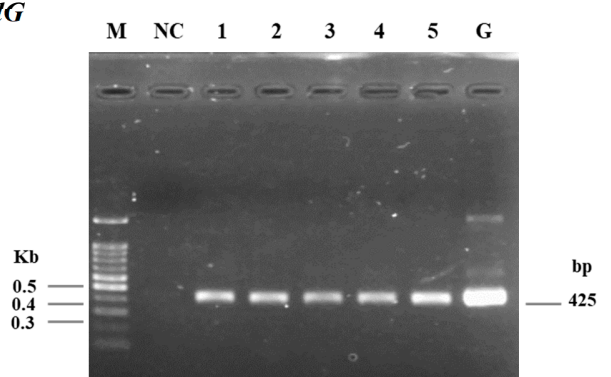
**G. *crtB***



**D. *lipA***

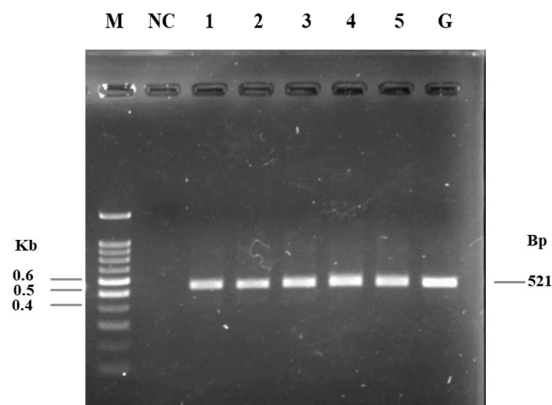


**H. *chlG***



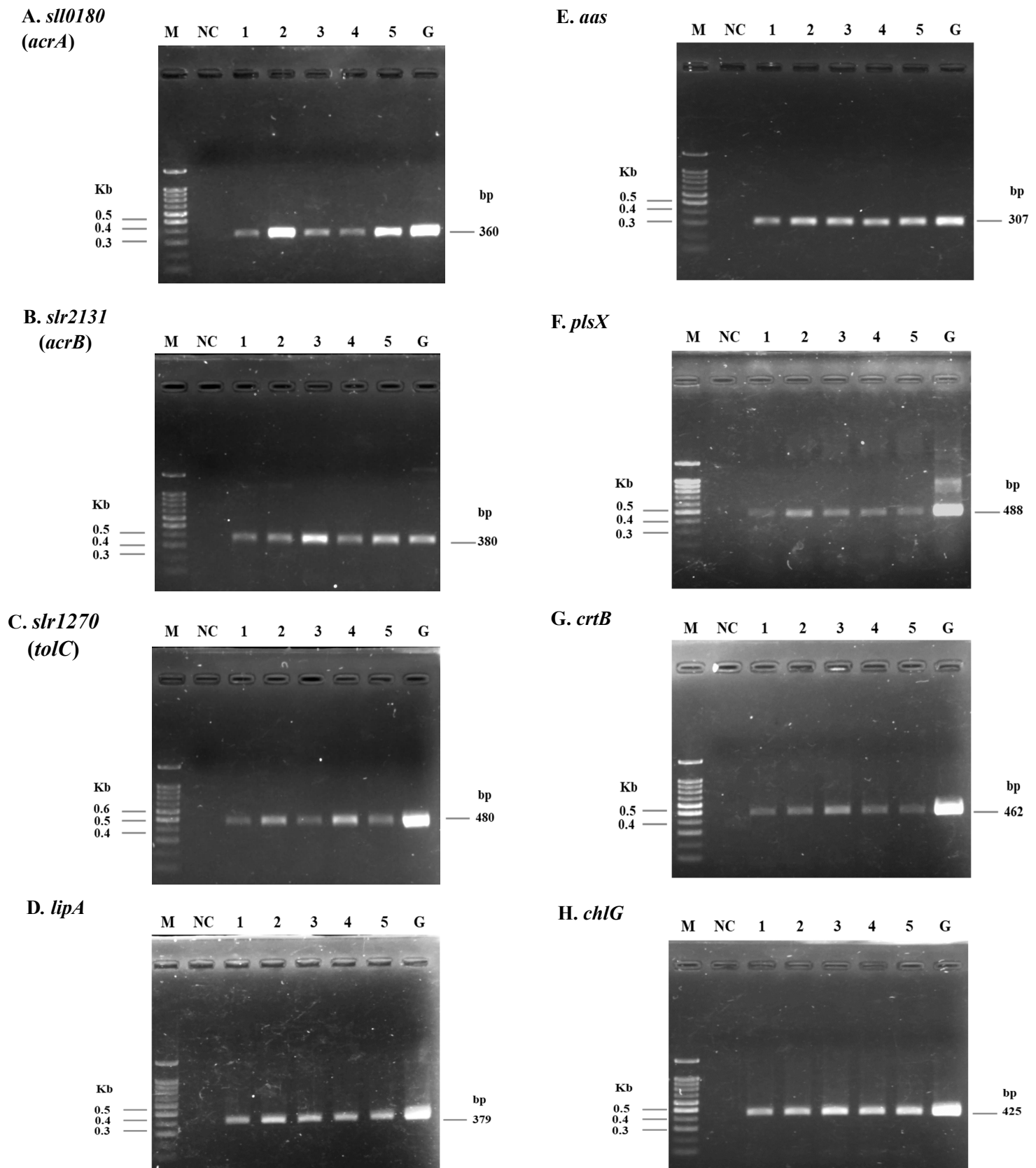
**Figure S1 (Continue):** The expression of genes in each strain cultured under normal BG<sub>11</sub> medium analyzed by RT-PCR analysis

### I. *16S rRNA*



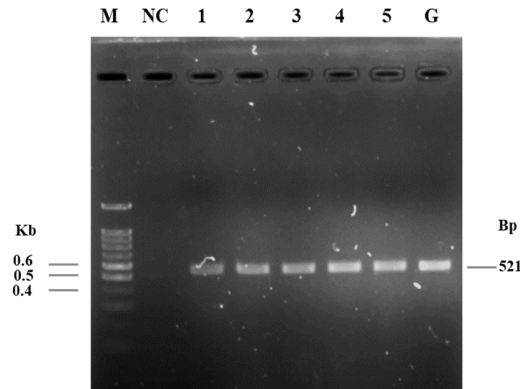
**Figure legend S1.** The figure displays images of 1% agarose electrophoresis gels stained by RedSafe™ Nucleic acid staining. The products were obtained from the RT-PCR analysis of all strains that were grown in normal BG<sub>11</sub> medium. The expression levels of nine genes were analyzed using specific primer pairs (listed in Table S2). The genes analyzed were A. *slr0180* (360 bp), B. *slr2131* (380 bp), C. *slr1270* (480 bp), D. *lipA* (379 bp), E. *aas* (307 bp), F. *plsX* (455 bp), G. *crtB* (462 bp), H. *chlG* (425 bp), and I. *16s rRNA* (521 bp). The gel electrophoresis included; Lane M: M23 Set of 100 bp + 1,5 Kb DNA ladder with stain, SibEnzyme®; Lane NC: Negative control, Lane 1-5: PCR products from studied cells, including WTc, OA, OB, OC, and OABC, respectively; and Lane G: PCR product of genomic DNA of *Synecocystis* sp PCC 6803 wild type.

**Figure S2:** The expression of genes in each strain cultured in BG<sub>11</sub> - N medium analyzed by RT-PCR analysis



**Figure S2 (Continue):** The expression of genes in each strain cultured in BG<sub>11</sub> - N medium analyzed by RT-PCR analysis

**I. *16S rRNA***

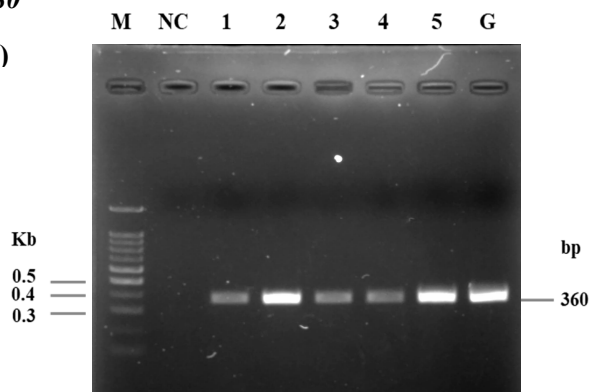


**Figure legend S2.** The figure displays images of 1% agarose electrophoresis gels stained by RedSafe™ Nucleic acid staining. The products were obtained from the RT-PCR analysis of all strains that were grown in BG<sub>11</sub> -N medium. The expression levels of nine genes were analyzed using specific primer pairs (listed in Table S2). The genes analyzed were A. *slr0180* (360 bp), B. *slr2131* (380 bp), C. *slr1270* (480 bp), D. *lipA* (379 bp), E. *aas* (307 bp), F. *plsX* (455 bp), G. *crtB* (462 bp), H. *chlG* (425 bp), and I. *16s rRNA* (521 bp). The gel electrophoresis included; Lane M: M23 Set of 100 bp + 1,5 Kb DNA ladder with stain, SibEnzyme®; Lane NC: Negative control, Lane 1-5: PCR products from studied cells, including WTc, OA, OB, OC, and OABC, respectively; and Lane G: PCR product of genomic DNA of *Synecocystis* sp PCC 6803 wild type.

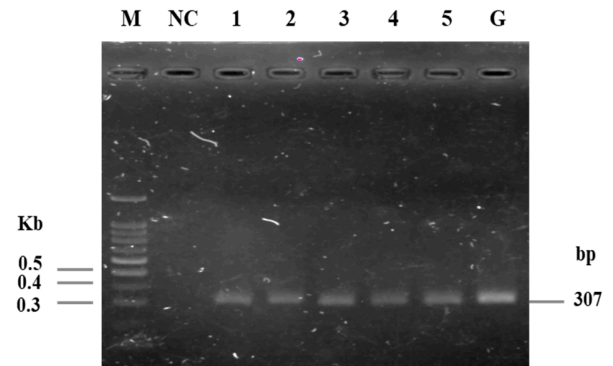
**Figure S3:** The expression of genes in each strain cultured in BG<sub>11</sub>+1.5% NaCl medium analyzed by RT-PCR analysis

**A. *slr0180***

(*acrA*)

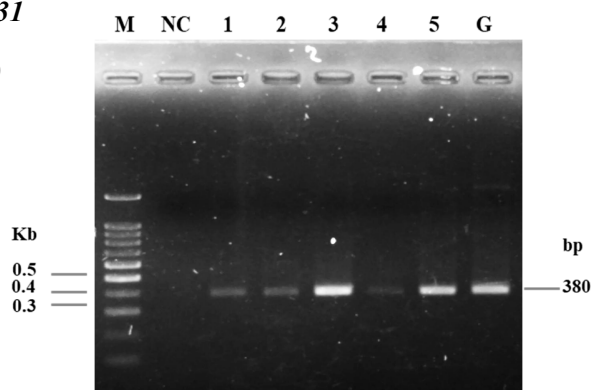


**E. *aas***

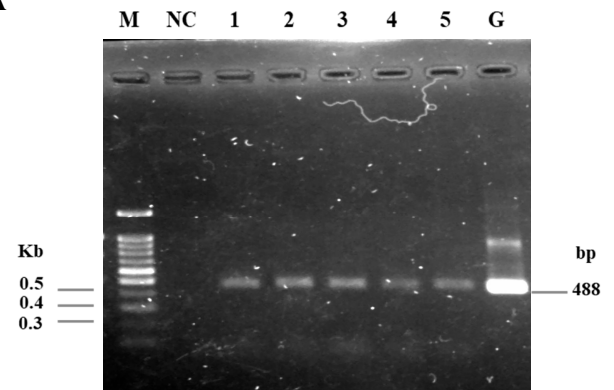


**B. *slr2131***

(*acrB*)

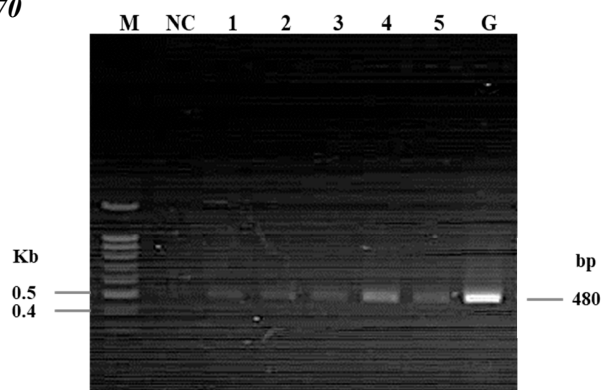


**F. *plsX***

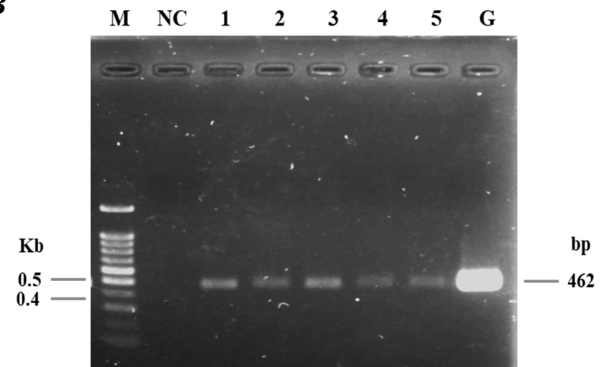


**C. *slr1270***

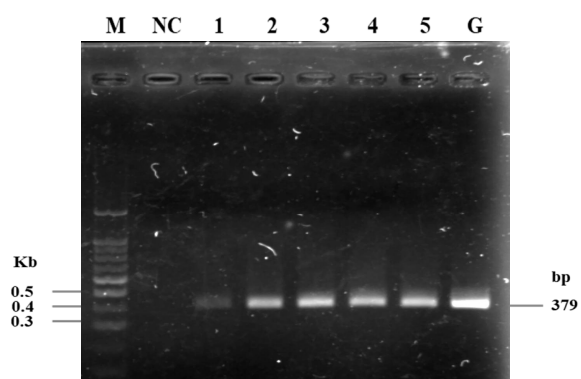
(*tolC*)



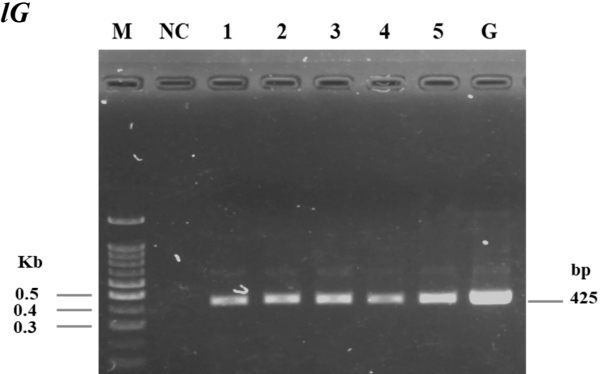
**G. *crtB***



**D. *lipA***



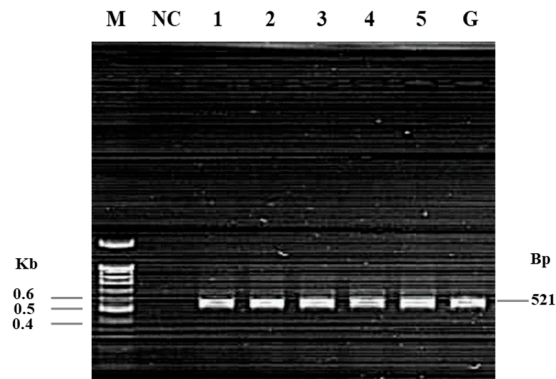
**H. *chlG***





**Figure S3 (Continue):** The expression of genes in each strain cultured in BG<sub>11</sub> +1.5% NaCl medium analyzed by RT-PCR analysis

**I. *16S rRNA***



**Figure legend S3.** The figure displays images of 1% agarose electrophoresis gels stained by RedSafe™ Nucleic acid staining. The products were obtained from the RT-PCR analysis of all strains that were grown in BG<sub>11</sub> + 1.5% NaCl medium. The expression levels of nine genes were analyzed using specific primer pairs (listed in Table S2). The genes analyzed were A. *sll0180* (360 bp), B. *slr2131* (380 bp), C. *slr1270* (480 bp), D. *lipA* (379 bp), E. *aas* (307 bp), F. *plsX* (455 bp), G. *crtB* (462 bp), H. *chlG* (425 bp), and I. *16s rRNA* (521 bp). The gel electrophoresis included; Lane M: M23 Set of 100 bp + 1,5 Kb DNA ladder with stain, SibEnzyme®; Lane NC: Negative control, Lane 1-5: PCR products from studied cells, including WTc, OA, OB, OC, and OABC, respectively; and Lane G: PCR product of genomic DNA of *Synecocystis* sp PCC 6803 wild type.