

Supplementary Files

Diguanylate cyclase and phosphodiesterase interact to maintain the specificity of c-di-GMP signaling in the regulation of antibiotic synthesis in *Lysobacter enzymogenes*

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Table S1. Differentially expressed genes by RNA-Seq

gene_id	average_ fpkm_ OH11	average_ fpkm_ LchP	diffexp_log2fc_ OH11-vs-LchP	Predicted function
OH11 3896	2.783	11.766	2.087995335	unknown
OH11 4760	11.086	2.743	-2.033020066	conserved hypothetical protein [<i>Bordetella petrii</i>]
OH11 5121	27.306	6.723	-2.042801087	M15 family metalloproteinase [<i>Lysobacter enzymogenes</i>]
OH11 5116	1223.996	292.356	-2.091782696	Ox3 [<i>Lysobacter enzymogenes</i>]
OH11 3439	93.656	21.58	-2.126074772	beta-lactamase [<i>Caulobacter</i> sp. K31]
OH11 5117	1565.753	355.156	-2.169384035	Ox4 [<i>Lysobacter enzymogenes</i>]
OH11 5115	1157.623	256.85	-2.198456808	Ox2 [<i>Lysobacter enzymogenes</i>]
OH11 4008	16.133	3.433	-2.258086621	hypothetical protein [<i>Dyella japonica</i>]
OH11 4941	55.29	11.453	-2.27149193	glutamate--cysteine ligase [<i>Rhodanobacter thiooxydans</i>]
OH11 5114	1520.62	300.27	-2.36527499	Ox1 [<i>Lysobacter enzymogenes</i>]
OH11 5118	49.51	9.113	-2.468662769	membrane transporter [<i>Pandoraea</i> sp. SD6-2]
OH11 5113(pk s)	1172.79	202.643	-2.554759045	hybrid polyketide synthase and nonribosomal peptide synthetase [<i>Lysobacter enzymogenes</i>]
OH11 4940	1300.68	214.42	-2.600751899	hypothetical protein [<i>Lysobacter enzymogenes</i>]
OH11 5111	1153.756	185.133	-2.667761099	ferredoxin reductase-like protein [<i>Lysobacter enzymogenes</i>]
OH11 5109	681.983	106.95	-2.697326158	arginase-like protein [<i>Lysobacter enzymogenes</i>]
OH11 5112	1031.64	155.42	-2.758764386	sterol desaturase-like protein [<i>Lysobacter enzymogenes</i>]

Red tagged genes belong to HSAF biosynthesis gene cluster.

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      1      10      20      30      40      50      60
3756 MAVLALWAVATIASAQSIVLPPVAAMSAAGAGVPARAPASEPAAARPIMSAALVA
1158 .....MERSWRLLWQTLLTLGLSA

      70      80      90      100     110     120
3756 AAPPSAAQAREAFDFIGYRAPSLSLRLAQDFVFNRVLAGEDGCRFEAVSGLVWGSK
1158 AALACAPFVVARLPG.....ADPPANQVLAGRMDARFAFVAGERIDYFD

      130     140     150     160     170     180
3756 GEPRWWRIVVNQVDPAIAPQLTIDRFSRREIELWRPGDELPRRSTYGPDIIDLNHSIRF
1158 RRTQWLRRTATADVGEDQLPOLVIDQFYRKFEDIWRHRDADPVRRALHGRGSEFQHSRF

      190     200     210     220     230     240
3756 IVEPTPKGLRKGDAIYLRMLAAIVLSQVEVEPLAKVQRDMMHVG LRSVVLTAMGVAV
1158 VVYPTPEGGLRKGVIYLRITYATEFTPSTLRHEPLAVHRQDMGHVALRSVVLTAGATAI

      250     260     270     280     290     300
3756 LAFGFWIGLRERGYAYLCLTLLIQILTLTSDGGEMRVVVPWIKDIAPDTRTNIVLTAATL
1158 LAFGFWVGLRERGYAYLCLTLLVQTVNLAIVEGGEIRMIPWIEVIEPNRRTNVVLTAAATL

      310     320     330     340     350     360
3756 ASIRFLIFELGLRRTQPRVTRADWCSYSLGALIVVSLFRTWKYSALYGNLNLVLAALI
1158 ASVRFIMFELDLRRTQAGVAKVINACSNVVGALLAVSLVQTWKLSASEGNLVLLVLIQAV

      370     380     390     400     410     420
3756 LYATVVAVWRRQREAYFLLAWVPLMVLLVVLVGANHEWWEFAWLEYTFVGLVFGGLG
1158 FYACAVAISSRQREAYFLAGAWVPLLAVLVVLVGFQKWWMF FAWLEYAVPLGLVFGGLG

      430     440     450     460     470     480
3756 LLLGLTSKIQQLRRDRDTANRLATYDSLTCAMTRATSQSLRSAVESAHRSQRPLSVVFF
1158 LLLGLAAKIQKLRQDHDATKHRATYDRLTSMNRQATEQSLREALEAHRSRRLIVVFF

      490     500     510     520     530     540
3756 DIDHFKRINDEHGRVGDERTLRIVALLRTRNRLRAYDLFGRYGGDEVLVVIADTYLIRDAAR
1158 DIDHFKRINDEHGRVAGDEALRTVAERTRNRLRATDLGCRYGGDEILVGIHPGTRLEQGLV

      550     560     570     580     590     600
3756 VAEHLRESVSGSPISIDGRLLPVSLSGVAELQPGETPEQLLERADAALYASKSAGRDRV
1158 VAEHLRAVAGANPFSVHGRALNLSLSGVAELRPGENFDQLLERADAALYASKSAGRDRV

      610
3756 TAHGSESHEVVS
1158 TVQRAAVEVAI.

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Figure S1. Multiple sequence alignment shows that 3756 and 1158 share 55% similarity of the amino acid sequence.

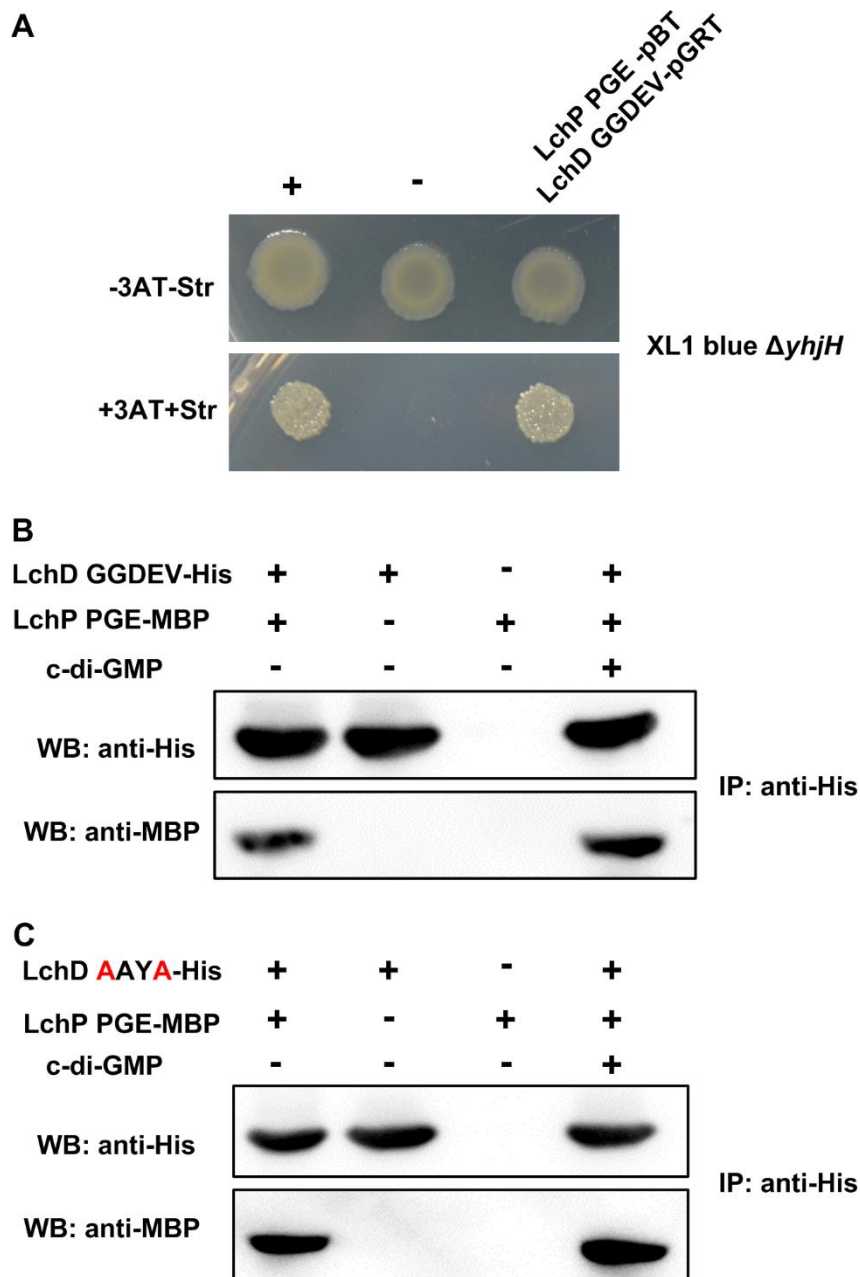


Figure S2. (A) B2H assay indicates LchP and LchD interact in the high c-di-GMP background strains. +, positive control (GacS-pBT and GacS-pTRG); -, negative control (vectors pBT and pTRG). (B) & (C) Protein pull-down assay.

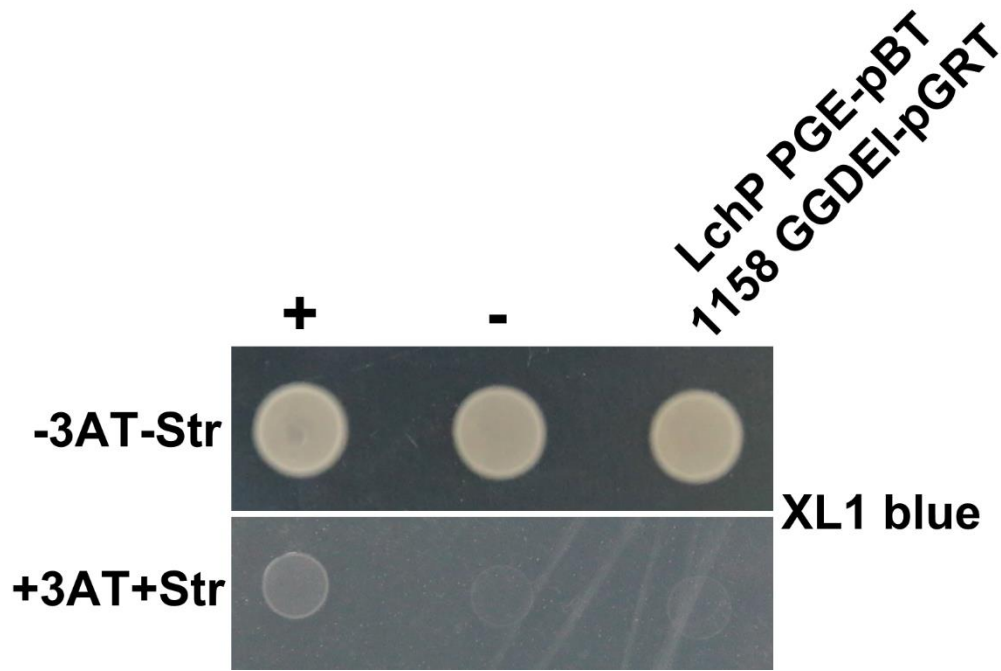


Figure S3. B2H assay indicates LchP does not interact with 1158. +, positive control (GacS-pBT and GacS-pTRG); -, negative control (vectors pBT and pTRG).