Supplementary Material:

A meet-up of acetyl phosphate and c-di-GMP modulates BldD activity for development and antibiotic production

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Protein	Helix	Antiparallel	Parallel	β-turn	Random coil	Total sum
	(%)	(%)	(%)	(%)	(%)	(%)
BldD	44.3	6.1	6.5	15.2	25.9	98.0
BIdD	61.8	3.5	4.0	12.7	17.6	99.5
BIdD	82.0	1.5	1.8	9.8	8.9	104.0

Table S1 Secondary structural elements in BldD

Table S2 Strains and plasmids used in this work

Strain or plasmid	Characteristics	Source or Reference
Strains		
S. erythraea NRRL2338	Used as parental strain, wild type	DSM 40517
<i>Ε. coli</i> DH5α	<i>E. coli</i> DH5α F-Ø80d lacZΔM (lacZ	Transgen Biotech
	YA -argF) U169 deoR	
E. coli BL21(DE3)	F'ompTr- Bm-B (DE3)	Transgen Biotech
E. coli BL21(DE3)- bldD	The strain for expression of BldD	This study
E. coli BL21(DE3)- bldD ^{K11Q}	The strain for expression of BldD ^{K11Q}	This study
E. coli BL21(DE3)- bldD ^{K11R}	The strain for expression of BldD ^{K11R}	This study
S. erythraea ObldD	The strain for over-expression of bldD,	This study
	NRRL2338 integrated with pIB139-bldD	
S. erythraea ObldD ^{K11Q}	The strain for over-expression of <i>bldD</i> ^{K11Q} ,	This study
	NRRL2338 integrated with pIB139-bldD ^{K11Q}	
S. erythraea ObldD ^{K11R}	The strain for over-expression of <i>bldD</i> ^{K11R} ,	This study
	NRRL2338 integrated with pIB139-bldD ^{K11R}	
plasmid		
pET28a(+)	vector with T7-RNA polymerase-	Thermo Scientific
	based promoter for expression in	
	E. coli BL21(DE3), hexahistidine	
	tag with thrombin cleavage	
pET- <i>bldD</i>	pET28a(+) with bldD inserted in Ndel and	This study
	HindIII	
рЕТ- <i>bldD</i> ^{к11Q}	pET28a(+) with <i>bldD</i> ^{K11Q}	This study
pET- <i>bldD</i> ^{K11R}	pET28a(+) with <i>bldD</i> ^{K11R}	This study
pIB139	pSET152 with integrase of phiC31	(25)
	and PermE, the strong promoter of	
	Streptomyces	
pIB139- <i>bldD</i>	pIB139 with <i>bldD</i> gene interted intoNdeI	This study
	and Xbal	
pIB139- <i>bldD</i> ^{K11Q}	pIB139 with <i>bldD</i> ^{K11Q}	This study
pIB139- <i>bldD</i> ^{K11R}	pIB139 with <i>bldD</i> ^{K11R}	This study

Oligonucle	otides Sequence (5'to 3')					
Primers for overproduction of BldD protein						
pET- <i>bldD</i> F	GTCGCGGATCCGAATTCATGGGCGACTACGCCAAG					
pET- <i>bldD</i> R	GGTGCTCGAGTGCGGCCGCAAGCTTTCACTCCTCCCGGGCCG					
Primers fo	Primers for the construction of the S. erythraea ObldD strain					
pIB- <i>bldD</i> F	GCCGGTTGGTAGGATCCACATATGCATCATCATCATCATCACAGCAGCG					
pIB- <i>bldD</i> R	CGCGCGCGGGCCGCGGATCCTCTAGAAGCTTCCTTTCGGGGCTTTGTTAG					
M13F	GTGCTGCAAGGCGATTAAGTT					
M13R	TTATGCTTCCGGCTCGTATGT					
The primers used in Site-Directed Mutagenesis of BldD						
K11R F	GCGGCAGGCTCCGCGC					
K11R R	CTGCCGCCCAGCGCCT					
K11Q F	GCGGCCAGCTCCGCGC					
K11Q R	GGCCGCCCAGCGCCTT					
Primers for PCR amplification of EMSAs probe with biotin labeling						
bldD_F	AGCCAGTGGCGATAAGTCCCGACGGCTGTCGGC					
bldD_R	AGCCAGTGGCGATAAGCCGTTTCATTCGCCCCGTC					
Primers for real-time RT-PCR						
SACE_810	1-F GTTGCGATGCCGTGAGGT					
SACE_8103	1-R CGGGTGTTACCGACTTTCA					
eryBIV-F	GCAGCCGCAGGATCACGC					
<i>eryBIV</i> -R	GCCGCCCGTGTTGCTCTA					
eryAI-F	CCGCTGATGCCGAACGAC					
eryAI-R	CACCCTTCCCCGCACTCTG					
<i>ermE</i> -F	CCTCCAGGCACCAGTCCAC					
<i>ermE</i> -R	AGTCGTTGCGGGAGAAGCT					
eryK-F	CCGATGGACCACGAGCAGTT					
<i>eryK</i> -R	AAGGCGGGAGATCAGGTCGT					
whiG-F	AGTTGCAGATGACCAGCGTG					
<i>whiG</i> -R	GAGACGTTCTACAGCCTCGG					
bldN-F	CTCTACGACGAGTACTCCCAGG					
<i>bldN</i> -R	GTTCTTGGCGATGGTGATGAAC					
bldM-F	GACTTGTCTCGGCCCACC					
bldM-R	CTCGGTCAGCTGCACACC					

Table S3 The oligonucleotides used in the study



Figure S1 K11 acetylation inhibits antibiotic production. (A) Growth curves of *S. erythraea* WT, ObldD, ObldD^{K11Q}, and ObldD^{K11R} strains grown in TSB medium. (B) The transcription level of *bldD* gene in *S. erythraea* WT, ObldD, ObldD^{K11Q}, and ObldD^{K11R} strains grown in TSB medium till the middle exponential phase. Fold change represented the expression level compared to WT strain. Error bars show the SDs of three independent experiments. (C) The antibiotic production of *S. erythraea* WT, ObldD, ObldD^{K11Q}, and ObldD^{K11Q}, and ObldD^{K11Q}, by the strains grown in TSB medium till the middle exponential phase. Fold change represented the expression level compared to WT strain. Error bars show the SDs of three independent experiments. (C) The antibiotic production of *S. erythraea* WT, ObldD, ObldD^{K11Q}, and ObldD^{K11Q}, and ObldD^{K11Q}, by the strains grown in TSB medium determined by bioassays.







Figure S3 MS/MS spectra for the identification of AcP- acetylated K11 by LC/MS/MS analysis.



Figure S4 MS/MS spectra for the identification of AcP- acetylated K35 by LC/MS/MS analysis.



Figure S5 MS/MS spectra for the identification of AcP- acetylated K53 by LC/MS/MS analysis.



Figure S6 MS/MS spectra for the identification of AcP- acetylated K83 by LC/MS/MS analysis.



Figure S7 MS/MS spectra for the identification of AcP- acetylated K98 by LC/MS/MS analysis.



Figure S8 MS/MS spectra for the identification of AcP- acetylated K119 by LC/MS/MS analysis.



Figure S9 MS/MS spectra for the identification of AcuA- acetylated K35 by LC/MS/MS analysis.



Figure S10 MS/MS spectra for the identification of AcuA- acetylated K53 by LC/MS/MS analysis.



Figure S11 MS/MS spectra for the identification of AcuA- acetylated K83 by LC/MS/MS analysis.





y8 y7 y6 y5 y4 y3 y2 y1 K119_BIdD G D Y N G K V L S I R in vitro AcuA-acetylation y₂*++ 136.0919 100₇ 90b₉⁺⁺ y₅ 488.7404 587.4272 У₇ 814.4878 80-У₄ 488.4109 70-632.3041 у₃ 375.3190 60-50-У₈ 929.5957 40 У₆ 757.6091 У₁ 175<u>.</u>2760 30-У₂ 288.2030 905.5842 976.7123 20-1078.8271 335.2087 460.2631 688.5313 10-1162,7966 البنابيات 1200 0diainth - il 200 300 500 600 700 800 900 1000 1100 400 m/z

Figure S13 MS/MS spectra for the identification of AcuA- acetylated K119 by LC/MS/MS analysis.



Figure S14 MS/MS spectra for the identification of K11 in vivo by LC/MS/MS analysis.



Figure S15 BldD acetylation level at different growth stage. Acetylation level of BldD of the *S. erythraea* WT strain under N⁻ conditions at the indicated time. Each lane was loaded with equal amount of BldD protein. The band intensities were quantified by densitometry using ImageJ software.