

Supplementary Material

Transcriptional regulator DasR represses daptomycin production through both direct and cascade mechanisms in *Streptomyces roseosporus*

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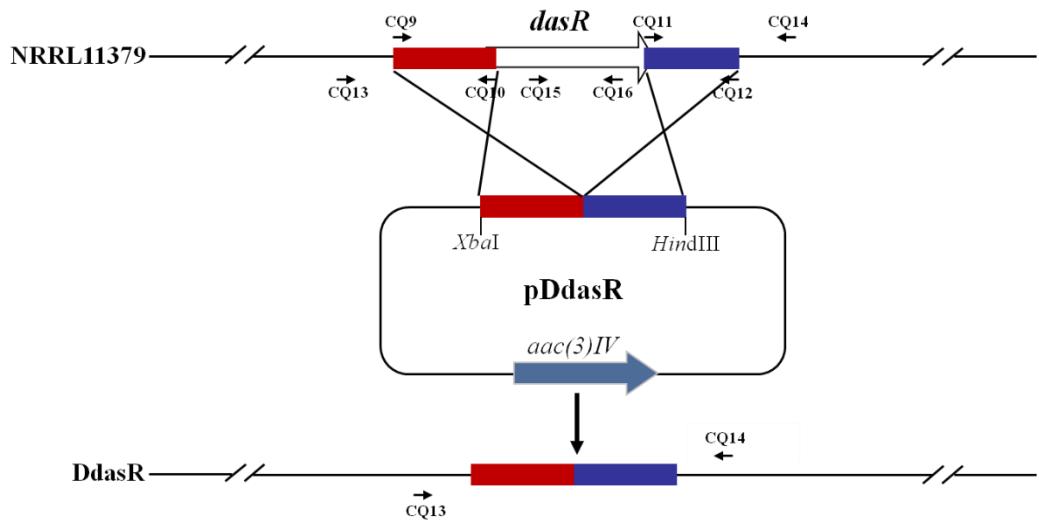
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Figure S1.

A



B

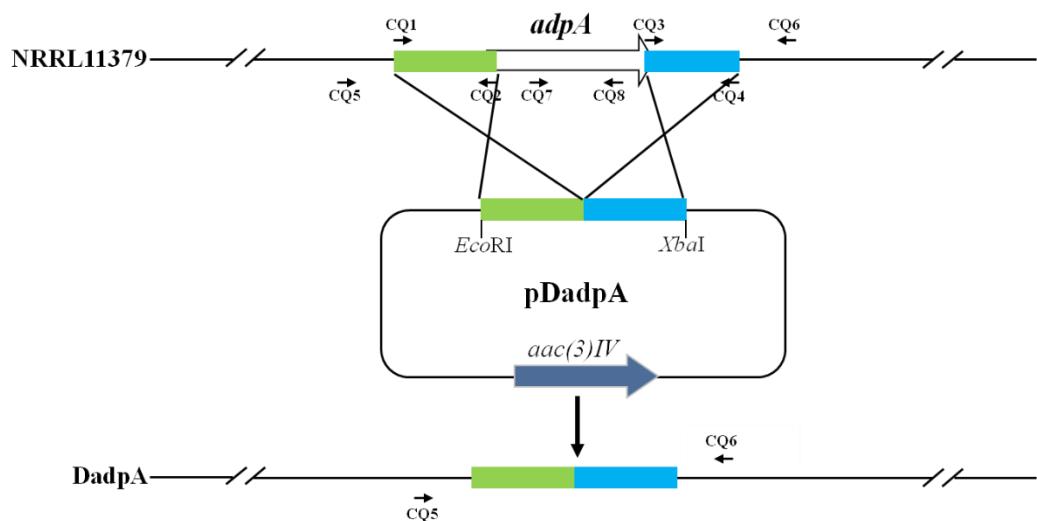
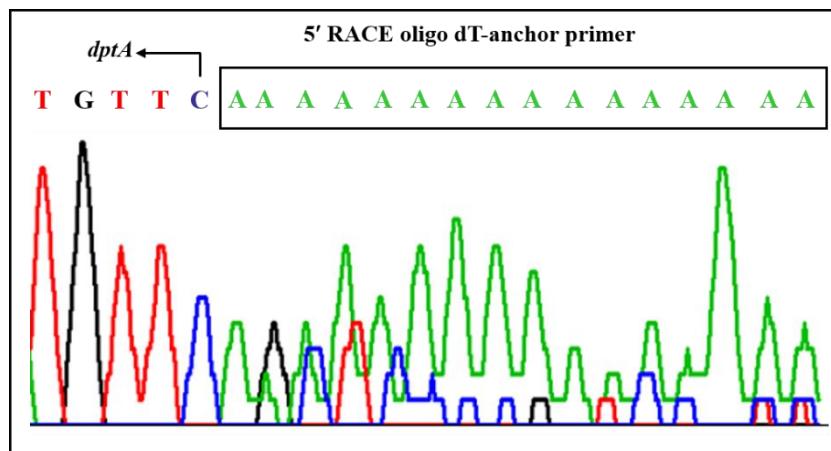


Figure S1. Strategy for deletion of *dasR* (A) and *adpA* (B) in WT (schematic). Large arrows: genes and their directions. Small arrows: positions of primers. Rectangles: homologous exchange regions used for gene deletion.

Figure S2.

A



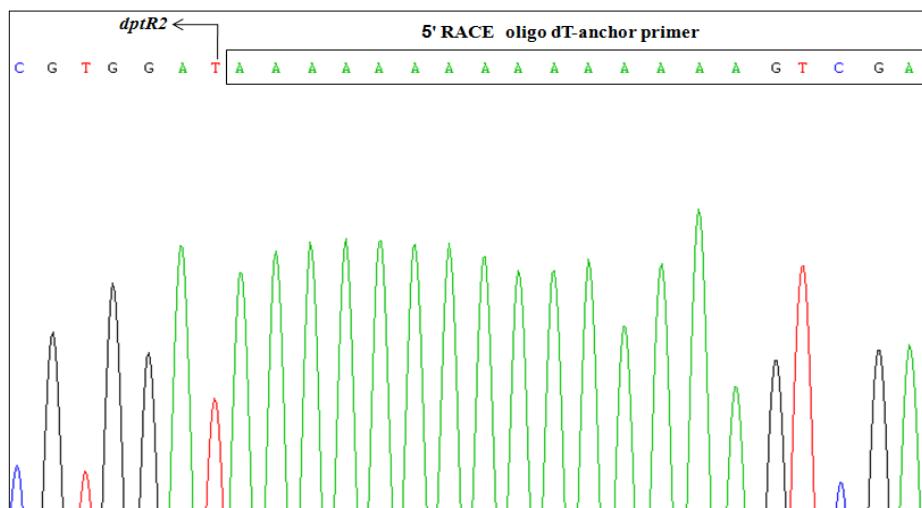
B



Figure S2. Determination of *dptA* TSS. (A) 5' RACE analysis of *dptA* TSS. Box: complementary sequence of oligo dT-anchor primer. Bent arrow: complementary base of TSS. (B) Promoter structure of *dptA*. Boxes: putative -10 and -35 regions. Bent arrow: *dptA* TSS. Yellow highlight: TSCs. Shading: translational stop codons.

Figure S3.

A



B



Figure S3. Determination of *dptR2* TSS. (A) 5' RACE analysis of *dptR2* TSS. Box: complementary sequence of oligo dT-anchor primer. Bent arrow: complementary base of TSS. (B) Promoter structure of *dptR2*. Boxes: putative -10 and -35 regions. Bent arrow: *dptR2* TSS. Yellow highlight: *dptR2* TSC.

Table S1. Strains and plasmids used in this study.

Strains or plasmids	Description	Source or reference
Strains		
<i>S. roseosporus</i>		
NRRL11379	WT strain, daptomycin producer	Laboratory stock
DdasR	<i>dasR</i> deletion mutant	This study
CdasR	<i>dasR</i> complemented strain	This study
OdasR	<i>dasR</i> overexpression strain	This study
DadpA	<i>adpA</i> deletion mutant	This study
CadpA	<i>adpA</i> complemented strain	This study
OadpA	<i>adpA</i> overexpression strain	This study
WT/pKC1139	WT strain carrying empty vector pKC1139	This study
WT/pSET152	WT strain carrying empty vector pSET152	This study
<i>E. coli</i>		
JM109	General cloning host	Laboratory stock
ET12567	Methylation-deficient strain	[1]
BL21 (DE3)	Host for protein overexpression	Novagen
Plasmids		
pKC1139	Multiple-copy <i>E. coli</i> - <i>Streptomyces</i> shuttle vector	[2]
pSET152	Integrative <i>E. coli</i> - <i>Streptomyces</i> shuttle vector	[2]
pET-28a (+)	Vector for His ₆ -tagged protein overexpression in <i>E. coli</i>	Novagen
pJL117	pIJ2925 derivative carrying promoter <i>ermE*</i> <i>p</i>	[3]
pDdasR	<i>dasR</i> deletion vector based on pKC1139	This study
pCdasR	<i>dasR</i> complemented vector based on pSET152	This study
pOdasR	<i>dasR</i> overexpression vector based on pKC1139	This study
pET28-dasR	His ₆ -DasR overexpression vector based on pET-28a (+)	This study
pDadpA	<i>adpA</i> deletion vector based on pKC1139	This study
pCadpA	<i>adpA</i> complemented vector based on pSET152	This study
pOadpA	<i>adpA</i> overexpression vector based on pKC1139	This study
pET28-adpA	His ₆ -AdpA overexpression vector based on pET-28a (+)	This study

Table S2. Primers used in this study.

Primer	DNA sequence * (5'-3')	Purpose
CQ9	GCT <u>CTAGATTT</u> CCCTGGGTCCCTCGG (<i>Xba</i> I)	Deletion of <i>dasR</i> gene
CQ10	CTTCAGACGCCACGAAGGTCTCGCTCCCCGTACT	
CQ11	AGTACGGGGAGCGAGACCTCGTGGCGCGTCTGAAG	
CQ12	CCC <u>AAGCTT</u> CCCGTCCGGTCGGAT (<i>Hind</i> III)	
CQ13	CGAGGGAGGTGTCCAGCTTC	Confirmation of <i>dasR</i> deletion in mu-
CQ14	CGTCGCGGCCATCTGAC	tant DdasR
CQ15	ACCTTCGTCGCCAAGCCG	
CQ16	GGGACAGCATGAGCATCGG	
CQ21	CCC <u>AAGCTT</u> ACGCAAGCGTCGGGAAGG (<i>Hind</i> III)	Overexpression of <i>dasR</i> in
CQ22	GCT <u>CTAGACGGTT</u> ACGTGATCCTGC (<i>Xba</i> I)	<i>S. roseosporus</i>
CQ75	CGGAATTCCCCACCGCGAAGACATT (<i>Eco</i> RI)	Complementation of <i>dasR</i> in DdasR
CQ76	GCT <u>CTAGAGTT</u> CACGTGATCCTGCTCC (<i>Xba</i> I)	Overexpression of His ₆ -DasR in <i>E. coli</i>
CQ25	CGGAATT <u>CAGTACGGGGAGCGAGACC</u> (<i>Eco</i> RI)	Deletion of <i>adpA</i> gene
CQ26	CCCTCGAGCGGTTACGTGATCCTGC (<i>Xho</i> I)	
CQ1	CGGAATT <u>CTGACCCCTTCGCGGGATG</u> (<i>Eco</i> RI)	
CQ2	GGAACGAACCGCTCAGGATAACAGCACGCCAA	
CQ3	TTGCCGTGCTGCTGTTCATCCTGACGCCGTTCC	
CQ4	GCT <u>CTAGAGTCACGGATGTCCGCCAG</u> (<i>Xba</i> I)	Confirmation of <i>adpA</i> deletion in mu-
CQ5	ACACGCCATGAGGCCGC	tant DadpA
CQ6	CACAACCAGGTGCTCTGCC	
CQ7	GAACTCACCACGCCGTACG	
CQ8	GCACATGCCGTCGTCCA	Overexpression of <i>adpA</i> in
CQ17	CCA <u>AGCTTACCGAGGGGGGCTTAGC</u> (<i>Hind</i> III)	<i>S. roseosporus</i>
CQ18	GCT <u>CTAGAGCGGGCGGATCACGATGT</u> (<i>Xba</i> I)	
CQ19	CGGAATT <u>CTGACCCCTTCGCGGGATG</u> (<i>Eco</i> RI)	Complementation of <i>adpA</i> in DadpA
CQ20	GCT <u>CTAGAGCGGGCGGATCACGATGT</u> (<i>Xba</i> I)	Overexpression of His ₆ -AdpA in <i>E. coli</i>
CQ23	CGGAATT <u>CATGAGCCAGGACTCCGCC</u> (<i>Eco</i> RI)	Amplification of <i>adpA</i> ORF for
CQ24	CCCTCGAGCGCAGTCGATCCACACCAT (<i>Xho</i> I)	RT-qPCR
CQ27	GCTTAGCGTCATGAGCCAG	
CQ28	TGAACAGCAGCACGCCAA	
ZQL75	TCCCAGGAATCGCGAGAG	Amplification of <i>dptR3</i> ORF for
ZQL76	CCCGGATTCCCCCGACTC	RT-qPCR
ZQL79	GAACAGACCACCCCTCTCG	Amplification of <i>dptBC</i> ORF for
ZQL80	CTGTGGCCGATGGGGTAG	RT-qPCR
ZQL81	CGCGTACATCATCCAGACC	Amplification of <i>dptA</i> ORF for
ZQL82	GTCATGCTCAGTCGGAGACG	RT-qPCR
ZQL83	GAGTGAGAGCCGCTGTGC	Amplification of <i>dptE</i> ORF for
ZQL84	GGTGTCCCGTACGAGAACCC	RT-qPCR
ZQL85	CCAGATCCTCTCGACGGTG	Amplification of <i>dptM</i> ORF for
ZQL86	CCGATAACAGGCCGTACCC	RT-qPCR
ZQL87	TTCCGGTACGAGCGGCTG	Amplification of <i>dptD</i> ORF for
ZQL88	CGTCAGATCGAAGCGGCG	RT-qPCR
ZQL89	TCCGCACCATCACGTTCAC	Amplification of <i>dptH</i> ORF for
ZQL90	GACTCCTGGGCCACCTG	RT-qPCR

ZQL93	GGCCAGGATCGTGACGTC	Amplification of <i>dptR2</i> ORF for RT-qPCR
ZQL94	CGGAACGGCAGGAGTCATC	Amplification of <i>dptF</i> ORF for RT-qPCR
ZQL115	GACAGATGCCGAGTCGT	RT-qPCR
ZQL116	GACGCTCACAGCAGCTC	Amplification of <i>dptII</i> ORF for RT-qPCR
ZQL117	CTACCACGTGACCGTCAAGG	Amplification of <i>dptG</i> ORF for RT-qPCR
ZQL118	GTCGTCGAACTCGTTCCCTC	RT-qPCR
ZQL119	CAACGACGGCAGCTACCTC	Amplification of <i>dptP</i> ORF for RT-qPCR
ZQL120	GGCGCATATCGGTCCAGTTC	RT-qPCR
ZQL121	CAATCCGCCGTACCAAGGC	Amplification of <i>hrdB</i> ORF for RT-qPCR and probe <i>hrdB</i> for EMSA
ZQL122	GGACACGCCGCTGTGG	for EMSA
GJ91	CCAAGGGCTACAAGTTCTCC	Amplification of probe <i>adpAp</i> for EMSA
GJ92	TTGATGACCTCGACCATGTG	Amplification of probe <i>dptEp</i> for EMSA
CQ49	ATGGCCGGACAACCCACC	Amplification of probe <i>dptAp</i> for EMSA
CQ50	CTGGCTCATGACGCTAACGC	Amplification of probe <i>dptR2p</i> for EMSA
ZQL39	GGCGTGGAACATACTGGCG	Amplification of probe <i>dptR3p</i> for EMSA
ZQL40	GCACAGCGGCTCTCACTC	Amplification of probe <i>dptIp</i> for EMSA
ZQL43	CGAGGTACCGCGTGGAT	Amplification of probe <i>dptP-M</i> for EMSA
ZQL44	GTCCATCTCTCGCGGATCC	Amplification of probe <i>dptR2p</i> for EMSA
ZQL51	CCGTTCCGATGCGAGTGC	Amplification of probe <i>dptEp</i> for EMSA
ZQL52	CGTGCAGGAAGGTGTTCGC	Amplification of probe <i>dptAp</i> for EMSA
ZQL37	TCCCAGGAATCGCGAGAG	Amplification of probe <i>dptR3p</i> for EMSA
ZQL38	GAAGAGGCCGAGGATGCG	Amplification of probe <i>dptIp</i> for EMSA
ZQL47	GCGCGGTCAACAAAGATTCTT	Amplification of probe <i>dptP-M</i> for EMSA
ZQL48	CCTTGACGGTCACGTGGTAG	Amplification of probe <i>dptR2p</i> for EMSA
ZQL57	CGGTCCGAACCGGCTCTTG	Amplification of probe <i>dptEp</i> for EMSA
ZQL58	AGGGCCTCGGATCGATG	Amplification of probe <i>dptAp</i> for DNase I footprinting
CQ61	ACCCGCCTCCCTGACCC, 5' FAM	Amplification of probe <i>dptEp</i> for DNase I footprinting
CQ62	CCTGGCTCATGACGCTAACGC	Amplification of probe <i>dptR2p</i> for DNase I footprinting
CQ63	CGCACCGGACGCCCTGAC, 5' FAM	Amplification of probe <i>dptAp</i> for DNase I footprinting
CQ64	GGCACAGCGGCTCTCACTC	Amplification of probe <i>dptR3p</i> for DNase I footprinting
CQ65	CCGTTCCGATGCGAGTGC	For 5' RACE
CQ66	AACAGCCGGTGAGTGTGC, 5' FAM	dptA-SP1 for 5' RACE
CQ67	CGAGGTCACCGCGTGGAT, 5' FAM	dptA-SP2 for 5' RACE
CQ68	GGTCGAGGATCTGCAGCAG	dptA-SP3 for 5' RACE
Oligo	GACCACGGTATCGATGTCGACTTTTTTTTTTTTV	dptR2-SP1 for 5' RACE
dT-anchor		dptR2-SP2 for 5' RACE
primer		dptR2-SP3 for 5' RACE
Anchor	GACCACGGTATCGATGTCGAC	For 5' RACE
primer		
CQ72	GGGGACGCTCCACAGCAG	
CQ73	CGCAGAGGGCAACTCCGG	
CQ74	GATCCGGTGGGTGTC	
ZQL69	GACGTTCAGCGAGCCCAG	
ZQL70	CGCTCGTAGGCCAGCG	
ZQL71	CGCGATAGGGAGGGTGACG	

* Underlining: sequence of restriction enzyme shown in parentheses.

References

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3. Li, L.; Guo, J.; Wen, Y.; Chen, Z.; Song, Y.; Li, J. Overexpression of ribosome recycling factor causes increased production of avermectin in *Streptomyces avermitilis* strains. *J. Ind. Microbiol. Biotechnol.* **2010**, *37*, 673-679.