

Supplemental Material

Figure S1. (A) Diagram showing *wblA_{ch}* disruption via double crossover. BstPI restriction sites were shown on *wblA_{ch}* locus. The probe for Southern blot is indicated (B) Confirmation of constructed *wblA_{ch}* mutant by PCR amplification. (C) Southern blot analysis of wild type and $\Delta wblA_{ch}$ mutant strains. Genomic DNA was digested with BstPI, WT strain showed a hybridized band of 587bp, and $\Delta wblA_{ch}$ showed a band of 471bp.

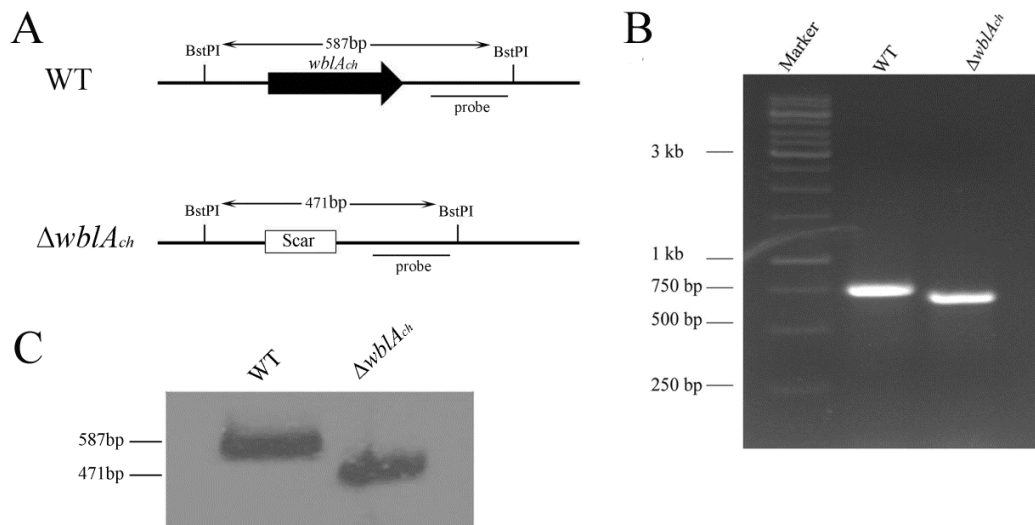


Figure S2. Effect of *wblA_{ch}* disruption on morphological differentiation. (A) Growth, aerial mycelium formation, sporulation of wild-type strain (WT), *wblA_{ch}* deletion mutant ($\Delta wblA_{ch}$) and *wblA_{ch}* complemented mutant (pYP2/*wblA_{ch}*). (B) Scanning electron micrographs of different strains.

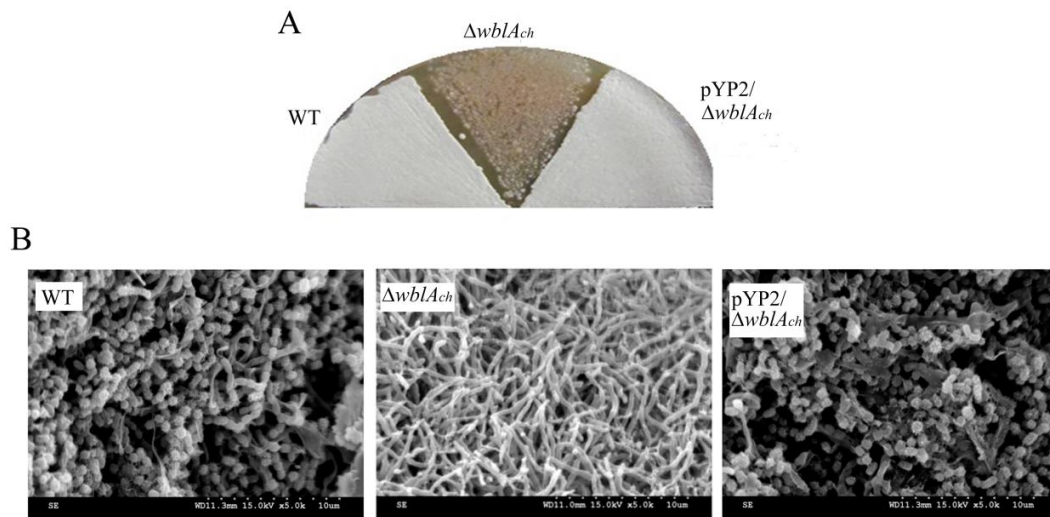


Figure.S3. HPLC analysis of culture filtrates from the wild-type strain (WT) (black line), and the *wblA_{ch}*-overexpression strain (pYP3/WT) (red line). The figure on the left represents the extractions of the WT and the pYP3/WT after centrifugation. The figures on the right are the spectrogram of natamycin and yellow pigment, respectively.

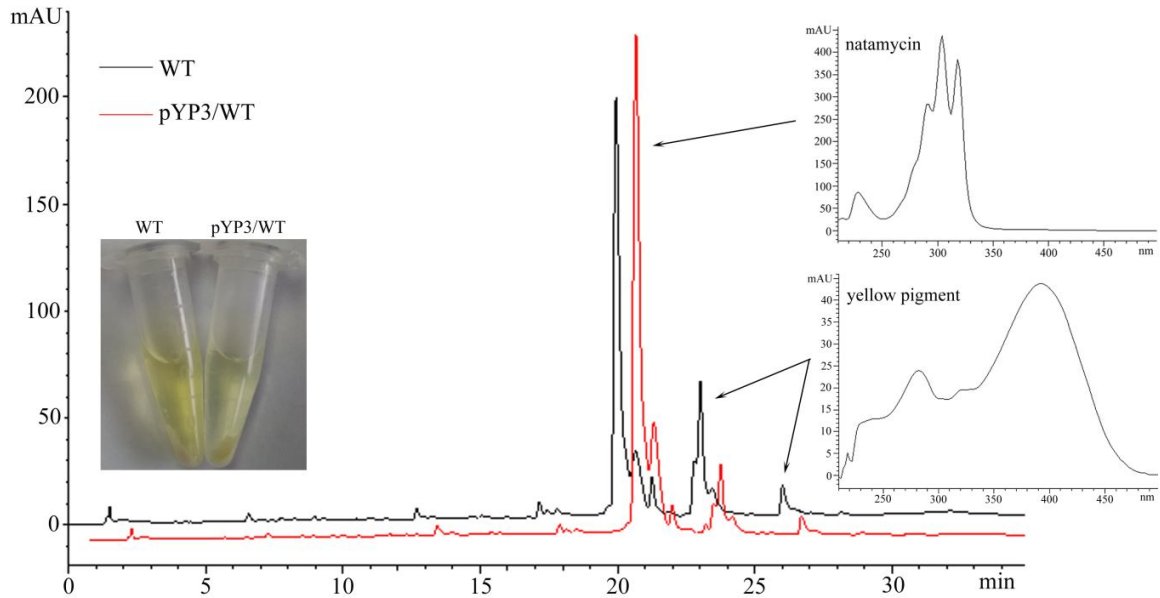


Figure S4. EMSA analysis of the AdpA_{ch} binding sequences and mutated sequences. (A) Mutations generated at the AdpA_{ch} binding sites. BamHI sites (GATATC) were used to replace the conserved AdpA_{ch}-binding sequence in each sequence. (B) EMSA analysis. probe A, probe B and probe C covered binding site A to C, respectively. probe mA, probe mB and probe mC covered mutated site A to C, respectively. Labeled fragments were carried out with 0.1 μg and 0.2 μg of purified His₆-AdpA_{ch} protein, respectively.

A

Site A 5' TCTTGAATGGCCCGAACGGACTATGCG 3' Site mutA 5' TCTTGAAGGATATCGAACGGACTATGCG 3'
 Site B 5' ACATGGGACTTCCGGCGACACAAGCG 3' Site mutB 5' ACATGGGACTTCCGATATCCCACAAGCG 3'
 Site C 5' CCTCTCTGTGCGGCCCTGCC 3' Site mutC 5' CCTCTCTGTGGATATCCTGCC 3'

B

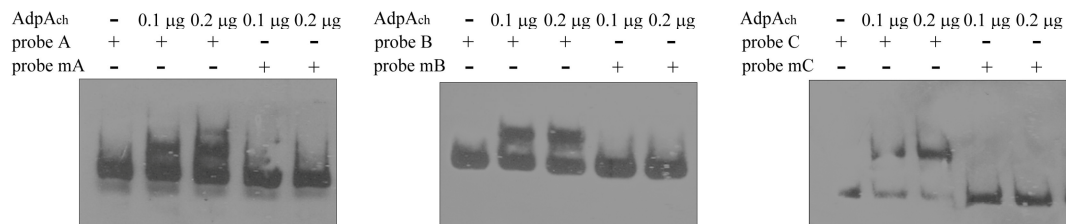


Table S1. The peak area of natamycin and yellow pigment determined by HPLC analysis from the WT strain and *wbla_{cht}*-overexpression strain.

	Natamycin		Yellow pigment	
	Peak area (mAU*s)	Fold change relative to WT	Peak area (mAU*s)	Fold change relative to WT
Wild-type (WT)	^a 3190.3	1	^c 870.9	1
pYP3 /WT	^b 4120.9	1.29	^d 234.6	1
			^e 412.2	0.47
			^f 97.2	0.41

a,b,c,d,e,f represent the peak area of natamycin and yellow pigment from the WT strain and *wbla_{cht}*-overexpression strain, respectively. They are determined by HPLC analysis.

The front peak of yellow pigment as shown in Fig.S3^{c,e}.

The later peak of yellow pigment as shown in Fig.S3^{d,f}.