Figure S1, related to Experimental Procedures and Fig. 1. Genetic organization of the PTM and PTN biosynthetic clusters in *S. platensis* MA7327 and MA7339 and the FASII loci in *S. platensis* MA7327 and *S. albus* J1074. (A) Genetic organization of the PTM and PTN biosynthetic cluster in in *S. platensis* MA7327 and MA7339. Four self-resistance candidates are shaded in light blue and are conserved in both *ptm* and *ptn* clusters. Functional annotations of the four genes are summarized in Table S1. (B) Genetic organization of the FASII loci in *S. platensis* MA7327 and *S. albus* J1074. The *fabH* and *fabF* genes were amplified and sequenced using primers based on homologous regions within the *fab* operons of *S. coelicolor*, *S. avermitilis*, and *S. griseus* (Table S4). Primers are depicted as small black arrows. The ORF downstream of *fabF* is a putative gene encoding a protein homologous to 3-hydroxyisobutryate dehydrogenases from *Streptomyces* spp.

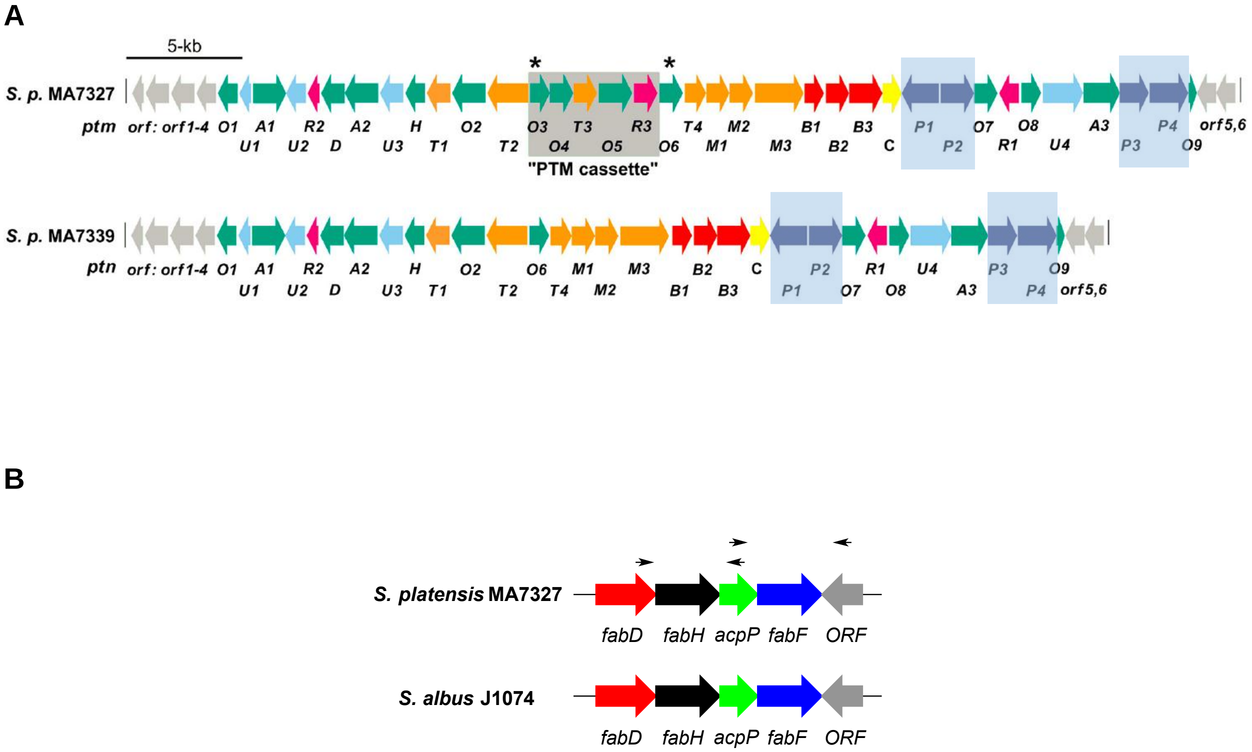

Fig. S2, related to Experimental Procedures and Fig. S2B. Protein sequence alignment of *Streptomyces* spp. and *E. coli* FabF and *Streptomyces platensis* MA7327 and MA7339 PtmP3. The conserved catalytic triad of Cys162, His300, and His334 are identified with red asterisks. Conserved residues throughout all protein sequences are shown in red text with yellow highlight; conserved residues to the consensus sequence are shown in blue text with cyan highlight; similar residues to the consensus sequence are shown in blue text with no highlight.

```
Consensus                 VSATNRTVVVTGIGATTPLGGDAASTWEGLLAGRSGVRPLXQEWAADLPV
S. platensis MA7327 PtmP3 -MADNGQVLVTGIGAMTPVGADASSSWSGLLAGKSGVRALVEEWAADLPV     49
S. platensis MA7339 PtmP3 -MAENGQVLVTGIGAMTPVGADASSSWSGLLAGKSGVRALVEEWAADLPV     49
S. platensis MA7327 FabF  VNATNRTVVVTGIGATTPLGGDSASSWEAMLAGRSGVGTLDQDWAAELPV     50
S. albus J1074 FabF       VSPTNRTVVVTGIGATTPLGGDAASTWEGLIAGRSGVRPLDDERYADLPV     50
S. avermitilis FabF       VSPTNRTVVVTGIGATTPLGGDVASTWEGLVAGRSGVRPLEQEWAAEQAV     50
S. coelicolor FabF        VSSTNRTVVVTGIGATTPLGGDAASTWEGLVAGRSGVRPLEQEWAADQAV     50
S. griseus FabF           VNSTNRTVVVTGIGATTPLGGDSASTWEGLMAGRSGVKPLEGERFAELPV     50
E. coli FabF              --MSKRRVVVTGLGMLSPVGNTVESTWKALLAGQSGISLIDHFDTSAYAT     48

Consensus                 RIAAQAAVDPAE-VLPRPQARKLDRSAQFALIAAREAWADAGXTXXAGED
S. platensis MA7327 PtmP3 SIAAGLTEDPAA-ALPRTQARKLDRGEQLAMLTSREAWQDAG-------A     91
S. platensis MA7339 PtmP3 GIAAGLTEDPAA-ALPRTQARKLDRGEQLAMLASREAWQDAG-------A     91
S. platensis MA7327 FabF  RIAAQAAVDPAD-VLPRAQARKLDRSAQLALIAAREAWADAGFTARAGED     99
S. albus J1074 FabF       RIAAQIAVEPAE-VLPRPLVRKLDRSAQFALIAAREAWADAGYTAMAGED     99
S. avermitilis FabF       RIAAQIAVEPGE-VIPRPQARRLDRSAQFALIAAKEAWADAGFTDKAGAD     99
S. coelicolor FabF        RIAAPAAVDPSE-VIPRPQARRLDRSAQFALIAAQEAWKDAGYAGKAGES     99
S. griseus FabF           RIAALAAVDPGD-VLPRPLARKLDRSAQFALIAAREAWADAGFTAKAGED     99
E. coli FabF              KFAGLVKDFNCEDIISRKEQRKMDAFIQYGIVAGVQAMQDSG-----LEI     93


Consensus                 PEVD------PERLGAVIASGIGGVTTLLDQYDVLKEKGVRRVSPHTVPM
S. platensis MA7327 PtmP3 PEVE------PERLAVVIGTGTGGVLTTLGQDDIFEESGARRLSPFAVPM    135
S. platensis MA7339 PtnP3 PEVE------PERLAVVIGTGTGGVLTTLGQDDLFEESGARRLSPFAVPM    135
S. platensis MA7327 FabF  TSVD------PDRLGAVIASGIGGVTTLLGQYDVLKEKGVRRVSPHTVPM    143
S. albus J1074 FabF       EQIS------PERLGTVIASGIGGVTTLLDQYDVLKEKGARRVSPHTVPM    143
S. avermitilis FabF       PAVD------PDRLGTVIASGIGGVTTLLDQYDVLKEKGVRRVSPHTVPM    143
S. coelicolor FabF        PAEDGAAHVDPDRLGAVIASGIGGVTTLLDQYDVLKEKGVRRVSPHTVPM    149
S. griseus FabF           ESVA------PERLGSVIASGIGGVTTLLDQYDVLKEKGVRRVSPHTVPM    143
E. coli FabF              TEEN------ATRIGAAIGSGIGGLGLIEENHTSLMNGGPRKISPFFVPS    137

                                                    *
Consensus                 LMPNGPXANVGLDVGARAGVHTPVSACASGAEAIGYAIEMIRTGRADVVV
S. platensis MA7327 PtmP3 LMPNGPAAWVSMDLGAKGGARTPVSACASGAEALAMGLDLLRAGRVDVVV    185
S. platensis MA7339 PtnP3 LMPNGPAAWVSMDLGAKGGARTPVSACASGAEALAMGLDLLRAGRVDVVV    185
S. platensis MA7327 FabF  LMPNGPSANVGLDVNARAGVHTPVSACASGSEAIGYAIEMIRTGRADFVI    193
S. albus J1074 FabF       LMPNSPSANVGLEVNARAGVHTPVSACASGAEAIGYAVEMIRTGRADVVV    193
S. avermitilis FabF       LMPNGPSANVGLAVGARAGVHTPVSACASGAEAIGYAIEMIRTGRADVVV    193
S. coelicolor FabF        LMPNGPSANVGLAVGARAGVHTPVSACASGAEAIGYAIEMIRTGRADVVV    199
S. griseus FabF           LMPNGPAANVGLEVNAQAGVHTPVSACASGAEAIGYAVEMIRTGRADVVV    193
E. coli FabF              TIVNMVAGHLTIMYGLRGPSISIATACTSGVHNIGHAARIIAYGDADVMV    187

Consensus                 AGGTEAAIHPLPIAAFXNMMAMSKNNDXPXGASRPFDTARDGFVLGEGAG
S. platensis MA7327 PtmP3 AGGVEACLHPFTIAAFAQMKALSTQCENPEAVSRPFDVARSGFVMGEGAG    235
S. platensis MA7339 PtnP3 AGGVEACLHPFTIAAFAQMKALSTQCENPESVSRPFDVARSGFVMGEGAG    235
S. platensis MA7327 FabF  AGGTEAAIHPLPIAAFGNMMAMSKSNDDPQGASRPFDTARNGFVMGEGAG    243
S. albus J1074 FabF       AGGTEAAIHPLPVVAFANMMAMSKNNDEPEKASRPYDTGRDGFVLGEGAG    243
S. avermitilis FabF       AGGTEAAIHPLPIAAFGNMMAMSKNNDDPQGASRPYDVARDGFVLGEGAG    243
S. coelicolor FabF        AGGTEAAIHPLPIAAFGNMMAMSKNNDDPQGASRPFDTARDGFVLGEGAG    249
S. griseus FabF           AGGTEAAIHPLPIAAFANMMAMSKNNEEPETASRPYDTGRDGFVLGEGAG    243
E. coli FabF              AGGAEKASTPLGVGGFGAARALSTRNDNPQAASRPWDKERDGFVLGDGAG    237
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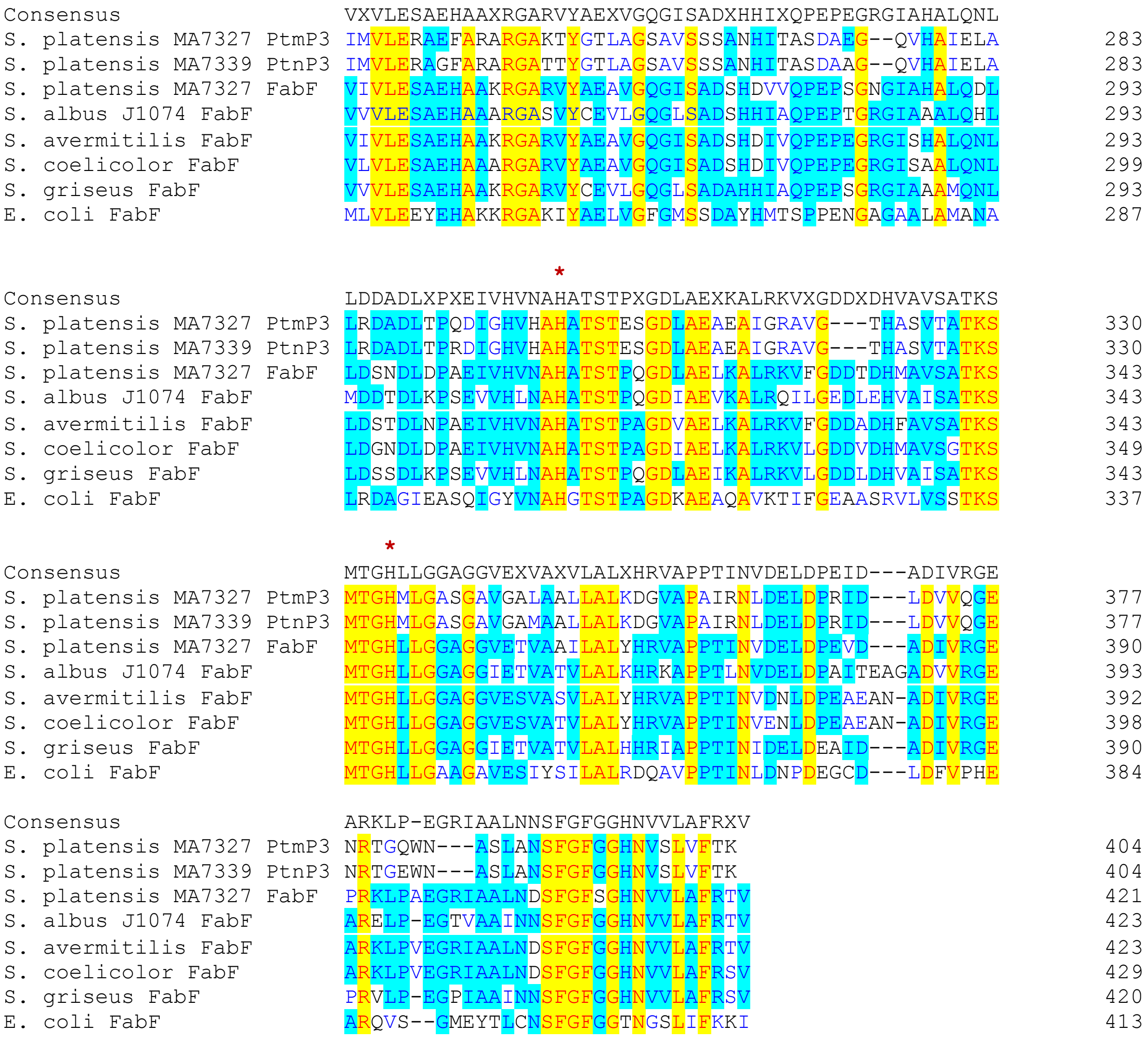
Fig. S2 continued.



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Consensus                 VXVLESAEHAAXRGARVYAEXVGQGISADXHHIXQPEPEGRGIAHALQNL
S. platensis MA7327 PtmP3 IMVLERAEFARARGAKTYGTLAGSAVSSSANHITASDAEG--QVHAIELA        283
S. platensis MA7339 PtnP3 IMVLERAGFARARGATTYGTLAGSAVSSSANHITASDAAG--QVHAIELA        283
S. platensis MA7327 FabF  VIVLESAEHAAKRGARVYAEAVGQGISADSHDVVQPEPSGNGIAHALQDL        293
S. albus J1074 FabF       VVVLESAEHAAARGASVYCEVLGQGLSADSHHIAQPEPTGRGIAAALQHL        293
S. avermitilis FabF       VIVLESAEHAAKRGARVYAEAVGQGISADSHDIVQPEPEGRGISHALQNL        293
S. coelicolor FabF        VLVLESAEHAAARGARVYAEAVGQGISADSHDIVQPEPEGRGISAALQNL        299
S. griseus FabF           VVVLESAEHAAKRGARVYCEVLGQGLSADAHHIAQPEPSGRGIAAAMQNL        293
E. coli FabF              MLVLEEYEHAKKRGAKIYAELVGFGMSSDAYHMTSPPENGAGAALAMANA        287

                                          *
Consensus                 LDDADLXPXEIVHVNAHATSTPXGDLAEXKALRKVXGDDXDHVAVSATKS
S. platensis MA7327 PtmP3 LRDADLTPQDIGHVHAHATSTESGDLAEAEAIGRAVG---THASVTATKS        330
S. platensis MA7339 PtnP3 LRDADLTPRDIGHVHAHATSTESGDLAEAEAIGRAVG---THASVTATKS        330
S. platensis MA7327 FabF  LDSNDLDPAEIVHVNAHATSTPQGDLAELKALRKVFGDDTDHMAVSATKS        343
S. albus J1074 FabF       MDDTDLKPSEVVHLNAHATSTPQGDIAEVKALRQILGEDLEHVAISATKS        343
S. avermitilis FabF       LDSTDLNPAEIVHVNAHATSTPAGDVAELKALRKVFGDDADHFAVSATKS        343
S. coelicolor FabF        LDGNDLDPAEIVHVNAHATSTPAGDIAELKALRKVLGDDVDHMAVSGTKS        349
S. griseus FabF           LDSSDLKPSEVVHLNAHATSTPQGDLAEIKALRKVLGDDLDHVAISATKS        343
E. coli FabF              LRDAGIEASQIGYVNAHGTSTPAGDKAEAQAVKTIFGEAASRVLVSSTKS        337

                             *
Consensus                 MTGHLLGGAGGVEXVAXVLALXHRVAPPTINVDELDPEID---ADIVRGE
S. platensis MA7327 PtmP3 MTGHMLGASGAVGALAALLALKDGVAPAIRNLDELDPRID---LDVVQGE        377
S. platensis MA7339 PtnP3 MTGHMLGASGAVGAMAALLALKDGVAPAIRNLDELDPRID---LDVVQGE        377
S. platensis MA7327 FabF  MTGHLLGGAGGVETVAAILALYHRVAPPTINVDELDPEVD---ADIVRGE        390
S. albus J1074 FabF       MTGHLLGGAGGIETVATVLALKHRKAPPTLNVDELDPAITEAGADVVRGE        393
S. avermitilis FabF       MTGHLLGGAGGVESVASVLALYHRVAPPTINVDNLDPEAEAN-ADIVRGE        392
S. coelicolor FabF        MTGHLLGGAGGVESVATVLALYHRVAPPTINVENLDPEAEAN-ADIVRGE        398
S. griseus FabF           MTGHLLGGAGGIETVATVLALHHRIAPPTINIDELDEAID---ADIVRGE        390
E. coli FabF              MTGHLLGAAGAVESIYSILALRDQAVPPTINLDNPDEGCD---LDFVPHE        384

Consensus                 ARKLP-EGRIAALNNSFGFGGHNVVLAFRXV
S. platensis MA7327 PtmP3 NRTGQWN---ASLANSFGFGGHNVSLVFTK                            404
S. platensis MA7339 PtnP3 NRTGEWN---ASLANSFGFGGHNVSLVFTK                            404
S. platensis MA7327 FabF  PRKLPAEGRIAALNDSFGFSGHNVVLAFRTV                           421
S. albus J1074 FabF       ARELP-EGTVAAINNSFGFGGHNVVLAFRTV                           423
S. avermitilis FabF       ARKLPVEGRIAALNDSFGFGGHNVVLAFRTV                           423
S. coelicolor FabF        ARKLPVEGRIAALNDSFGFGGHNVVLAFRSV                           429
S. griseus FabF           PRVLP-EGPIAAINNSFGFGGHNVVLAFRSV                           420
E. coli FabF              ARQVS--GMEYTLCNSFGFGGTNGSLIFKKI                           413
```

Fig. S3, related to Experimental Procedures. Disk diffusion assay for PTM and PTN susceptibility of naïve *Streptomyces* spp. *Streptomyces* spp. were assayed for resistance against PTM and PTN. *S. albus* J1027, *S. avermitilius* SUK-A4, *S.* lividans K4-114, S. *coelicolor* CH999, *S. platensis* MA7327, and S. *platensis* MA7339 were challenged with (1) 0 µg, (2) 200 µg, (3) 150 µg, (4) 100 µg, (5) 50 µg, and (6) 25 µg or (A) 5 µg, (B) 10 µg, (C) 20 µg, and (D) 40 µg of PTM or PTN.

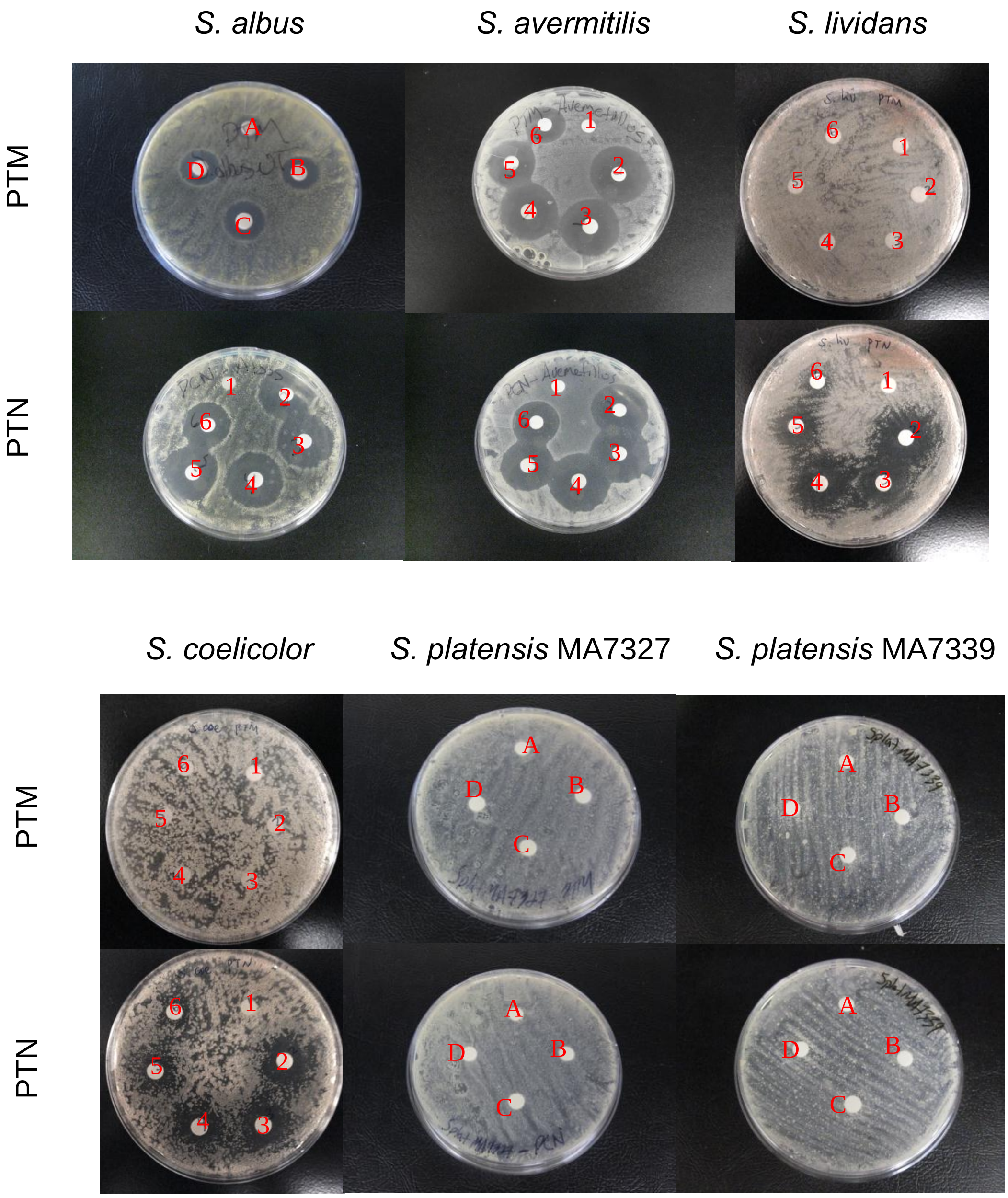


Fig. S4, related to Table 1. Minimum inhibitory concentrations (MIC) to PTM and PTN for selected Streptomyces species by 96-well plate assay. *S. albus* J1074*, S. platensis* MA7327, *S. platensis* MA7339, *S. albus* SB12011, *S. albus* SB12017, *S. albus* SB12013, *S. albus* SB12014, *S. albus* SB12018, *S. albus* SB12019, and *S. platensis* SB12021 (rows 1-10, respectively) challenged with PTM (panel A) or PTN (panel B). Final concentrations of PTM and PTN were 0, 256, 128, 64, 32, 16, 8, 4, 2, 1, 0.5, and 0.25 µg/mL (columns 1-12, respectively) and 0, 64, 32, 16, 8, 4, 2, 1, 0.5, 0.25, 0.125, and 0.0625 µg/mL, respectively (columns 1-12, respectively). The asterisk denotes a well (i.e., *S. a.* SB12019 at 4) with poor growth; however, it was ignored as the adjacent wells showed no inhibition.

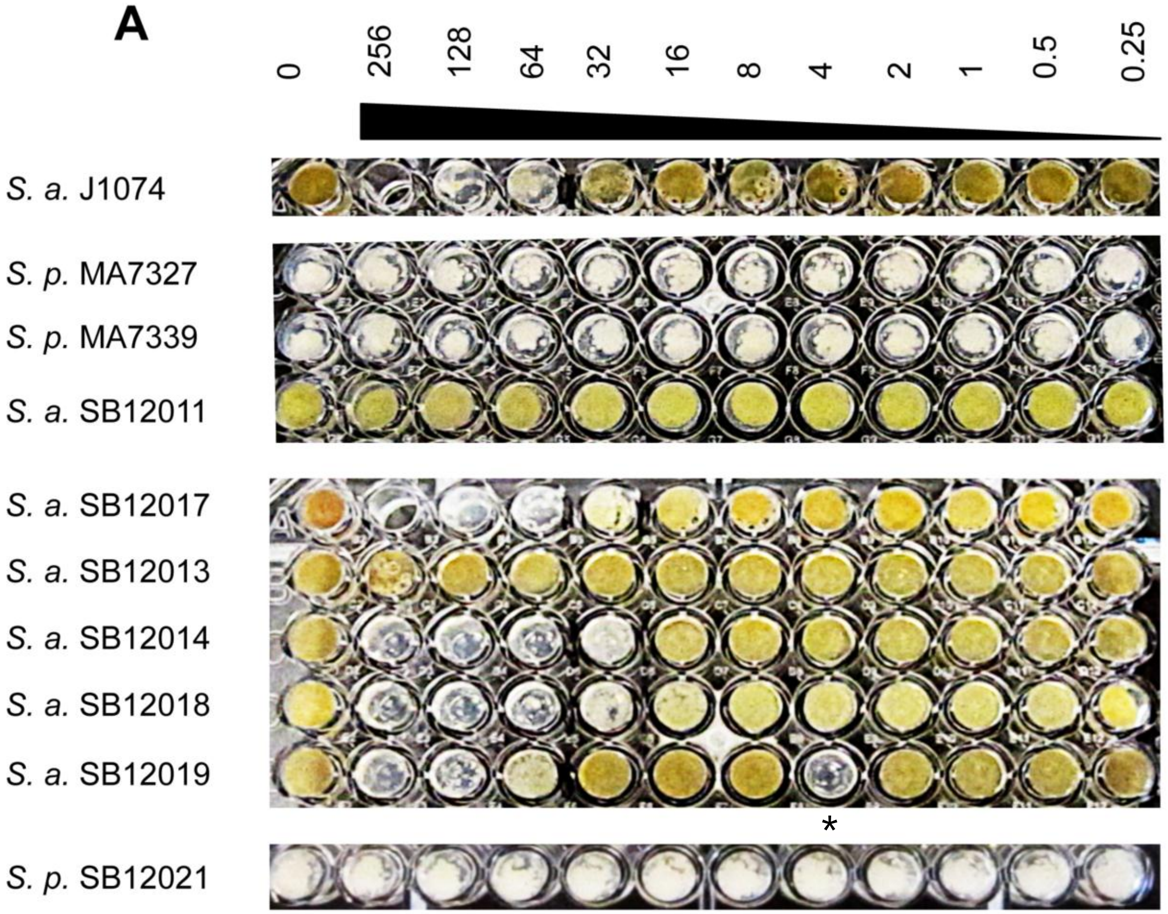


Fig. S4 continued**.**

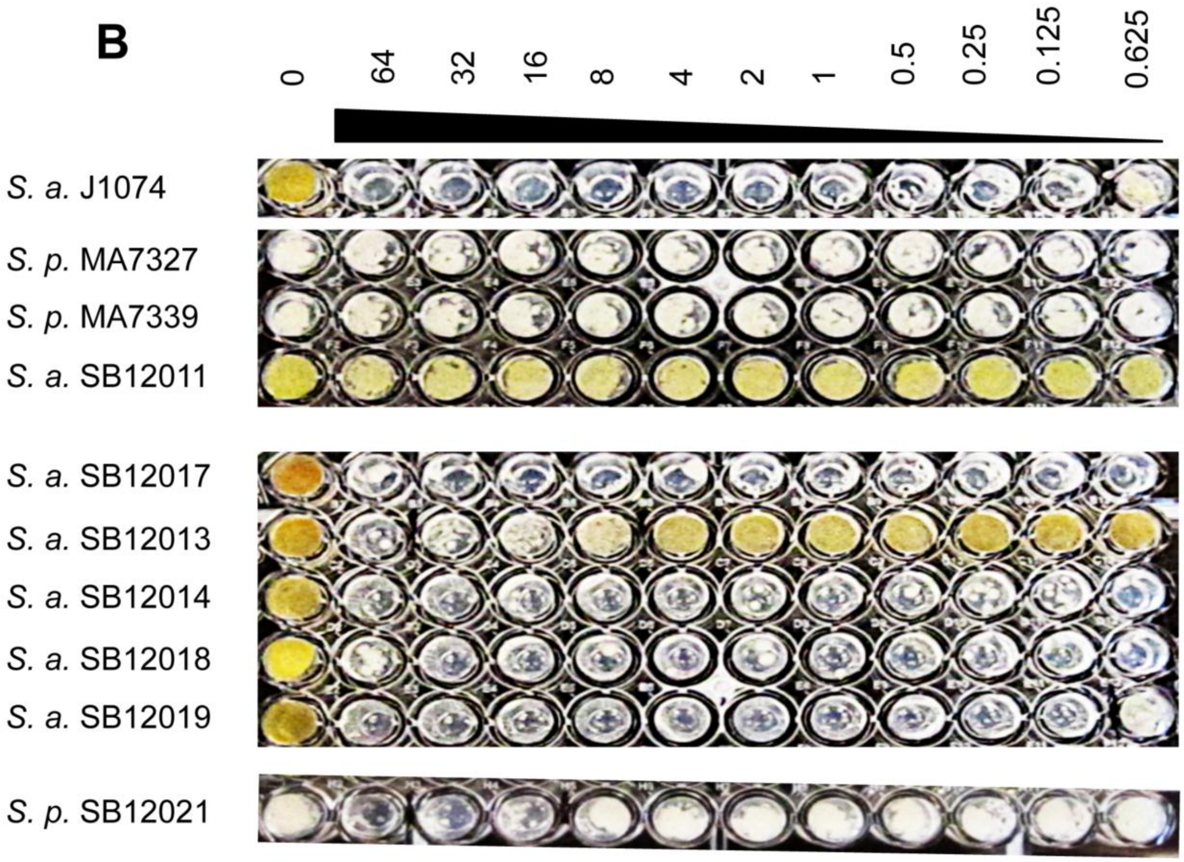
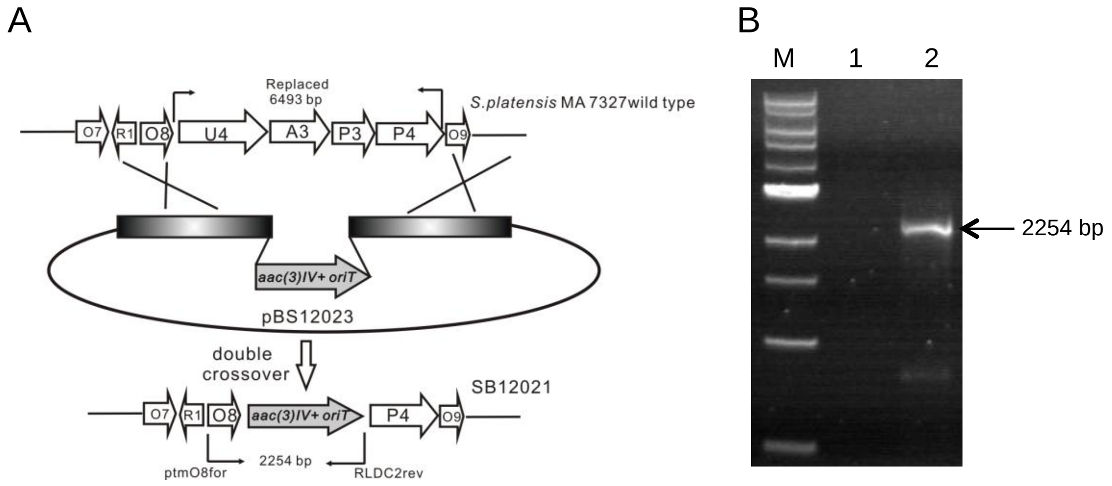
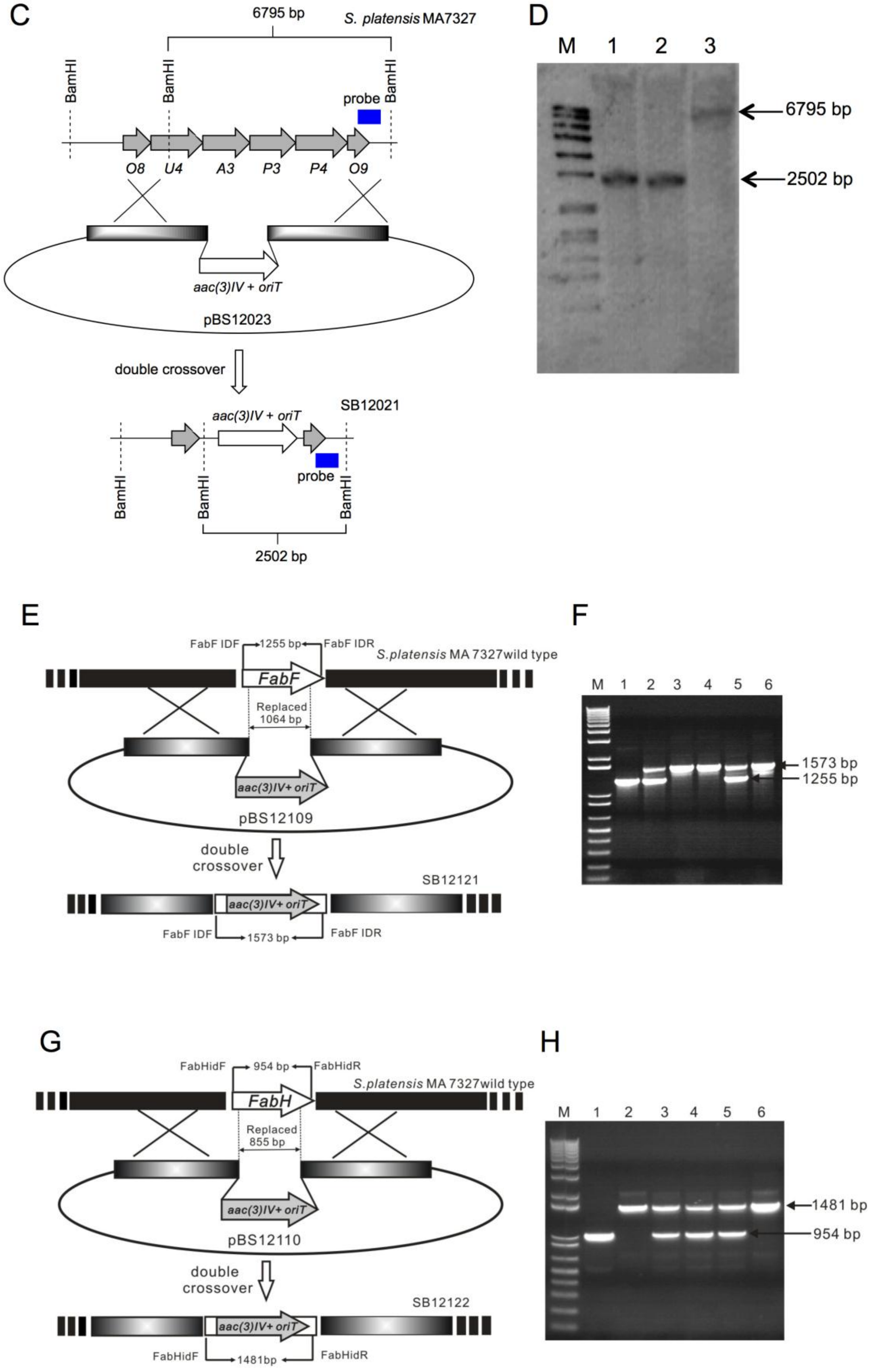


Fig. S5, related to Experimental Procedures and Table 1. Construction and Southern analyses of the Δ*ptmU4-ptmP4* mutant *S. platensis* SB12021, the Δ*fabF* mutant *S. platensis* SB12022, the Δ*fabH* mutant of *S. platensis* SB12023. (A) Schematic representation of the deletion of *S. platensis ptmU4-ptmP4* by insertion of an apramycin resistance-oriT cassette *(aac(3)IV +oriT*). (B) PCR verification of WT and double crossover mutant genotypes, using the primers ptmO8for and RLDC2rev. Lane 1, *S. platensis* MA7327; lane 2, *S. platensis* SB12021. (C) Schematic representation of the Southern analysis constructs for *S. platensis* SB12021. (D) Southern blot verification of WT (6795 bp) and double crossover (2502 bp) mutant genotypes. Lanes 1-2, *S. platensis* SB12021; lane 3, *S. platensis* MA7327. (E) Schematic representation of the inactivation of *S. platensis fabF*. (F) PCR verification of WT, single crossover mutant, and double crossover mutant genotypes, using the primers FabF_IDF and FabF_IDR. Lane 1, *S. platensis* MA7327; lanes 2 and 5, single crossover mutants; lanes 3 and 4, double crossover mutants, *S. platensis* SB12022 and SB12024; lane 6, pBS12024 positive control. (G) Schematic representation of the inactivation of *S. platensis fabH.* (H) PCR verification of WT, single crossover mutant, and double crossover mutant genotypes, using the primers FabF_IDF and FabF_IDR. Lane 1, *S. platensis* MA7327; lane 2, double crossover mutants, *S. platensis* SB12023 (or SB12025); lanes 3-5, single crossover mutants; lane 6, pBS12025 positive control. (I) Schematic representation of the inactivation of *S. platensis fabH*. (J) Schematic representation of the inactivation of *S. platensis fabF*. (K) Southern blot verification of WT (2780 bp) and double crossover mutants of *fabH* (1764 bp) and *fabF* (2283 bp) genotypes. Lanes 1 and 4, *S. platensis* MA7327; lane 2, *S. platensis* SB12023; lane 3, *S. platensis* SB12022.




C
6795 bp
S. platensis MA7327
BamHI
BamHI
probe
BamHI
O8
U4
A3
P3
P4
O9
aac(3)IV + oriT
pBS12023
double crossover
aac(3)IV + oriT
SB12021
probe
BamHI
BamHI
BamHI
2502 bp
D
M
1
2
3
6795 bp
2502 bp
E
FabF IDF
1255 bp
FabF IDR
S.platensis MA 7327wild type
FabF
Replaced
1064 bp
aac(3)IV+ oriT
pBS12109
double crossover
SB12121
aac(3)IV+ oriT
FabF IDF
1573 bp
FabF IDR
F
M
1
2
3
4
5
6
1573 bp
1255 bp
G
FabHidF
954 bp
FabHidR
S.platensis MA 7327wild type
FabH
Replaced
855 bp
aac(3)IV+ oriT
pBS12110
double crossover
SB12122
aac(3)IV+ oriT
FabHidF
1481bp
FabHidR
H
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2
3
4
5
6
1481 bp
954 bp

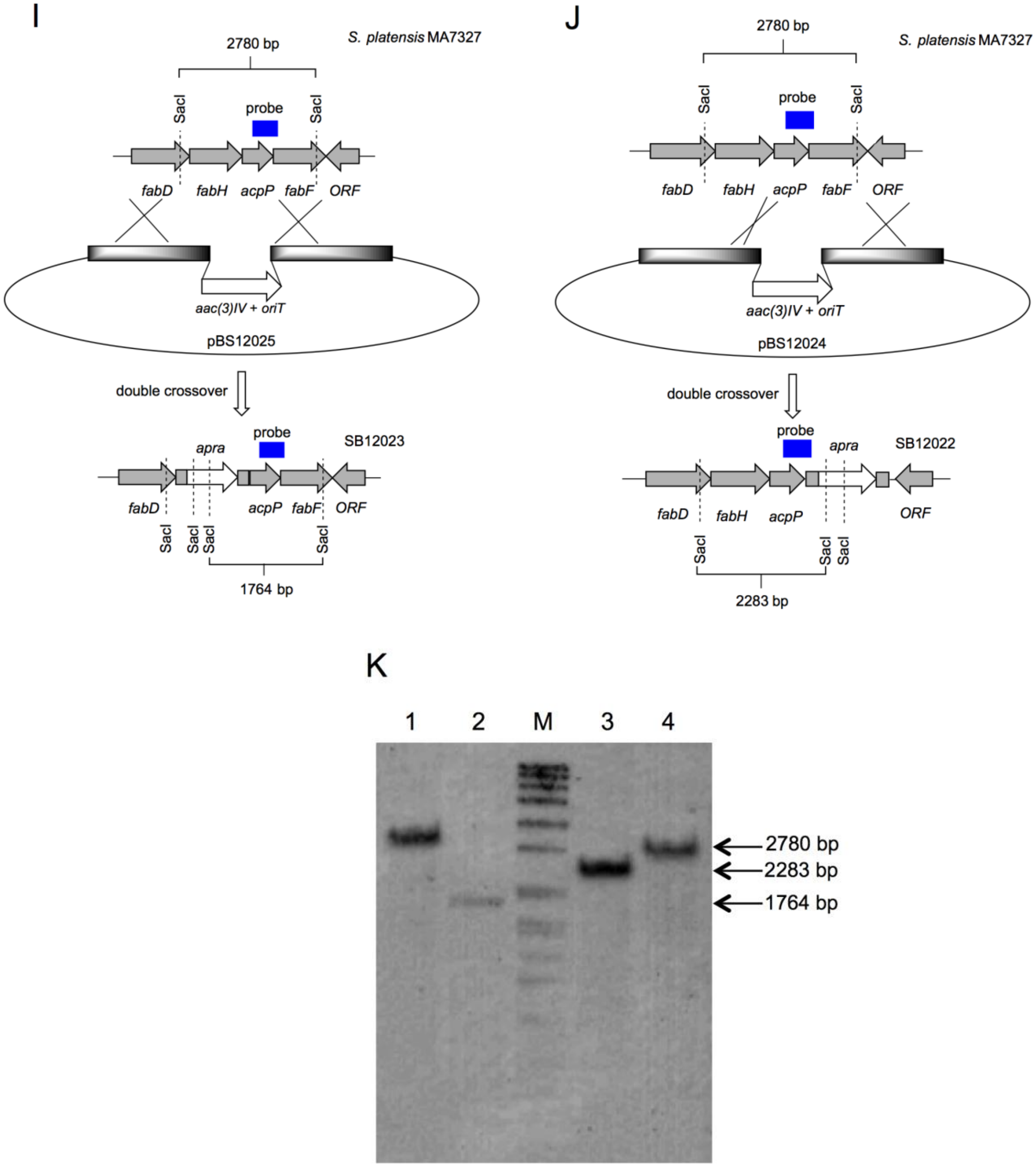
I
2780 bp
S. platensis MA7327
SacI
probe
SacI
fabD
fabH
acpP
fabF
ORF
aac(3)IV + oriT
pBS12025
double crossover
probe
apra
SB12023
fabD
acpP
fabF
ORF
SacI
SacI
SacI
SacI
1764 bp
J
2780 bp
S. platensis MA7327
SacI
probe
SacI
fabD
fabH
acpP
fabF
ORF
aac(3)IV + oriT
pBS12024
double crossover
probe
apra
SB12022
fabD
fabH
acpP
ORF
SacI
SacI
SacI
2283 bp
K
1
2
M
3
4
2780 bp
2283 bp
1764 bp

Table S1, related to Fig. 2A. Functional analysis of four candidate resistance genes from the *ptm*/*ptn* gene clusters in *Streptomyces platensis* MA7327 and *Streptomyces platensis* MA7339.

Gene	# of AA*	PTM/PTN % Identity	Protein homolog	% Identity/ % Similarity	Proposed function
ptmP1/*ptnP1*	474	96	PhlA (AAB48109)	23/34[§]	Putative resistance
			PhlB (AAB48107)	21/36[¶]	Unknown
ptmP2/*ptnP2*	414	99	PhlC (AAB48108)	22/35	Putative resistance
ptmP3/*ptnP3*	405	96	TiKASII (1J3N_A)	46/63	Putative resistance
ptmP4/*ptnP4*	520	97	Pep (AAG31689)	30/48	Efflux pump

*AA, amino acids.

[§] Values from alignment of full-length PhlA with residues 1-334 of PtmP1.

[¶] Values from alignment of full-length PhlB with residues 335-474 of PtmP1.

Table S2, related to Experimental Procedures. Strains and plasmids used in this study.

Strain	Genotype, Description	Reference/Source
E. coli DH5α	*E. coli* host for cloning	Commercial
S. platensis MA7327	Wildtype PTM/PTN producer	(Singh, et al., 2006; Wang, et al., 2006)
S. platensis MA7339	Wildtype PTN producer	(Singh, et al., 2007; Wang, et al., 2007)
S. platensis SB12001	PTM/PTN overproducing strain	(Smanski, et al., 2009)
S. platensis SB12002	PTM/PTN overproducing strain	(Smanski, et al., 2009)
E. coli ET12567/pUZ8002	Methylation-deficient *E. coli* host for intergeneric conjugation; contains pUZ8002, a nontransmissible *oriT* mobilizing plasmid	(MacNeil, et al., 1992)
E. coli BW25113/pIJ790	*E. coli* host for PCR targeting	(Gust, et al., 2003)
E. coli BW25113/pIJ790/pBS 12005	*E. coli* host for PCR targeting of the *ptm* cluster	This study
S. albus J1074	Naïve host for expression constructs	(Chater and Wilde, 1980)
S. avermitilis SUK-A4	Naïve host for susceptibility assay	(Komatsu, et al., 2010)
S. lividans K4-114	Naïve host for susceptibility assay	(Ziermann and Betlach, 1999)
S. coelicolor CH999	Naïve host for susceptibility assay	(Kieser T, et al., 2000; McDaniel, et al., 1993)
S. albus SB12009	*S. albus* J1074 harboring pBS12016	This study
S. albus SB12010	*S. albus* J1074 harboring pBS12017	This study
S. albus SB12011	*S. albus* J1074 harboring pBS12018	This study
S. albus SB12012	*S. albus* J1074 harboring pBS12019	This study
S. albus SB12013	*S. albus* J1074 harboring pBS12020	This study
S. albus SB12014	*S. albus* J1074 harboring pBS12021	This study
S. albus SB12015	*S. albus* J1074 harboring pBS12026	This study
S. albus SB12016	*S. albus* J1074 harboring pBS12027	This study
S. albus SB12017	*S. albus* J1074 harboring pBS12028	This study
S. albus SB12018	*S. albus* J1074 harboring pBS12029	This study
S. albus SB12019	*S. albus* J1074 harboring pBS12030	This study
S. platensis SB12020	*S. platensis* MA7327 harboring pBS12022	This study
S. platensis SB12021	*S. platensis* MA7327 Δ*ptmU4-ptmP4::aac(3)IV*	This study
S. platensis SB12022	*S. platensis* MA7327 Δ*fabF::aac(3)IV*	This study
S. platensis SB12023	*S. platensis* MA7327 Δ*fabH::aac(3)IV*	This study
S. platensis SB12024	*S. platensis* SB12020 Δ*fabF::aac(3)IV*	This study
S. platensis SB12025	*S. platensis* SB12020 Δ*fabH::aac(3)IV*	This study

Plasmid	Description	Reference/Source
pGEM-T Easy	TA cloning vector	Promega
pCR2.1-TOPO	TA cloning vector	Invitrogen

Table S2 continued**.**

pIJ773	Construct containing the apramcin resistance cassette (*aac (3)IV*+oriT)	(Gust, et al., 2003)
pBS12005	Cosmid harboring partial *ptm* gene cluster	(Smanski, et al., 2011)
pBS12013	The ermE* promotor cloned as an 0.3 kb EcoRI/BamHI fragment from pWHM860pro into the same site of pBS9010 (Galm, et al., 2009)	This study
pBS12014	Cosmid harboring *fab* cluster from *S. platensis* MA7327	This study
pBS12015	0.3 kb EcoRI/BamHI fragment from pWHM1250 containing the constitutive ermE* promotor cloned into the same sites of pSET152	This study
pBS12016	pSET152ermE* derivative pBS12015 harboring *ptmP1*	This study
pBS12017	pSET152ermE* derivative pBS12015 harboring *ptmP2*	This study
pBS12018	pSET152ermE* derivative pBS12015 harboring *ptmP3*	This study
pBS12019	pSET152ermE* derivative pBS12015 harboring *ptmP4*	This study
pBS12020	pSET152ermE* derivative pBS12015 harboring *S. platensis* MA7327 *fabF*	This study
pBS12021	pSET152ermE* derivative pBS12015 harboring *S. platensis* MA7327 *fabH*	This study
pBS12022	pSET152ermE* derivative pBS12013 harboring *ptmP3*	This study
pBS12023	pBS12005 Δ*ptmU4-ptmP4::aac(IV)3*, generated by PCR targeting with primers RLDC2for and RLDC2rev	This study
pBS12024	pBS12014 Δ*fabF::aac(IV)3*, generated by PCR targeting with primers ΔFabF-Forward and ΔFabF-Reverse	This study
pBS12025	pBS12014 Δ*fabH::aac(IV)3*, generated by PCR targeting with primers ΔFabH-Forward and ΔFabH-Reverse	This study
pBS12026	pSET152ermE* derivative pBS12015 harboring *ptmP3*(C162A)	This study
pBS12027	pSET152ermE* derivative pBS12015 harboring *ptmP3*(C162Q)	This study
pBS12028	pSET152ermE* derivative pBS12015 harboring *ptmP3*(C162L)	This study
pBS12029	pSET152ermE* derivative pBS12015 harboring *S. albus* J1074 *fabF*	This study
pBS12030	pSET152ermE* derivative pBS12015 harboring *S. albus* J1074 *fabH*	This study

Table S3, related to Experimental Procedures. Primers used in this study.

Primer	Nucleotide Sequence (5'-3')	Function
PtmP1For	GACCTCGACGTCGCTGAC	Amplification of *ptmP1*
PtmP1Rev	TGGTTCCGTGCGCAGTAC	Amplification of *ptmP1*
PtmP2For	CGTGGTGTTGATGACCCGTC	Amplification of *ptmP2*
PtmP2Rev	GCCAGTTCGACGGCCATG	Amplification of *ptmP2*
PtmP3For	TGTGGAAGGGACACAACTTACC	Amplification of *ptmP3*
PtmP3Rev	GTGGTCACTTGGTGAACACCAGG	Amplification of *ptmP3*
PtmP4For	TGTTCACCAAGTGACCACGGC	Amplification of *ptmP4*
PtmP4Rev	CGTCATCACTCACTCCAGGATG	Amplification of *ptmP4*
PtmP3C162AFor	GCCCGTCAGCGCCGCCGCGTCCGGTGCCG	Site-directed mutagenesis of *ptmP3*
PtmP3C162ARev	CGGCACCGGACGCGGCGGCGCTGACGGGC	Site-directed mutagenesis of *ptmP3*
PtmP3C162QFor	GCCCGTCAGCGCCCAGGCGTCCGGTGCCG	Site-directed mutagenesis of *ptmP3*
PtmP3C162QRev	CGGCACCGGACGCCTGGGCGCTGACGGGC	Site-directed mutagenesis of *ptmP3*
SeqC162mutUp	GACGACATCTTCGAGGAGTCCG	Sequencing of PtmP3 C162 mutations
SeqC162mutDown	CGGACTCCTCGAAGATGTCGTC	Sequencing of PtmP3 C162 mutations
RLDC2for	ACACCAGCCGTACTACGCGGATCGGAGGGCCGAGTCGTGATTCCGGGGATCCGTCGACC	Amplification of *ptmU4-ptmP4* disruption cassette
RLDC2rev	CTACTTGCCGGGCTGCCGGGTACGGACGAGCAGTCCGGCTGTAGGCTGGAGCTGCTTC	Amplification of *ptmU4-ptmP4* disruption cassette
ptmO8for	AAAACCTCTATTTCCAGTCGGTAGCGTTAAATCAGTTAACTAAG	Confirmation of Δ*ptmU4-ptmP4* in *S. platensis*
U4-P4SouthF	GTCGAGGCCATCTTCTACGA	Probe for Southern analysis of Δ*U4-P4*
U4-P4SouthR	GAACATCCAGCGGTTCTCC	Probe for Southern analysis of Δ*U4-P4*
UpstreamFabH(2)	TGGGACCTGTGCATGGAGAC	Amplification/sequencing of *Streptomyces*/sequencing *fabH*
DownstreamFabH(1)	GGTCGTCGGTGAAGGACTTGTC	Amplification/sequencing of *Streptomyces fabH*
DownstreamFabH(2)	TCGACCATGGACAGCGAGTCG	Amplification/sequencing of *Streptomyces fabH*
UpstreamFabF(1)	GGACAAGTCCTTCACCGACGAC	Amplification/sequencing of *Streptomyces fabF*
UpstreamFabF(2)	GCTGTCCATGGTCGAGGTCG	Amplification/sequencing of *Streptomyces fabF*
DownstreamFabF(1)	TCCGCTGGCTGCACCAGG	Amplification/sequencing of *Streptomyces fabF*
DownstreamFabF(2)	ACGACGAACTGGAGCCCTTCC	Amplification/sequencing of *Streptomyces fabF*

Table S3 continued**.**

Primer	Nucleotide Sequence (5'-3')	Function
FabFinFor	GCGGCCAGTACGACGTGCTC	Sequencing of *Streptomyces fabF*
FabFinRev	AGCCGTCTCAAGCTCGTCGTC	Sequencing of *Streptomyces fabF*
ΔFabH-Forward	GGCGGCTACCGCCCGACCCGGGTCGTGCCCAACGAGGAGATTCCGGGGATCCGTCGACC	Amplification of *fabH* disruption cassette
ΔFabH-Reverse	CAACAGTCGCTCCATGGCGAGCGGAATGGAGGCGGCCGATGTAGGCTGGAGCTGCTTC	Amplification of *fabH* disruption cassette
ΔFabF-Forward	ACACCGCTGGGTGGCGACAGCGCTTCGTCCTGGGAGGCCATTCCGGGGATCCGTCGACC	Amplification of *fabF* disruption cassette
ΔFabF-Reverse	CTCGGCGGGCAGCTTGCGGGGCTCGCCGCGGACGATGTCCTGTAGGCTGGAGCTGCTTC	Amplification of *fabF* disruption cassette
FabHscreen For	TCCACCGTTTCGCACTTCA	Isolation of cosmids containing *S. platensis fabH*
FabHscreen Rev	GGCCGTTGGGCATCAGCAT	Isolation of cosmids containing *S. platensis fabH*
FabFscreen For	ATCGCACCGTGGTCGTCAC	Isolation of cosmids containing *S. platensis fabF*
FabFscreen Rev	GGCCGTTGGGCATCAGCAT	Isolation of cosmids containing *S. platensis fabF*
FabH_IDF	GACCTCGAAGGTCAAGCCC	Confirmation of Δ*fabH* in *S. platensis*
FabH_IDR	GTCGCCAACAGTCGCTCCA	Confirmation of Δ*fabH* in *S. platensis*
FabF_IDF	AACGCGACCAATCGCACCG	Confirmation of Δ*fabF* in *S. platensis*
FabF_IDR	TCCGGAAGGCCAGCACCAC	Confirmation of Δ*fabF* in *S. platensis*
fabFH_South F	CGGATCTTCACCGCAAGTAA	Probe for Southern analysis of Δ*fabF/H*
fabFH_South R	GTTCACGGGAATTCTTACTCCA	Probe for Southern analysis of Δ*fabF/H*

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