

Biochemical Analysis of the Biosynthetic Pathway of an Anticancer Tetracycline SF2575

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Abstract: SF2575 **1** is a tetracycline polyketide produced by *Streptomyces* sp. SF2575 and displays exceptionally potent anticancer activity toward a broad range of cancer cell lines. The structure of SF2575 is characterized by a highly substituted tetracycline aglycon. The modifications include methylation of the C-6 and C-12a hydroxyl groups, acylation of the 4-(S)-hydroxyl with salicylic acid, C-glycosylation of the C-9 of the D-ring with D-olivose and further acylation of the C4'-hydroxyl of D-olivose with the unusual angelic acid. Understanding the biosynthesis of SF2575 can therefore expand the repertoire of enzymes that can modify tetracyclines, and facilitate engineered biosynthesis of SF2575 analogues. In this study, we identified, sequenced, and functionally analyzed the *ssf* biosynthetic gene cluster which contains 40 putative open reading frames. Genes encoding enzymes that can assemble the tetracycline aglycon, as well as installing these unique structural features, are found in the gene cluster. Biosynthetic intermediates were isolated from the SF2575 culture extract to suggest the order of pendant-group addition is C-9 glycosylation, C-4 salicylation, and O-4' angelicylation. Using in vitro assays, two enzymes that are responsible for C-4 acylation of salicylic acid were identified. These enzymes include an ATP-dependent salicylyl-CoA ligase SsfL1 and a putative GDSE family acyltransferase SsfX3, both of which were shown to have relaxed substrate specificity toward substituted benzoic acids. Since the salicylic acid moiety is critically important for the anticancer properties of SF2575, verification of the activities of SsfL1 and SsfX3 sets the stage for biosynthetic modification of the C-4 group toward structure–activity relationship studies of SF2575. Using heterologous biosynthesis in *Streptomyces lividans*, we also determined that biosynthesis of the SF2575 tetracycline aglycon **8** parallels that of oxytetracycline **4** and diverges after the assembly of 4-keto-anhydrotetracycline **51**. The minimal *ssf* polyketide synthase together with the amidotransferase SsfD produced the amidated decaketide backbone that is required for the formation of 2-naphthacenecarboxamide skeleton. Additional enzymes, such as cyclases C-6 methyltransferase and C-4/C-12a dihydroxylase, were functionally reconstituted.

Introduction

Bacterial aromatic polyketide natural products comprise a group of molecules that displays diverse structures and bioactivities yet share common biosynthetic origins. The poly- β -ketone backbone is synthesized by a minimal polyketide synthase (PKS) consisting of a ketosynthase (KS or KS $_{\alpha}$), a chain-length factor (CLF or KS $_{\beta}$), and an acyl carrier protein (ACP).¹ Additional tailoring enzymes are required to fix the regioselectivity of sequential cyclization steps and perform a multitude of decorating reactions to afford the various polycyclic bioactive compounds. A small, yet extremely important group of aromatic polyketides is the tetracycline family. Tetracyclines are characterized by the linearly fused four-ring structure and a heavily oxidized 2-naphthacenecarboxamide carbon skeleton.

Other common features include the planar phenyldiketone arrangement and the tricarbonylmethane moiety in the A ring. This family is exemplified by the well-known tetracyclines chlorotetracycline **5** and oxytetracycline **4**² (Scheme 1). Discovered in 1948 from *Streptomyces aureofaciens*³ and in 1950 from *S. rimosus*,⁴ respectively, these compounds were commercialized as broad-spectrum antibiotics and used successfully until bacterial resistance prompted the need for the creation of analogues to combat drug resistant strains.⁵ The natural tetracycline scaffold has since been used to create second- and third-generation tetracyclines semisynthetically. The third-generation tetracycline tigecycline gained FDA approval in

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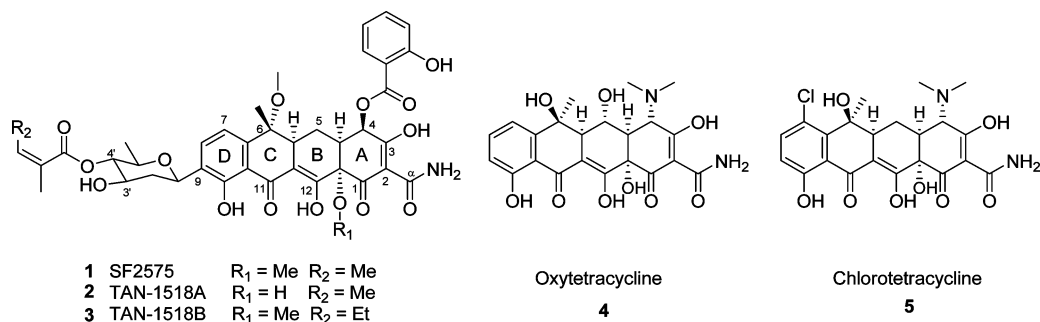
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Scheme 1



2005,^{6,7} demonstrating the continued utility of the tetracycline scaffold. Remarkably, since the initial discovery of **4** and **5** over 60 years ago, there have been only a few natural tetracyclines discovered. Among these are SF2575^{8,9} **1** and related compounds, TAN-1518A **2** and TAN-1518B **3**,¹⁰ chelocardin,¹¹ and dactylocycline.¹² Each of these compounds contains the tetracycline core and exhibits novel structural features not observed in **4** or **5**. Given the rarity of tetracycline natural products, understanding the biosynthesis of these newly discovered compounds may provide a route to the generation of new tetracycline antibiotics through the use of combinatorial biosynthesis and metabolic engineering strategies.

SF2575 was first isolated by Hatsu et al. from the producing strain *Streptomyces* sp. SF2575.⁹ The 2-naphthacene-carboxamide carbon framework of **1** is identical to that of **4** and **5**. In addition, there are a number of unique tailoring modifications decorating the tetracyclic aglycon including two methoxy groups at C-6 and C-12a, a 4-(*S*)-salicylate that replaces the more common 4-(*R*)-dimethylamine substituent, a C-9 *C*-glycoside of 2-6-dideoxy-*arabino*-hexopyranose (D-olivose), and acylation of the O-4' of D-olivose with (*Z*)-2-methyl-2-butenate (angelate). The angelate and salicylate moieties are unusual polyketide modifications which add to the intrigue of the biosynthesis of **1**. In addition to its unique structure, **1** also introduces potent anticancer bioactivity to the tetracycline family. Screening by Hatsu et al. demonstrated that **1** has very weak antibiotic activity, which is most likely due to, among others, methylation of the C-12a hydroxyl group that disrupts interactions with the bacterial 30S ribosomal subunit.¹³ SF2575 was, however, found to have exceptionally potent anticancer activity both through an in vitro cytotoxicity assay with P388 leukemia cells and during an in vivo assay using mouse xenografts.⁹ More recently, a 60-cell line screening by the National Cancer Institute demonstrated the potent activity of **1** against nearly all types of cancer cell

lines tested, resulting in an average IC₅₀ value of 11.2 nM. The mechanism of action of several closely related SF2575 analogues, **2** and **3** has been identified as inhibition of DNA topoisomerase I.¹⁰ As these structures are nearly identical to that of **1**, it is likely that this family of compounds shares a common molecular target. As key enzymes during DNA replication, both DNA topoisomerases I and II are known targets for current anticancer therapies in clinical use such as doxorubicin, a topoisomerase II poison,¹⁴ and camptothecin derivatives which target topoisomerase I.¹⁵ Elucidation of the SF2575 biosynthetic pathway can therefore be useful toward future structure–activity relationship (SAR) studies and engineered biosynthesis of new anticancer compounds.

In this report we have identified and sequenced the *ssf* gene cluster responsible for the biosynthesis of **1**. This *ssf* gene cluster is only the third tetracycline family gene cluster to be identified and sequenced following chlorotetracycline¹⁶ and oxytetracycline.^{17,18} The genetic information offers valuable opportunities to further enhance our understanding of tetracycline biosynthesis and to investigate an entirely new set of tetracycline-tailoring modifications that distinguish **1** from the previously studied **4** and **5**. Bioinformatic analysis of the gene cluster along with identification of the possible biosynthetic intermediates from *Streptomyces* sp. SF2575 fermentation extract led to the assembly of a putative biosynthetic pathway for **1**. We have identified key tailoring enzymes involved in the attachment of salicylate to the tetracycline aglycon and verified their function through in vitro assays. Additionally, we have reconstituted the early portions of the *ssf* pathway in a heterologous host and demonstrated the biosynthesis of the tetracycline core of **1** parallels the biosynthetic pathway of **4**.^{18–20}

Results and Discussion

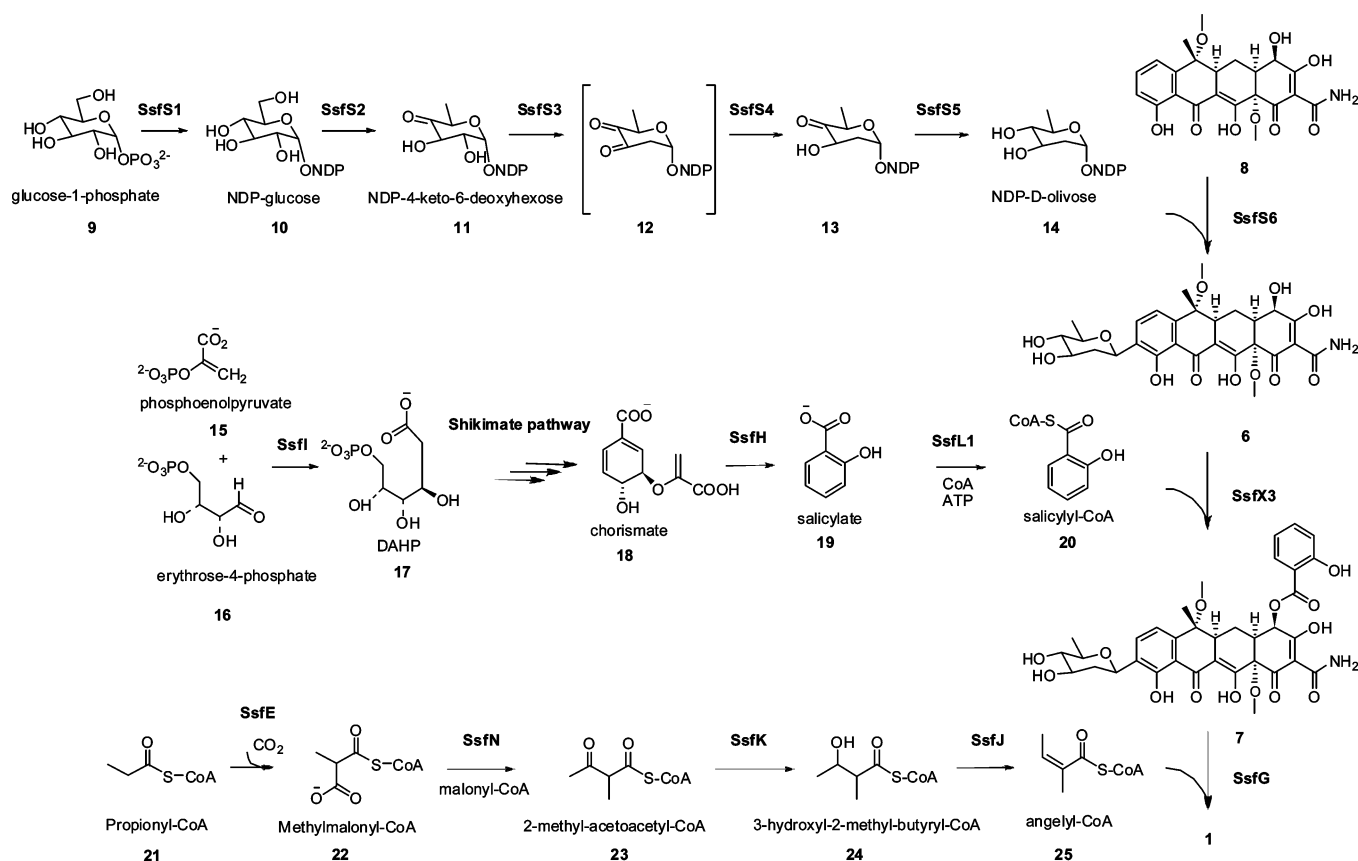
Identification of SF2575 Intermediates from Crude Extract.

Comparing the core structures of **1** and **4**, biosynthesis of the naphthacene-carboxamide carbon framework of **1** is predicted to parallel that of the oxytetracycline (*oxy*) biosynthetic pathway^{17,18} and may share a number of common intermediates.

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Scheme 2



As shown in Scheme 2, the putative aglycon is likely to be **8**, which exhibits the typical features of a tetracycline except replacement of 4-(*R*)-dimethylamine with 4-(*S*)-hydroxyl, inversion of stereochemistry at C-6 and *O*-methylations at C-6 and C-12a. Downstream tailoring of **1** is therefore likely to occur following assembly of **8**. In order to decipher the timing of the three unique post-PKS tailoring reactions leading to the biosynthesis of **1**: glycosylation with D-olivose **14**, *O*-4' acylation of angelic acid and C-4 acylation of salicylic acid **19**, crude extract of *Streptomyces* sp. SF2575 culture was prepared and analyzed on HPLC and LC/MS to try to identify any potential stable intermediates that may be present. *Streptomyces* sp. SF2575 culture was grown on solid Bennette's media for 10 days at 30 °C. A sample was extracted each day starting with day 4 to analyze the metabolic profile. Using selected ion monitoring, two potential intermediates identified were **6** ($[M + H]^+$ at m/z 576, RT = 18.3 min) and **7** ($[M + H]^+$ at m/z 696, RT = 26.8 min), in addition to the parent compound **1** ($[M + H]^+$ at m/z 778, RT = 34.2 min) (Figure 1). The UV spectrum of each compound was similar to that of **1** with a characteristic tetracycline λ_{\max} at 358 nm, and a λ_{\max} at 302 nm for **1** and **7** characteristic of the salicylate. The UV spectrum of **6** lacks this contribution at 302 nm, resulting in a smooth peak at 358 nm, and is indicative of the loss of salicylate compared to **7** as suggested by the molecular weight difference. To confirm the identity of these compounds as shown in Figure 1, authentic standards were prepared from base hydrolysis of purified **1** as described by Hatsu et al.⁸ Treatment of **1** with 0.5 M NaOH led to the hydrolysis of the angelate and afforded **7**, while complete conversion to **6** was obtained by treating **1** with 1.0 M NaOH for 15 h. Following purification of **6** and **7** from the base hydrolysis reactions, proton NMR and HRMS were used

to confirm the structures by comparison to published data (Supporting Information).⁸ These prepared samples were then used as standards to verify the identities of **6** and **7** in the fermentation extract of *Streptomyces* sp. SF2575 by HPLC retention times, mass fragmentation patterns and UV spectra.

Other potential intermediates, such as **6** acylated with angelate, or **8** acylated with salicylate, were not detected in the crude extracts using selected ion monitoring by LC/MS. This evidence, along with the positive detection of **6** and **7** were used to construct a proposed aglycon-tailoring pathway of **1** as shown in Scheme 2. Therefore, the likely order of the tailoring modifications starts with C-glycosylation of **8** with **14** that results in **6**, followed by attachment of salicylic acid **19** at C-4 to produce **7**, and capped by the acylation of *O*-4' of **7** with angelate to produce the final product **1**. It is noteworthy that each of these isolated intermediates has already been *O*-methylated at the C-12a and C-6 hydroxyl groups, which indicates that these modifications likely take place early in the biosynthesis, providing further support for **8** as an advanced intermediate. While **8** was not identified in the fermentation extract, this could be due either to the potential instability of **8** or the rate of the glycosylation reaction which may not permit the accumulation of **8** in detectable quantities.

Bioactivity of SF2575 and Putative Biosynthetic Intermediates. Since the potent antiproliferative activity of **1** is new to the tetracycline family, we sought to gain insight to the structural features of **1** that may contribute to this activity. The angelate and salicylate modifications of **1** are unique structural features among tetracyclines and bacterial aromatic polyketides. To probe whether these moieties are the "warheads" that contribute to the antitumor activities of **1**, we performed in vitro cytotoxicity assays with Nalm-6 pre-B cells using **6**, **7** and **1** (Supporting

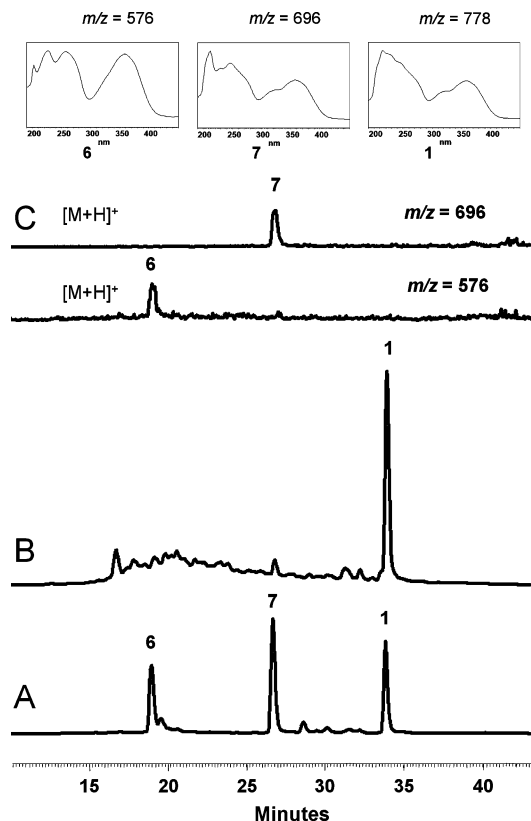


Figure 1. Production of **1** and biosynthetic intermediates by *Streptomyces* sp. SF2575. The data were collected on the Shimadzu LC/MS. (A) LC trace (358 nm) for a mixture of standards **6**, **7**, and **1**. (B) LC trace (358 nm) of the extract after 7 days growth on solid Bennette's media. (C) Selected ion monitoring was used to confirm the identification of **7** ($[M + H]^+$ $m/z = 696$) and **6** ($[M + H]^+$ $m/z = 576$). The UV spectra of these compounds are shown for comparison.

Information Figure S5). While the parent compound **1** had a potent IC_{50} of 8.8 nM, removal of the angelate resulted in a significantly attenuated IC_{50} of 327 nM for **7**. Further hydrolysis of the salicylate as in **6** led to an additional 15-fold decrease of potency with an IC_{50} of 5.2 μ M. Similar trends were observed when other cell lines, including MCF-7, HeLa, and M249 were subjected to the cytotoxicity assays (Supporting Information Figure S5). Hence, both pendant groups are critically important for the bioactivity of **1** and are attractive targets for SAR studies. Identification of the enzymes responsible for these additions may therefore provide useful biosynthetic approaches toward functionalizing these positions, especially considering the densely functionalized tetracycline core may be difficult to assess synthetically.

Identification and Sequencing of the *ssf* Biosynthetic Gene Cluster. To construct a blueprint of SF2575 biosynthesis, the *ssf* gene cluster was identified by screening a cosmid library prepared from *Streptomyces* sp. SF2575 genomic DNA using degenerative primers published by Wawrik et al. for screening the type II polyketide KS_{α} gene.²¹ Several PCR products from different cosmids were sequenced and were found to encode an identical KS fragment, which indicates that there is likely only one aromatic PKS gene cluster present in the *Streptomyces* sp. SF2575 genome. Three overlapping cosmids were sequenced by a combination of shotgun sequencing and primer walking

(Figure 2). The cluster spans a 47.2 kb region and contains 40 ORFs putatively involved in SF2575 biosynthesis, including the essential KS_{α} – KS_{β} heterodimer for synthesis of the polyketide backbone. To confirm that this cluster is responsible for SF2575 biosynthesis, the *ssfB* gene encoding KS_{β} was inactivated by an insertion of a kanamycin resistance gene (*aphII*) through a double crossover recombination. Disruption of this gene resulted in complete loss of SF2575 production (Supporting Information Figure S6), hence confirming the link between **1** and the sequenced *ssf* gene cluster.

A map of the *ssf* gene cluster is shown in Figure 2. The putative boundaries are determined on the basis of sequence analysis and biosynthetic logic. The *ssf* genes identified along with their proposed function are listed in Table 1. Represented within are genes likely responsible for the biosynthesis of the aglycon **8**, pendant groups **14**, **19**, and **25**, as well as regulation and self-resistance. Based on the putative functions of these genes, the proposed biosynthetic pathways of **8** and the subsequent tailoring of **8** to **1** are shown in Scheme 4 and Scheme 2, respectively.

Genes Putatively Involved in the Biosynthesis of D-Olivose **14.** Deoxysugar decoration is an important tailoring modification of bacterial secondary metabolites and is usually essential for the bioactivity of the natural products.²² The C-9 of **1** is modified with a C-glycoside D-olivose, which is also found among other polyketides such as urdamycin A²³ and simocyclinone.²⁴ Putative enzymes encoded in the *ssf* gene cluster that can convert glucose to NDP-D-olivose are SsfS1 (NDP-glucose synthase), SsfS2 (4',6'-dehydratase), SsfS3 (2',3'-dehydratase), SsfS4 (C-3' reductase), and SsfS5 (C-4' reductase) (Scheme 2). The proposed pathway includes the unstable intermediate **12** which is reduced at the 3' position by SsfS4.²⁵ NDP-D-olivose is subsequently transferred to the C-9 of the aglycon **8** by a C-glycosyltransferase to yield **6**. C-glycosyltransferases are more rare than O-glycosyltransferases, and are found in a number of aromatic PKS biosynthetic gene clusters such as urdamycin,²³ hedamycin,²⁶ and simocyclinone.²⁴ The putative *ssf* glycosyltransferase, SsfS6, has high sequence homology to HedJ, a C-glycosyltransferase from the hedamycin biosynthetic pathway.²⁶ Since SsfS6 is the first glycosyltransferase that can modify the tetracycline scaffold, it can potentially be a useful enzyme toward increasing the structural diversity of the D-ring, and in particular the C-9 position, of tetracycline compounds.

Genes Putatively Involved in the Biosynthesis of Salicylate **19.** The C-4 salicylate substitution in **1** is unusual not just among tetracyclines but quite rare among aromatic polyketides. One known example is that of thermorubin, in which the salicylate moiety is thought to be incorporated as a starter unit.²⁷ A related modification is the addition of a 6-methylsalicylic acid which is typically synthesized via a dedicated type I PKS, such as

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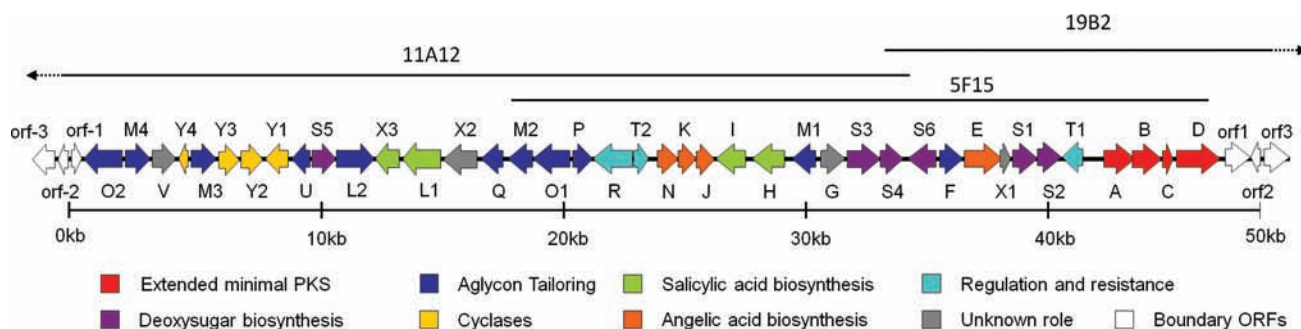


Figure 2. Organization of the *ssf* biosynthetic gene cluster. Genes are categorized according to their proposed role. The gene cluster spans 47.2 kb and contains 40 ORFs. Details of proposed functions are shown in Table 1.

Table 1. Putatively Assigned Functions of Enzymes Encoded in the *ssf* Biosynthetic Gene Cluster

name	closest homologue	putative role	size (kDa)	identity (%) / similarity (%)	accession number
SsfA	OxyA	ketosynthase	45	76/86	CAA80985
SsfB	OxyB	chain length factor	43	64/77	AAZ78326
SsfC	OxyC	acyl carrier protein	9.5	54/73	AAZ78327
SsfD	OxyD	amidotransferase	68	68/79	AAZ78328
SsfE	ChIJ	carboxytransferase	58	81/89	AAZ77684
SsfF	Npun_F4742	ketoreductase	34	55/70	ACC83094
SsfG	ChIB3	ketosynthase III	36	37/56	DQ116941
SsfH	MbtI	salicylate synthase	48	42/57	Q7D785
SsfI	PlmI	DAHP-7-phosphate synthase	45	56/67	AY354515
SsfJ	SAV_2786	enoyl CoA hydratase/isomerase	28	61/75	BAC70497
SsfK	Athe_1156	3-ketoacyl-(ACP) reductase	26	38/59	ACM60257
SsfL1	SdgA	Salicylyl-AMP ligase	58	75/84	BAG78380
SsfL2	OxyH	acyl-CoA ligase	56	51/67	DQ143963
SsfM1	OxyT	O-methyltransferase	36	48/62	DQ143963
SsfM2	DauK	O-methyltransferase	35	38/53	AAB16938
SsfM3	MtmMII	methyltransferase	37	38/55	CAK50790
SsfM4	OxyF	C-methyltransferase	37	51/68	AAZ78330
SsfN	PpzT	ketosynthase III	31	46/63	CAX48662
SsfO1	OxyS	oxygenase	55	42/54	AAZ78342
SsfO2	OxyL	oxygenase	59	57/70	AAZ78335
SsfP	CmmQ	dehydrogenase	29	49/54	YP_118212
SsfQ	Lct52	SAM synthetase	43	84/90	ABX71135
SsfR	Krad_0275	MFS transporter	58	33/51	ABS01765
SsfS1	StrD	dTDP glucose synthase	39	72/83	BAG22759
SsfS2	CalS3	glucose-4,6-dehydratase	36	69/80	AAM94770
SsfS3	Sim20	hexose-2,3-dehydratase	53	58/72	AF322256
SsfS4	ChlC4	hexose-3-ketoreductase	33	49/59	AAZ77681
SsfS5	NanG4	hexose-4-ketoreductase	37	42/53	AAZ77681
SsfS6	HedJ	glycosyltransferase	41	40/55	AAZ77683
SsfT1	SnorA	regulation	31	44/61	CAA12016
SsfT2	SAML0351	regulation (TetR family)	23	48/62	CAJ89338
SsfU	OxyJ	ketoreductase	27	76/86	AAZ78333
SsfV	ZhuC	acyltransferase	34	54/64	AAG30190
SsfX1	ChII	unknown function	8.5	50/60	AAZ77683
SsfX2	RemJ	carbohydrate kinase	36	64/72	CAE51179
SsfX3	AviX9	acyltransferase	40	48/61	AAK83171
SsfY1	OxyK	aromatase/cyclase	34	57/67	AAZ78334
SsfY2	NcnE	cyclase	33	56/68	AAD20271
SsfY3	CmmQ	cyclase	31	29/42	CAE17552
SsfY4	OxyI	cyclase	13	66/76	AAZ78332
Orf-1	hypothetical protein SGR_5601	unknown	12	84/94	BAG22430
Orf-2	SSEG_08767	FeS assembly protein	17	89/96	EDY55253
Orf-3	SSEG_03816	cysteine desulfurase	46	90/94	EDY65440
Orf1	hypothetical conserved protein	unknown	66	60/69	EEL13034
Orf2	hypothetical protein SCO3803	unknown	14	78/88	NP_627922
Orf3	SSEG_08979	AraC transcriptional regulator	35	82/90	EDY56197

those found in the chlorothricin²⁸ or polyketomycin²⁹ pathways. Sequence analysis of *ssf* gene cluster revealed a likely mech-

anism of salicylate **19** synthesis from the shikimate pathway (Scheme 2), similar to that utilized in the biosynthesis of siderophores yersinobactin³⁰ and mycobactin.³¹ SsfH was found to be homologous to the salicylate synthase genes Irp³⁰ and

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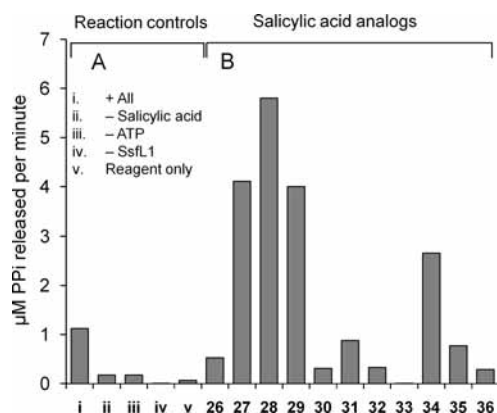
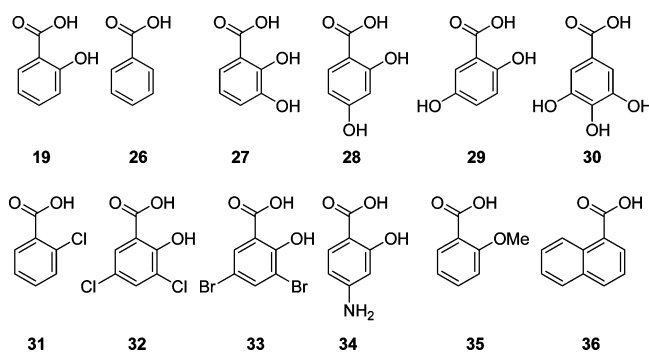


Figure 3. In vitro assay of SsfL1 activity and substrate specificity. (A) Synthesis of salicylyl-AMP as indicated by the release of PP_i in the presence of ATP, salicylate **19** and the salicylyl-CoA ligase SsfL1. (i) all reaction components; (ii) no **19**; (iii) no ATP; (iv) no SsfL1; and (v) pyrophosphate reagent only. (B) Utilization of substituted benzoic acids by SsfL1 as indicated by PP_i release assay. The structures of compounds indicated by number here are shown in Scheme 3.

Mtbl³¹ from yersinobactin and mycobactin biosynthesis respectively, which convert chorismate **18**, a byproduct of the shikimate pathway, to **19** in a two step reaction that proceeds through an isochorismate intermediate.³⁰ In addition, the *ssf* gene cluster contains *ssfI* which encodes 3-deoxy-d-arabino-heptulosonate-7-phosphate (DAHP) synthase that condenses erythrose-4-phosphate **16** and phosphoenolpyruvate **15** into DAHP **17**,³² which is the first step in the shikimate pathway. Genes encoding the remainder of the shikimate pathway that converts **17** to **18** are absent from the *ssf* gene cluster and are likely shared with the endogenous metabolism of *Streptomyces* sp. SF2575. The *ssfI* gene is therefore likely an extra copy dedicated for the biosynthesis of **1** and serves to direct carbon flow through the shikimate pathway when SF2575 biosynthesis is induced.

Genes Involved in the Transfer of Salicylate to C-4. Attachment of **19** to **6** is proposed to occur through an ATP-dependent activation of **19** to salicylyl-CoA **20** by a salicylyl-CoA ligase, and subsequent transfer catalyzed by an acyltransferase. SsfL1 has high sequence homology to NcsB2³³ and MdpB2,³⁴ which catalyze formation of the CoA-ester of naphthoic acid and 3,6-dimethylsalicylic acid in the enediyne biosynthetic pathways of neocarzinostatin and maduropeptin, respectively. To verify that SsfL1 is involved in the activation of **19**, the enzyme was expressed from *Escherichia coli* BL21(DE3) as an N-terminal hexahistidine tag fusion protein and purified using Ni-NTA chromatography (~5 mg/L, Supporting Information Figure S7). ATP and **19** were added to SsfL1 and the release of pyrophosphate (PP_i) was monitored spectrophotometrically at 340 nm using a coupled assay that oxidizes NADH. As shown in Figure 3A, significant PP_i release was observed only in the presence of SsfL1, ATP and **19**. To demonstrate the CoA ligase properties of SsfL1, enzymatic synthesis of **20** was performed by introducing CoA into the assay. After overnight incubation, a new compound consistent with the retention time of **20** was purified

Scheme 3



from the reaction mixture by HPLC and mass analysis confirmed the identity ($[M + H]^+$ at $m/z = 888$, Supporting Information Figure S8).

For the ligation of **20** to **6**, no clear enzyme candidate emerged during the bioinformatic analysis. One of the initially unassigned enzymes, SsfX3, has high sequence homology to only one enzyme from a published natural product biosynthetic pathway, which is AviX9 from the avilamycin gene cluster (56%/44% similarity/identity). However, the role of AviX9 in avilamycin biosynthesis has not been identified.³⁵ Several proteins with lower homology to SsfX3 were reported as hypothetical proteins in the GDSL lipase/acyl-hydrolase family (PF00657). Characteristic features of this class of acyltransfer enzymes are (i) the active site motif GDSL, (ii) the lack of a nucleophilic elbow formed by the GX SXG motif of typical hydrolases, and (iii) a flexible substrate binding pocket.^{36,37} Despite the low sequence homology, residues strictly conserved in this family (Ser, Gly, Asn, His)³⁶ can be predicted to be S174, G209, N236, and H338 in SsfX3. Residues which form the catalytic triad were also identified by sequence homology and are predicted to be S174, D333, and H338. Therefore, SsfX3 was considered as a potential acyltransferase that may catalyze the acyltransfer of either **20** or an activated form of angelate during the biosynthesis of **1**.

To probe the potential role of SsfX3, we first assayed the reverse hydrolysis reaction using different products. **1** was treated with purified SsfX3 overnight, and the assay mixture was analyzed by LC/MS. The result showed the presence the parent compound **1** and a second compound with mass corresponding to the loss of **19** ($[M + H]^+$ at $m/z = 658$, Supporting Information Figure S9). A control reaction without SsfX3 did not afford this compound, as determined by selected ion monitoring. The UV of this compound showed λ_{\max} of 358 nm and the loss of the shoulder at 302 nm, consistent with the hydrolysis of **19**. Despite the low conversion, this result was the first indication that SsfX3 may be involved in C-4 salicylation. To examine if the intermediate **7** may be the endogenous product of SsfX3, we repeated the same hydrolysis reaction using purified **7**. Analysis of the product mixture showed that nearly all **7** was converted to **6** in the presence of SsfX3, while no **6** was recovered in the absence of the enzyme (Supporting Information Figure S9). To confirm the SsfX3-catalyzed acyltransfer reaction, an in vitro assay was performed in which SsfX3 and SsfL1 were added to **6** with **19**, ATP, and free CoA.

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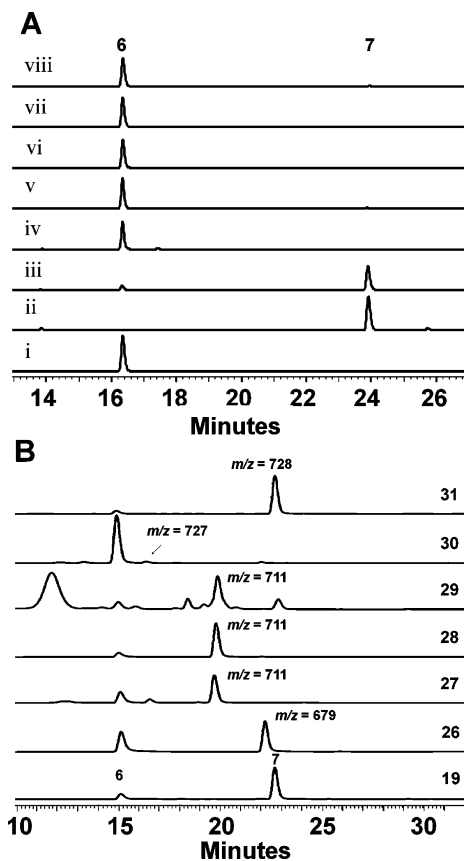


Figure 4. In vitro assay of SsfX3 activity and substrate specificity. (A) The tandem actions of SsfL1 and SsfX3 transfer **19** to the aglycon substrate **6** to yield **7**. The assays are performed in 50 mM HEPES, pH 7.9 and 10 mM MgCl₂. (i) the semisynthetic **6** standard; (ii) the semisynthetic **7** standard; (iii) Complete reaction containing 50 mM HEPES pH 7.9, 10 mM MgCl₂, 2 mM ATP, 2 mM free CoA, 2 mM **19**, 20 μM **6**, 1.5 μM SsfX3 and 15 μM SsfL1. Control reactions were performed as (iii) with the following exclusions: (iv) no SsfL1; (v) no ATP; (vi) no **19**; (vii) no SsfX3; and (viii) no CoA. The reactions were examined with HPLC (358 nm). (B) Synthesis of analogues of **7** using salicylic acid analogues, SsfL1 and SsfX3. All reactions were performed at 25 °C for 30 min, extracted with organic solvent and analyzed by LC/MS (358 nm, positive ionization).

The reaction was incubated for 30 min at room temperature and analyzed by HPLC (Figure 4A). The reaction containing all components showed nearly quantitative conversion of **6** to **7** (Figure 4A, trace iii). Omission of any of the enzyme, substrate, or cofactor component of the assay did not lead to the synthesis of **7**, as shown in Figure 4A, traces iv–viii. Together, these results confirmed that SsfX3 is responsible for the conversion of **6** to **7** using **20** as the acyl donor.

Substrate Specificity of SsfL1 and SsfX3. Exploiting the substrate tolerance of SsfX3 and SsfL1 may be useful toward diversifying the C-4 functionality of **1**. To probe this, differently substituted benzoic acids (Scheme 3) were tested for activation and acyltransfer by SsfL1 and SsfX3, respectively. Since SsfL1 is the initial gatekeeper in these reactions, the different substrates were first examined for recognition by SsfL1 using the PP_i release assay as described above (Figure 3B). Interestingly, nearly all the substrates examined showed levels of PP_i release above background (except **33**), demonstrating SsfL1 has relaxed substrate specificity. The 2-OH substituent is clearly not essential for binding, as benzoic acid **26**, 2-chlorobenzoic acid **31** and 2-methoxy benzoic acid **35** all supported similar rates of pyrophosphate release. Surprisingly, three dihydroxybenzoic

acids (**27–29**), as well as 4-aminosalicylic acid **34** were significantly better substrates than **19**, indicating substantial plasticity in the binding pocket of SsfL1.

Acyltransferases from the GSDL family are often found to have broad substrate specificity, which is proposed to be the result of a flexible substrate binding pocket.³⁶ Therefore, SsfX3 may be similarly tolerant and use different aryl-CoAs as substrates. Given nearly all substrates shown in Scheme 3 can be activated by SsfL1, we tested whether new variants of **7** can be synthesized in a coupled assay using both SsfL1 and SsfX3. To do so, 2 mM of each analogue was combined with SsfL1 (15 μM), and SsfX3 (1.5 μM) in an in vitro assay containing 2 mM free CoA, 2 mM ATP, 10 mM MgCl₂, and 20 μM **6** in 50 mM HEPES buffer pH 7.9. The reaction was incubated at room temperature for 30 min and analyzed by LC/MS for emergence of analogues of **7** (Figure 4B). The CoA-activated forms of the dihydroxybenzoic acids **27–29** were readily recognized by SsfX3 and led to the synthesis of new analogues of **7**. This demonstrates that the additional hydroxyl group is well tolerated at all three positions and this finding may be used to produce more hydrophilic derivatives of **1**. However, the trihydroxybenzoic acid **30**, which was a poor substrate in the SsfL1 activation assay, only afforded trace amounts of the adduct in the coupled assay as revealed by selected ion monitoring. The coupled assay also reveals SsfL1 and SsfX3 have significant differences in substrate tolerance. Whereas **34** and **35** were each well-activated by SsfL1, neither compound was transacylated to **6** by SsfX3. To test if SsfX3 can accept membrane permeable aryl thioesters, we mixed benzoyl-*S*-*N*-acetylcysteamine (benzoyl-SNAC) with **6** and SsfX3. The resulting extract showed that the C-4 benzoyl analogue of **7** was synthesized in similar yield as that using **26** and CoA in the coupled-enzyme system. This demonstrated SsfX3 also has relaxed substrate tolerance toward the acyl carrier. Taken together, these results indicate SsfL1 and SsfX3 are attractive enzymes in the biocatalytic synthesis of analogues of **1** for structural-activity relationship studies. Mutasynthesis of **1** containing different substituents at C-4 may also be accomplished by inactivating the endogenous salicylic biosynthetic pathways, such as deletion of *ssfH*.

Genes Putatively Involved in the Biosynthesis of Angelyl-CoA **25.** Little has been reported on the biosynthesis of angelic acid among bacterial natural products. Angelate is commonly found to be associated with plant metabolites and is biosynthesized from the isoleucine catabolic pathway.^{38,39} No genes were found in the *ssf* cluster that indicate a plant-like pathway for this unusual substitution in **1**. Instead, a set of genes encoding enzymes involved in the formation and tailoring of a short-chain acyl group was found. These genes include SsfE (carboxyltransferase), SsfJ (enoyl-CoA hydratase/isomerase), SsfN (KSIII), and SsfK (3-ketoacyl-ACP reductase). These genes resemble those found in fatty acid biosynthesis and may be responsible for synthesizing angelyl-CoA **25** from a propionyl-CoA **21**, or other short-chain acyl building blocks. One possible pathway is shown in Scheme 2.

SsfE contains a carboxyltransferase domain (PF01039) and is homologous to biotin-dependent methylmalonyl-CoA decarboxylase and propionyl-CoA carboxylase. Several of these homologues are present in polyketide gene clusters such as

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chlorothricin²⁸ (ChlJ), jadomycin⁴⁰ (JadN), simocyclinone²⁴ (SimA12), medermycin⁴¹ (med-ORF22), and others. One possible role for SsfE is to synthesize methylmalonyl-CoA **22** from **21**. The next set of steps in the biosynthesis of **25** are proposed to be catalyzed by *ssfK*, *ssfN*, and *ssfJ*, which are cotranscribed as a tricistronic cassette on the same operon. SsfN is homologous to KS III enzymes such as FabH, which catalyzes the condensation between acetyl-CoA and malonyl-ACP to initiate fatty acid biosynthesis.⁴² FabH homologues have been found in a number of polyketide gene clusters such as in R1128,⁴³ frenolicin,⁴³ and daunorubicin⁴⁴ to catalyze the decarboxylative condensation of short acyl groups. SsfN may therefore catalyze the condensation of **22** with acetyl-CoA to form 2-methyl-acetoacetyl-CoA **23**. β -Ketoreduction of **23** catalyzed by SsfK, which is homologous to 3-oxoacyl-ACP reductases such as FabG,⁴⁵ yields 3-hydroxyl-2-methyl-butyryl-CoA **24**. Stereospecific dehydration of **24** by SsfJ, which is a member of the enoyl-CoA hydratase/isomerase family (PF00378), results in **25**. As an alternative start to this pathway, SsfN may directly condense malonyl-CoA with acetyl-CoA to form acetoacetyl-CoA. The α -methyl group may then be incorporated by SsfM3, which is homologous to C-methyltransferases, to afford **23**.

Transfer of **25** to **7** is predicted to be catalyzed by an acyltransferase using similar mechanisms as for other acylated deoxysugars present in chromomycin⁴⁶ or mannopeptimycin.⁴⁷ Those belong to a large acyltransferase family (PF01757) that contains proteins with *O*-acyltransferase activity, including the deoxyhexose *O*-acyltransferases MdmB.⁴⁸ Unexpectedly, no similar acyltransferase is present in the *ssf* gene cluster. One acyltransferase homologue, SsfV, however, remains unassigned. SsfV has homologues in many type II polyketide gene clusters including OxyP from the *oxy* pathway and ZhuC from the R1128 pathway. A Pfam homology search revealed that it contains an acyltransferase domain (PF00698) from a family of proteins that includes bacterial malonyl-CoA-ACP transacylase (MAT). In vitro experiments with homologue ZhuC showed that it did indeed have malonyl-CoA ACP transacylase activity, however it was much slower than endogenous MAT from the fatty acid biosynthetic pathway.^{49,50} Additional in vitro studies demonstrated that ZhuC could efficiently hydrolyze acetyl and propionyl primed ACPs and therefore acts to ensure that the R1128 PKS is primed with the correct medium chain length acyl-ACPs.⁵⁰ Similarly, SsfV may be involved in ensuring the biosynthesis of **1** is initiated with malonamyl starter unit and is hence unlikely to be involved in angelate attachment.

The *ssf* gene cluster encodes another KS III homologue SsfG, which resembles ChlB3 and ChlB6 from the chlorothricin

biosynthetic cluster.²⁸ The role of these genes in the processing and attachment of the 5-chloro-6-methyl-*O*-methylsalicylic acid during chlorothricin biosynthesis has recently been published.⁵¹ ChlB3 is utilized to transfer 6-methylsalicylic acid from the type I PKS ChlB1 to a discrete ACP for further tailoring. ChlB6 is shown to transfer the tailored 5-chloro-6-methyl-*O*-methylsalicylic acid to D-olivose of desmethylsalicyl chlorothricin to form chlorothricin.⁵¹ Considering SsfG displays high sequence similarity to ChlB6 (52%) and the same deoxysugar substrate D-olivose is involved, SsfG therefore likely catalyzes the attachment of angelate in the *ssf* pathway. Instead of using a discrete ACP as the acyl carrier, the CoA-activated angelate **25** may directly serve as the substrate of SsfG.

Genes Encoding Enzymes That Synthesize the Polyketide Backbone 40. The *ssf* minimal PKS consists of SsfA (KS α), SsfB (KS β or CLF), and SsfC (ACP) that are highly homologous to the *oxy* minimal PKS.¹⁸ The amidotransferase SsfD, which is responsible for producing the malonamate starter unit unique to tetracyclines, is found adjacent to the *ssf* minimal PKS. The C-2 amidated starter unit is one of the signature moieties of tetracyclines, and the revelation of SsfD as an OxyD homologue with 68% sequence identity was one of the earliest convincing pieces of evidence that this gene cluster indeed encodes a tetracycline compound. Like OxyD, SsfD is highly similar to class II asparagine synthases that utilize ATP to convert aspartate to asparagine using glutamine as the nitrogen source.⁵² Zhang and co-workers demonstrated that the “extended minimal PKS”, which includes OxyABCD, is sufficient for producing the amidated polyketide chain **38**.¹⁸ In addition, SsfU, which is 76% identical to OxyJ, is predicted to be the C-8 (or C-9* using biosynthetic carbon numbering as shown in Scheme 4) ketoreductase that regioselectively reduces the nascent backbone to yield **40**.²⁰

To verify the function of the *ssf* minimal PKS, genes encoding SsfA, SsfB and SsfC, SsfD, and SsfU were placed into a pRM5-derived *Streptomyces*–*E. coli* shuttle vector⁵³ (Table 2). Shuttle plasmid pLP27 was subsequently transformed into *S. lividans* strain K4-114.⁵⁴ The resulting organic extract was analyzed by HPLC and is shown in Figure 5A. The product profile of K4-114/pLP27 was indistinguishable from that of K4-114/pWJ35, which contained the corresponding enzymes from the *oxy* biosynthetic pathway.¹⁸ By comparison to an authentic standard, the major product of the extract (RT = 13.5 min) was confirmed to be the isoquinolone **42** (20 mg/L), which can form via the spontaneous cyclization of the C-9* reduced amidated polyketide **40**.¹⁸ We further investigated whether the *oxy* and *ssf* extended minimal PKS components are functionally interchangeable. Three additional shuttle vectors were prepared with a combination of *oxy* and *ssf* genes as shown in Table 2 and transformed into K4-114. Each of these host/vector combinations was capable of producing **42** in similar quantities as K4-114/pLP27, indicating that each of the *ssf* components is functionally compatible and equivalent to its *oxy* counterpart. These results confirm (i) the extended *ssf* minimal PKS (SsfABCD) is capable of synthesizing the full length amidated polyketide precursor **38**, (ii) the hypothesis that the carbon backbone of **1** is

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Scheme 4

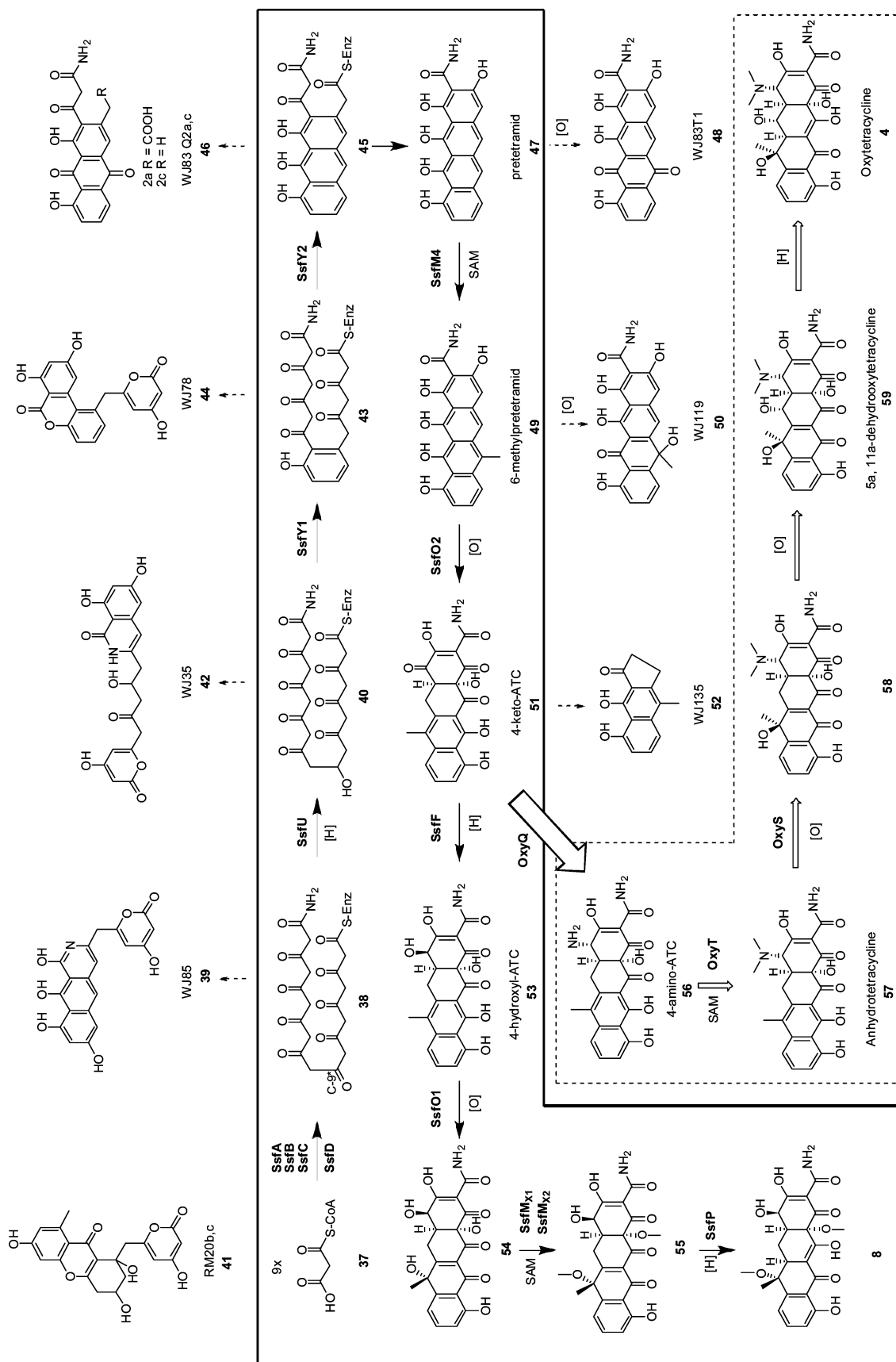


Table 2. Plasmids and Major Metabolites Produced by *S. lividans* K4-114 Transformed with Each Plasmid

plasmid	<i>ssf</i> genes	<i>oxy</i> genes	major products
pLP24	<i>ssfD</i>	<i>oxyABCJ</i>	41,42
pLP25	<i>ssfDC</i>	<i>oxyABJ</i>	41,42
pLP26	<i>ssfABD</i>	<i>oxyCJ</i>	41,42
pLP27	<i>ssfABCDU</i>		41,42
pLP27/pLP77	<i>ssfABCDUYI</i>		44
pLP27/pLP113	<i>ssfABCDUYIY2M4</i>		46
pLP27/pLP115	<i>ssfABCDUYIY2M4Y4</i>		46
pLP27/pLP118	<i>ssfABCDUYIY2M4Y4Y3</i>		46
PLP27/pLP126	<i>ssfABCDUYIY2M4L2</i>		50
pLP36	<i>ssfO2</i>	<i>oxyABCDJKNF</i>	52
pLP75	<i>ssfO2</i>	<i>oxyABCDJKNFQT</i>	57

biosynthesized via a tetracycline-like pathway, and (iii) SsfU as the C-9* KR that affords **40**. Also detected from these extracts was the acetate-primed product RM20b **41** (RT = 17.7 min), consistent with the previous report of *oxy* minimal PKS being able to initiate polyketide biosynthesis with the acetate starter unit.⁵⁵

Genes Encoding Enzymes That Synthesize 6-Methylpretetramid 49. Sequential cyclizations of the four rings are the next steps following biosynthesis of the full length polyketide chain. In the *oxy* cluster three cyclases were identified on the basis of sequence homology; however, only two were shown to be required to yield the intermediate pretetramid **47**.²⁰ Diverging from the *oxy* cluster, the *ssf* gene cluster contains four genes that have homology to cyclases. SsfY1 is highly similar to OxyK

(67% sequence similarity) and is predicted to be responsible for D ring cyclization to afford **43**. SsfY4 is similar to OxyI, itself similar to fourth ring cyclase MtmX from the mithramycin pathway. However OxyI was found to be unnecessary in the biosynthesis of **47**.²⁰ Although SsfY2 has low sequence homology (25% similarity and 14.5% identity) to the second ring cyclase (OxyN) from the *oxy* pathway, it displays stronger homology to second ring cyclases from benzoisochromanquinone (BIQ) pathways such as granaticin (68% similarity, 56% identity)⁵⁶ and medermycin (66% similarity, 55% identity).⁴¹ SsfY2 is therefore predicted to be the second ring cyclase in the *ssf* pathway. Intriguingly, an additional cyclase, SsfY3, also displays sequence similarity to first ring cyclase/aromatases, with 42% similarity to CmmQ⁴⁶ and 39% similarity to OxyK. Completion of the biosynthesis of **49** requires C-6 methylation of **47**, which is catalyzed by the OxyF homologue SsfM4.

To deduce the role, or lack thereof, of each of these cyclases in the biosynthesis of **49**, we heterologously expressed different combinations of cyclases found in the *ssf* gene cluster with SsfABCDU. We first constructed a pSET152-derived integrating vector⁵⁷ containing *ssfY1* and cotransformed the resulting plasmid pLP77 with pLP27 into K4-114. We detected the complete disappearance of **42** in the extract and emergence of a single major product that corresponds to the benzopyrone WJ78 **44** (Figure 5B), which is the shunt product of the amidated polyketide intermediate **43** that has been regioselectively cyclized at the D ring.⁵⁸ Cotransformation of K4-114 with pLP27 and an integrating vector containing *ssfY3*, did not lead to the recovery of **44**, indicating SsfY3 cannot substitute for SsfY1 and likely serves a different role in the biosynthesis of **1**.

We next set out to reconstitute the biosynthesis of **49** in K4-114 using entirely *ssf* genes. SsfM4 was chosen to be the likely C-6 methyltransferase because of its high sequence homology to OxyF. The integrating vector pLP113 bearing *ssfY1Y2M4* was cotransformed with pLP27 and resulting extract was intensely yellow and contained the anthraquinone carboxylic acid WJ83Q2a **46**. This confirmed SsfY2 was responsible for the cyclization of the second (or C) ring, while the third ring is likely spontaneously cyclized. However, to our surprise, the expected tetracyclic product **49**, which can be isolated in the oxidized form WJ119 **50**, was not found. This observation is different from what was observed for the *oxy* pathway, in which the equivalent set of *oxy* enzymes yielded **50**.²⁰ To determine if the *ssf* pathway requires the additional cyclases found in its gene cluster toward the formation of **47**, pLP115 and pLP118 were constructed, which contained in addition to genes encoded in pLP113, *ssfY4*, and *ssfY3Y4*, respectively. K4-114 cotransformed with pLP27, and these constructs continued to produce **46** only, suggesting that for the *ssf* pathway, different enzyme(s) may be needed to facilitate cyclization of the fourth ring. We tested this possibility by inserting additional *ssf* genes juxtaposed to the *ssf* cyclase genes in the cluster into K4-114 and examined the metabolic profiles. Fortunately, upon insertion of *ssfL2* into pLP113 to afford pLP126, and cotransformation of pLP27 and

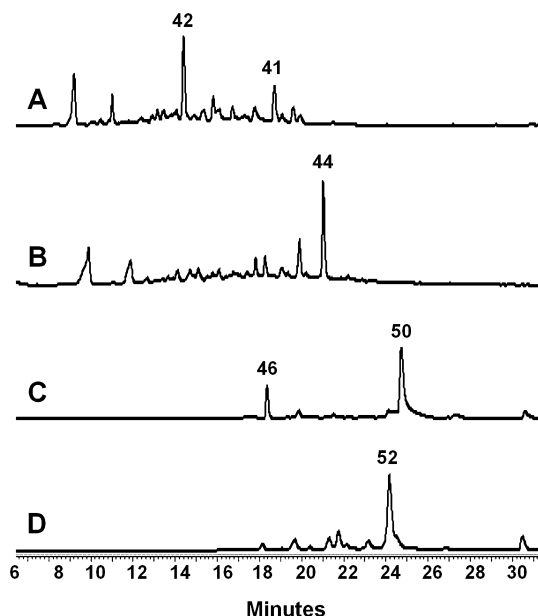


Figure 5. Reconstitution of tetracycline intermediates using *ssf* genes expressed in *S. lividans* K4-114. (A) HPLC analysis (245 nm) of the K4-114/pLP27 extract shows the amidated, reduced polyketide **42** is the major product, confirming the biosynthesis of the polyketide backbone **40** by SsfABCD and the subsequent C-9* reduction by SsfU. (B) HPLC analysis (253 nm) of the K4-114/pLP27/pLP77 extract shows addition of the putative cyclase SsfY1 leads to complete cyclization and aromatization of the D and formation of the shunt benzopyrone **44**. (C) HPLC analysis (430 nm) of K4-114/pLP27/pLP126 extract shows **50**, the oxidized form of **49**, as the dominant product. Biosynthesis of **49** using entirely *ssf* genes (SsfABCDUYIY2M4L2) indicates the tetracycline nature of the *ssf* biosynthetic pathway. (D) HPLC analysis (395 nm) of K4-114/pLP36 extract confirms the function of SsfO2 as the oxygenase that dihydroxylated C-4 and C-12a of **49**. The resulting product **51** undergoes spontaneous degradation to afford the observed product **52**.

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pLP126 into K4-114, the formation of **50** was detected as shown in Figure 5C. SsfL2 has homology to long-chain fatty acyl-CoA ligases as well as putative acyl-CoA ligases from several aromatic polyketide pathways such as CmmLII from the chromomycin gene cluster,⁴⁶ PokL from the polyketomycin gene cluster,²⁹ MtmL from the mithramycin gene cluster,⁵⁹ as well as OxyH.¹⁸ The role of these enzymes in their respective biosynthetic pathways has not been determined and has been suggested to function as an accessory protein.⁴⁶ Interestingly, biosyntheses of these compounds all require the equivalent Claisen cyclization of the A rings. The mechanism of SsfL2 in the heterologous biosynthesis of **49** with *ssf* PKS components is yet to be determined.

Tailoring Enzymes Putatively Involved in the Production of the Aglycon 8. During biosynthesis of **4**, the ring A of **49** is doubly hydroxylated by OxyL at C-12a and C-4 to produce the cyclohexenone-containing **51**, which is unstable and degrades into observed product WJ135 **52**.¹⁹ SsfO2, which is found at the boundary of the *ssf* gene cluster, is an OxyL homologue, and is most likely to perform this role in the *ssf* pathway. Compound **51** is likely the last common intermediate between the *oxy* and the *ssf* biosynthetic pathways. In the *oxy* pathway, reductive amination of the C-4 ketone group by OxyQ to yield 4-amino-ATC **56** and subsequent dimethylation by OxyT afford the stable intermediate anhydrotetracycline **57**.¹⁹ The C-4 position in **1** lacks the dimethylamino group and is instead acylated with a salicylic acid group. This requires ketoreduction of **51** at C-4 to produce 4-hydroxyl-ATC **53** for the downstream silylation reaction.

To determine whether this hydroxyl is directly installed by SsfO2 or whether an additional ketoreduction is required, the *oxyL* gene was replaced with *ssfO2* in the shuttle plasmid pWJ135, which contains all the *oxy* genes required to synthesize **51** (Table 2).¹⁹ K4-114 transformed with the resulting plasmid pLP36 produced the tricyclic ketone **52** (Figure 5D), which is a spontaneously degraded product of **51** as observed previously.¹⁹ To further confirm that the product of SsfO2 contains the C-4 ketone functionality as in **51**, we examined if SsfO2 can complement the role of OxyL in the biosynthesis of **57**, which requires reductive amination of the C-4 ketone in **51**. The genes *oxyQ* and *oxyT* were introduced to pLP36 to afford pLP75 (Table 2). As expected, K4-114/pLP75 produced ~10 mg/L of **57** as the dominant product, demonstrating that OxyL and SsfL2 catalyze the identical transformation of **49** to **51**. These results support the proposal that a dedicated C-4 ketoreductase is required to reduce **51** to **53**. SsfF is a ketoreductase with sequence homology to NADPH-dependent oxidoreductases with specificity for aromatic and nonpolar substrates (PF00248) and is therefore assigned as a candidate to catalyze this step.

The last tailoring enzyme in the *ssf* pathway that shares resemblances to enzymes found in *oxy* pathway is SsfO1 which has 54% similarity to OxyS. OxyS is known to be responsible for the C-6 hydroxylation of **57** to form 5a,11a-dehydrotetracycline **58**,^{60,61} and SsfO1, therefore, likely plays the parallel role to oxidize the aromatic C-ring in **53** to **54**. SsfO1, however, most likely catalyzes the C-6 hydroxylation with stereochemistry

opposite that of OxyS, based on X-ray crystallographic structure of **1**.⁸ Two *O*-methyltransferases are then needed to methylate the C-6 and the C-12a hydroxyl groups. Three methyltransferases (other than the C-6 methyltransferase SsfM4) are present in the *ssf* gene cluster. SsfM1 and SsfM2 bear strong resemblance to *O*-methyltransferases, while SsfM3 is similar to both *O*-methyltransferases and *C*-methyltransferases. The C12a-OH methylation modification can take place either prior to SsfO1 oxidation (using either **51** or **53** as substrate) or after C-6 oxidation (as shown in Scheme 4). The gene encoding SsfM2 is transcribed from the same operon that encodes *ssfO1* and is therefore the likely C-6 *O*-methyltransferase. In the same operon is the gene *ssfQ*, which encodes an *S*-adenosylmethionine (SAM) synthases and likely serves in an auxiliary role to produce sufficient SAM for the methyltransfer reactions. It is known that 6-deoxy analogues of tetracyclines, such as doxycycline, have enhanced stability toward acid and base degradation.⁶² The C-6-OH methylation may have a similar stabilizing effect on **1**. Once identified, the C-6 *O*-methyltransferase may potentially be useful to generate C-6-methoxytetracycline analogues that have enhanced stability.

The last step in the biosynthesis of **4** is the reduction of 5a,11a-dehydroxytetracycline **59** to **4**. This reductive modification required for the biosynthesis of **4** and **5** has been postulated to involve a gene located outside their respective gene clusters.⁶³ The *tchA* gene encodes a flavin-dependent oxidoreductase with reported cofactor 7,8-didemethyl-8-hydroxy-5-deazariboflavin (FO) and has been identified in *S. aureofaciens* to be involved for the biosynthesis of **5**.⁶⁴ An identical reduction step is also needed to complete the biosynthesis of aglycon **8** from, for example, **55**. One candidate for this reaction in the *ssf* gene cluster is a putative dehydrogenase SsfP. SsfP shares 54% sequence similarity to a putative F420-dependent methylenetetrahydromethanopterin reductase, but shares no sequence resemblance to TchA. Experimental evidence will be needed to determine if this reduction step is catalyzed by an enzyme encoded in the *ssf* gene cluster such as SsfP or if an external gene is required as in chlorotetracycline biosynthesis.

Genes Encoding Regulatory and Resistance Determinants.

The *ssf* gene cluster encodes two regulatory proteins, SsfT1 and SsfT2, and a resistance protein SsfR. SsfT2 is predicted to be a TetR family⁶⁵ repressor protein with a DNA-binding helix–turn–helix motif at the N-terminus. SsfR is an efflux protein from the major facilitator superfamily (MFS) class of ATP-independent transporters which utilizes a chemiosmotic gradient to transport small molecules (PF07690).⁶⁶ The *SsfT2* gene is located directly adjacent to *ssfR* with opposite polarity. Therefore the transcription of *ssfR* may be controlled by SsfT2 in a similar fashion as the TetR/TetA pair.⁶⁵ The second regulatory protein SsfT1 is a positive regulator in the *ssf* gene cluster, and is predicted to be a member of the pathway-specific

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Streptomyces antibiotic regulatory protein (SARP) family of transcriptional activators.⁶⁷ These activators have been the subject of metabolic engineering efforts as evidenced by the recent publication on the fredericamycin pathway which demonstrated a greater than 5 fold increase in antibiotic yield by overexpression of FdmR1.⁶⁸

Conclusions

We have identified the *ssf* biosynthetic gene cluster and biochemically characterized key steps in the biosynthesis of **1**. Biosynthesis of **1** from the aglycon **8** requires a new set of tetracycline-tailoring enzymes including the C-9 glycosyltransferase SsfS6 and the C-4 salicylyl transferase SsfX3. In vitro assays with SsfL1 and SsfX3 have shown that both enzymes have relaxed substrate flexibility toward different aromatic substrates, a feature that was exploited in the chemoenzymatic synthesis of several analogues of **7**. Using heterologous biosynthesis we have also verified the tetracycline nature of the gene cluster by reconstituting the biosynthesis of key intermediates. The identification of the *ssf* gene cluster and formulation of a putative biosynthetic pathway will therefore enable engineered biosynthesis of new tetracycline analogues.

Materials and Methods

Bacterial Strains and DNA Manipulation. *Streptomyces* sp. SF2575 was obtained from Meiji Co. *E. coli* XL-1 Blue (Stratagene) was used for the manipulation of plasmid DNA. *E. coli* strain BL21(DE3) was used for protein expression. Fosmids 11A12 and 5F15 were used as templates to amplify DNA by PCR. PCR fragments were cloned into pCR-Blunt vector obtained from Invitrogen and sequenced (Laragen). All restriction enzymes were purchased from New England Biolabs. PCR reagents for *pfx* DNA polymerase were purchased from Invitrogen. PCR Primers are listed in Supporting Information, Table S1. *S. lividans* strain K4-114⁵⁴ was used as a host for the transformation of shuttle vector constructs containing *ssf* genes. Protoplast preparation and PEG-mediated DNA transformation techniques were performed as published by Hopwood et al.⁶⁹

Spectroscopic Analysis. NMR of compounds was obtained on a Bruker ARX400 at the University of California Department of Chemistry and Biochemistry NMR facility. Accurate high resolution mass spectrometry was performed at the University of California Riverside Mass Spectrometry Facility. HPLC spectra were obtained on a Beckman Gold HPLC using a reverse-phase C18 column (Alltech Apollo C18 5 μ m column; 250 mm \times 4.6 mm) and a linear gradient of 5% CH₃CN in water (0.1% trifluoroacetic acid [TFA]) to 95% CH₃CN in water (0.1% TFA) in 30 min at a flow rate of 1 mL/min. LC/MS spectra were obtained on a Shimadzu 2010 EV liquid chromatography mass spectrometer using positive and negative electrospray ionization and a Phenomenex Luna 5 μ m, 2.0 mm \times 100 mm C18 reverse-phase column. Samples were separated on a linear gradient of 5 to 95% CH₃CN in water (0.1% formic acid) for 30 min at a flow rate of 0.1 mL/min unless otherwise noted.

Cultivation of *Streptomyces* sp. SF2575 and Purification of **1.** *Streptomyces* sp. SF2575 was cultured in R5 media for subculture and seed culture. Modified Bennett's agar (per 1 L, beef extract 1 g, bacto-peptone 2 g, yeast extract 1 g, glucose 10 g, agar 20 g) was used as a production media. For isolation of **1**, *Streptomyces* sp. SF2575 was precultured in 50 mL of R5 liquid media in a 250

mL baffled Erlenmeyer flask at 30 °C and 250 rpm for 3 days. One milliliter of precultures were inoculated on plates (4 L) of modified Bennett's agar in 150 mm \times 10 mm Petri dishes and incubated at 30 °C for 8 days. The cultured agar was harvested and extracted with the same volume of ethyl acetate twice. Organic solvent was dried *in vacuo* to obtain 875.2 mg of oily crude extract. The crude extract was fractionated with an open silica column (200–430 mesh, 50 mm Φ \times 300 mm) using a methanol and chloroform gradient. Fractions containing **1** were collected and purified by preparative HPLC to obtain 22 mg of **1**. HPLC purification was performed using an HPLC Alltech Alltima reverse-phase column (5 μ m, 10 mm \times 250 mm) with an isocratic gradient of 75% CH₃CN in water (0.1% TFA).

Preparation of Authentic Standards **6 and **7**.** **7** was prepared by a 2-h incubation of a 10 mg/mL solution of **1** with 0.5 M NaOH. Complete conversion of **1** to **6** was obtained by incubation of a 10 mg/mL solution of **1** in 1.0 M NaOH for 15 h. To isolate **6** and **7**, the reaction mixture for each was adjusted to pH 7 by addition of HCl, and the products were extracted with ethyl acetate/acetic acid (99%/1%). Following the evaporation of the solvent, the product was resuspended in methanol and purified by HPLC (Alltech Alltima reverse-phase column 5 μ m, 10 mm \times 250 mm) with an isocratic gradient of 78% CH₃CN in water (0.1% TFA). Purified **6** and **7** were characterized by LC/MS, HRMS, and proton NMR (see Supporting Information).

Bioactivity Assays. Cell proliferation was determined by (3-(4,5-dimethylthiazol-2-yl)-5-(3-carboxymethoxyphenyl)-2-(4-sulphophenyl)-2H-tetrazolium) (MTS) assay for adherent HeLa, MCF-7, and M249 cells. Five thousand cells per well (4000 HeLa) were plated in 100 μ L media in a 96-well plate and allowed to incubate for 18 h. Following incubation, 10 mM stock solution of **1**, **6**, or **7** solubilized in DMSO was added to media to prepare dilutions containing three times the final concentration. Fifty microliters of the appropriate dilution was added to each well. Cell proliferation was assayed 72 h after treatment using CellTiter 96 Aqueous OneSolution cell proliferation assay reagent (Promega). Direct cell counting was used for Nalm-6 suspension cells by Vi-CELL analyzer (Beckman). In a 24-well plate were plated 400 μ L cells (500,000 cells/mL). After 20 h 400 μ L of media containing twice the desired final drug concentration was added. Cells were analyzed 72 h after treatment. All cells were cultured according to ATCC or DSMZ guidelines. Prism (GraphPad) was used for analysis.

Identification and Sequencing of the *ssf* Gene Cluster. A fosmid library containing *Streptomyces* sp. SF2575 genomic DNA was prepared using the CopyControl Fosmid library production kit from Epicenter. Fosmids were screened using degenerate primers for the KS α gene as reported by Wawrik et al.²¹ Fosmids 5F15, 11A12 and 19B2 were sequenced by a combination of shotgun sequencing and primer walking. ORFs were identified using Frameplot software (<http://www.nih.go.jp/~jun/cgi-bin/frameplot.pl>), and functions of the encoded proteins were assigned by sequence similarity using NCBI protein–protein BLAST. Pfam protein family database was also used to identify functional domains.⁷⁰ The sequence has been deposited in the GenBank database under accession number GQ409537.

Inactivation of *ssfB* gene. For *ssfB* (CLF) disruption, approximately 1 kb of the 5' region of *ssfB* gene was amplified from genomic DNA of *Streptomyces* sp. SF2575 by PCR using a forward primer KS2-LEK-S which introduces an *EcoRI* site, and a reverse primer KS2-LEK-A2 which introduces a *KpnI* site. The PCR product obtained was cloned into pCR-Blunt vector to produce pCR-KSII-LEK. Approximately 1 kb of the 3' region of *ssfB* was also amplified by PCR using primer set KS2-RPH-S and KS2-RPH-A to add *PstI* and *HindIII* site to its 5' and 3' ends, respectively. The PCR product obtained was cloned to produce pCR-KSII-RPH. The

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1.1 kb of *aphII* gene was obtained from pFD-neoS plasmid.⁷¹ Plasmid pCR-KSII-LEK was digested with *EcoRI* and *KpnI*; plasmid pCR-KSII-RPH was digested with *PstI* and *HindIII*. Fragments were ligated together with *KpnI-PstI* digested *aphII* gene into plasmid pKC1139 digested with *EcoRI* and *HindIII* to produce about 9.5 kb of pKC-SF2-KSII. The construct was delivered into *Streptomyces* sp. SF2575 by conjugation with *E. coli* ET12567-(pUZ8002). Intergeneric conjugation between *E. coli* and *Streptomyces* was performed as described previously with minor modification.⁵⁷ The transformant was resistant to both apramycin and kanamycin and was grown in fresh R2YE/kanamycin liquid medium at 37 °C for 1–2 days in order to force chromosomal integration of the gene-disruption constructs. The resulting disruption mutant (*Streptomyces* sp. SF2575 Δ *ssfB*) was selected on kanamycin-containing plates. Gene disruption in *Streptomyces* sp. SF2575 Δ *ssfB* was confirmed by PCR of total genomic DNA. *Streptomyces* sp. SF2575 Δ *ssfB* did not produce SF2575 or intermediates when grown on Bennett's plates as confirmed by LC/MS analysis.

Expression and Purification of Recombinant Enzymes. SsfX3 and SsfL1 were cloned into a pET28 vector with an *N*-terminal His tag and expressed in *E. coli* BL21(DE3) strain. For each enzyme, a 5 mL overnight culture of BL21(DE3) transformed with expression plasmid was grown in LB medium containing 35 mg/L kanamycin. This overnight culture was used to inoculate a 500 mL flask of LB containing 35 mg/L kanamycin. Cultures were grown at 37 °C until OD₆₀₀ of 0.5 at which point IPTG was added to a final concentration of 120 μ M to induce protein expression. The induced cultures were further shaken overnight at 16 °C.

Protein purification was carried out at 4 °C. Cell pellets were resuspended in Buffer A (50 mM Tris-HCl, pH 7.9, 10 mM imidazole and 50 mM NaCl). Cell membranes were disrupted by sonication. Cell lysate was centrifuged at 16,000 rpm, and the soluble fraction was collected and incubated with Ni-NTA resin (Qiagen) for 2 h with gentle rotation. Protein–resin mixture was added to a gravity flow column, and buffers containing increasing step gradients of imidazole were applied. The target proteins were eluted in Buffer A containing 250 mM imidazole. A 30 kDa MWCO Amicon filtration column (Millipore) was used for buffer exchange and concentration of the protein solution. Purified enzymes were stored in Buffer B (50 mM Tris-HCl pH 7.9, 2 mM EDTA, 2 mM DTT). Proteins were aliquoted, flash frozen on dry ice, and stored at –80 °C. Protein concentrations were measured by Bradford assay using bovine serum albumin (BSA) as a standard.⁷²

In Vitro Assay. PP₁ assay reagent was purchased from Sigma (P7275) and was performed according to manufacturer instructions. Typical reaction mix includes: 33% PP₁ reagent, 100 mM Tris-HCl pH 7.5, 2 mM ATP, 2 mM salicylic acid and 10 μ M SsfL1. Reaction progress was monitored at 340 nm using a BioTek PowerWave XS plate reader for 30 min at room temperature. All in vitro assays containing SsfX3 were performed with the following conditions unless otherwise specified: 50 mM HEPES pH 7.9, 10 mM MgCl₂, 2 mM ATP, 2 mM free CoA, 2 mM salicylic acid, 20 μ M **6**, 1.5 μ M SsfX3 and 15 μ M SsfL1. Reaction mixture was incubated at room temperature for 30 min. A 100 μ L reaction volume was extracted with 200 μ L acetonitrile (1% acetic acid). Organic phase was then removed, and solvent was evaporated *in vacuo*. Samples were then resuspended in 30 μ L methanol and analyzed by HPLC or LC/MS as described in Spectroscopic Analysis.

Heterologous Biosynthesis of Polyketides Using *S. lividans*. *S. lividans* K4-114 strain⁵⁴ transformed with different constructs shown in Table 2 were grown on R5 agar plus 50 μ g/mL thiostrepton. Cultures were grown at 30 °C for approximately one week until colonies were well formed. For HPLC analysis, colonies were streaked out on 40 mL of fresh R5 agar (plus 50 μ g/mL thiostrepton) and incubated for 7–10 days until the plate was well pigmented. The agar was then finely chopped and extracted with 40 mL of organic solvent (99% ethyl acetate, 1% acetic acid). Sodium sulfate was added to the extract to remove residual water, the solvent was evaporated, and the products were resuspended in 400 μ L DMSO. The extracts were analyzed by reverse-phase HPLC. Compounds were identified by matching retention time and UV spectra to those of authentic standards.

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Supporting Information Available: Additional experimental procedures and compound characterizations. This material is available free of charge via the Internet at <http://pubs.acs.org>.

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