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Bifunctional Acyltransferase/Decarboxylase LnmK as the Missing Link for β -Alkylation in Polyketide Biosynthesis

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Both α - and β -alkylations contribute to the vast structural diversity displayed by polyketide natural products (Figure 1A).¹ While the α -alkyl branches are typically derived from extender units, the choice of which is dictated by the acyltransferase (AT) domain of modular polyketide synthases (PKSs),¹ the β -alkyl branches often result from the activities of hydroxymethylglutaryl-CoA (HMG-CoA) synthase homologues (HCSs).² For a β -methyl branch, HCS catalyzes condensation of acetyl-S-acyl carrier protein (acetyl-S-ACP) with the β -carbonyl group of the PKS-ACPtethered growing polyketide intermediate to afford an HMG-S-ACP intermediate, which is subsequently dehydrated and decarboxylated by two enoyl-CoA hydratase homologues (ECH1 and ECH2) sequentially to afford a β -methylated intermediate in either olefinic form (Figure 1B). This pathway has been experimentally confirmed in the biosynthesis of bacillaene (1),³ curacin (2),⁴ and myxovirescin A (also known as TA) (3)⁵ and a dedicated set of three proteins—an ACP, an AT, and a ketosynthase homologue (KS)-that derives acetyl-S-ACP from malonyl-CoA for this pathway has been identified (Figure 1C).2-5

A parallel pathway replacing acetyl-S-ACP with propionyl-S-ACP could be envisaged for introduction of a β -ethyl branch, and this proposal has been supported for 3 using chemoenzymatically prepared propionyl-S-ACP as a substrate (Figure 1B).^{5b} However, counterparts for propionyl-S-ACP biosynthesis from methylmalonyl-CoA, such as the AT and KS enzymes required to generate acetyl-S-ACP from malonyl-CoA, are absent from gene clusters known to encode biosynthesis of polyketides with β -ethyl branches (Table 1); the origin of propionyl-S-ACP remains unknown.²⁻⁵

Leinamycin (Lnm, 4), a potent antitumor antibiotic, possesses a β -branched C3 unit that is part of its unique five-membered 1,3dioxo-1,2-dithiolane moiety. We have previously cloned, sequenced, and characterized the *lnm* biosynthetic gene cluster from *Strepto*myces atroolivaceus S-140.6 Close examination of the lnm cluster revealed a subset of four genes-lnmL, lnmM, lnmF, and InmK-encoding an ACP (LnmL), an HCS (LnmM), an ECH1 (LnmF), and a protein of unknown function (LnmK). Counterparts of LnmL, LnmM, and LnmF are present in biosynthetic clusters of polyketides with both β -methyl and β -ethyl branches,²⁻⁶ supporting the proposal that the C3 β -branch in **4** is likely installed by LnmL/ LnmM/LnmF in a mechanistic analogy to the β -methyl branch in 1, 2 and 3. Homologues of LnmK, however, can only be found in gene clusters encoding the biosynthesis of ethyl-branch-bearing polyketides, suggesting LnmK as a candidate for propionyl-S-ACP biosynthesis (Table 1, Figure 1C). Here we report the characterization of LnmK as a bifunctional acyltransferase/decarboxylase (AT/ DC) that derives propionyl-S-ACP from methylmalonyl-CoA.



Figure 1. (A) Selected polyketides bacillaene (1), curacin (2), myxovirescin A (3), and leinamycin (4) with (blue) α - or (red) β -alkyl branches. (B) Unified pathway for β -alkylation utilizing both acetyl-S-ACP and propionyl-S-ACP as substrates. (C) Distinct pathways for acetyl-S-ACP and propionyl-S-ACP biosynthesis.

Table 1. Enzymes That Generate Acetyl-S-ACP and Propionyl-S-ACP and Incorporate Them into Polyketides with a β -Alkyl Branch (Methyl for 1, 2, and 3 at C-12 or Ethyl for 3 at C-16 and Propionyl for 4)^a

compd	AT/DC	AT	KS	ACP	HCS	ECH1	ECH2
1 2	_	PksC	PksF CurC	AcpK CurB	PksG CurD	PksH CurE	PksI CurF
3 (C-12)	-	TaV	TaK	TaB	TaC	TaX	TaY
3 (C-16) 4	TaD LnmK	_	_	TaE LnmL	TaF LnmM	TaX LnmF	1a¥ —

^{*a*} See refs 2-6

Hence, LnmK represents a new family of AT/DC enzymes supplying a key substrate for β -alkylation in polyketide biosynthesis.

We first overproduced both LnmL and LnmK in Escherichia coli BL21(DE3) and purified them to near homogeneity (Figure

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Figure 2. (A) HPLC analysis of LnmK-catalyzed formation of propionyl-*S*-LnmL: (I) apo-LnmL (\bullet); (II) holo-LnmL (\checkmark); (III) holo-LnmL and propionyl-*S*-LnmL (\diamond); (IV) methylmalonyl-*S*-LnmL (\diamond); (V) propionyl-*S*-LnmL. (B) LnmK-catalyzed loading of acyl-CoA's to holo-LnmL and (C) LnmK-catalyzed self-acylation as judged by (I) 4–15% SDS-PAGE and (II) autoradiogram: lane 1, molecular weight standards; lane 2, [1,3-¹⁴C₂]methylmalonyl-CoA; lane 3, [1,3-¹⁴C₂]malonyl-CoA; lane 4, [1-¹⁴C]propionyl-CoA; lane 5, [1-¹⁴C]acetyl-CoA.

S1 in the Supporting Information). The purified LnmL was eluted as a single peak upon HPLC analysis (Figure 2A, panel I) and confirmed to be in its apo form by electrospray ionization mass spectrometry (ESI-MS) analysis (Table S1). In vitro phosphopantetheinylation was carried out by incubating apo-LnmL with CoA in the presence of the known promiscuous phosphopantetheinyltransferase Svp,⁷ and the resultant holo-LnmL was confirmed by HPLC (Figure 2A, panel II) and ESI-MS (Table S1) analyses.

We then established that LnmK is a bifunctional AT/DC catalyzing the formation of propionyl-S-LnmL. Holo-LnmL was incubated with [1-¹⁴C]acetyl-, [1-¹⁴C]propionyl-, [1,3-¹⁴C₂]malonyl-, or [1,3-¹⁴C₂]methylmalonyl-CoA in the presence of LnmK, and the reaction mixtures were subjected to SDS-PAGE and phosphorimaging. LnmK specifically and efficiently catalyzed the loading of methylmalonyl-CoA to holo-LnmL, and no loading was observed with the other acyl-CoA's tested (Figure 2B). To verify the molecular identity of the acyl-S-LnmL species, the reaction was repeated with cold methylmalonyl-CoA, and the resultant product was subjected to HPLC and ESI-MS analyses. A distinct new product was formed (Figure 2A, panel III), which ESI-MS analysis remarkably identified as propionyl-S-LnmL (Table S1); LnmK apparently acts as bifunctional AT/DC, catalyzing both methylmalonyl transfer to form the methylmalonyl-S-LnmL intermediate and its subsequent decarboxylation to yield propionyl-S-LnmL (Figure 1C).

We finally determined the precise timing of the acyl transfer and decarboxylation events catalyzed by LnmK. The fact that LnmK cannot decarboxylate methylmalonyl-CoA and loads only methylmalonyl-CoA (but not propionyl-CoA) to holo-LnmL indicates that decarboxylation most likely occurs on methylmalonyl-S-LnmL. To directly verify this mechanism, we prepared methylmalonyl-S-LnmL via in vitro phosphopantetheinylation by incubating apo-LnmL with methylmalonyl-CoA in the presence of Svp.⁷ Methylmalonyl-S-

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LnmL formation was monitored by HPLC (Figure 2A, panel IV) and confirmed by ESI-MS (Table S1) analyses. Incubation of methylmalonyl-*S*-LnmL with LnmK allowed us to investigate LnmK's DC activity directly. LnmK catalyzes specific and efficient decarboxylation of methylmalonyl-*S*-LnmL to yield propionyl-*S*-LnmL, whose identity was confirmed by HPLC (Figure 2A, panel V) and ESI-MS (Table S1) analyses. Taken together, these results unambiguously establish that LnmK first transfers methylmalonyl from methylmalonyl-CoA to holo-LnmL to form methylmalonyl-*S*-LnmL and then decarboxylates the latter to form propionyl-*S*-LnmL (Figure 1C).

LnmK homologues are known but to date have all been annotated as hypothetical proteins (Figure S2).^{2–5} We now propose that LnmK represents a new family of AT/DC enzymes supplying substrates for β -alkylation in polyketide biosynthesis. To further probe the catalytic mechanism of this newly discovered family of AT/DC enzymes, LnmK was incubated with [1,3-¹⁴C₂]methylmalonyl-CoA in the absence of holo-LnmL, and the reaction mixtures were subjected to SDS-PAGE and phosphorimaging. Specific and efficient loading of [1,3-¹⁴C₂]methylmalonyl-CoA onto LnmK was observed (Figure 2C), indicative of a transient acyl-LnmK intermediate in LnmK catalysis. This is reminiscent of ATs with Ser at their active sites,⁸ although no conserved AT or DC active-site motif is apparent in LnmK (Figure S2).

In summary, LnmK has been characterized as a bifunctional AT/ DC that catalyzes the formation of propionyl-S-ACP from methylmalonyl-CoA, accounting for the missing link of the β -ethyl or propionyl branch in polyketide biosynthesis. LnmK therefore could be exploited by combinatorial biosynthesis methods to engineer novel polyketides, especially those with β -alkyl branches. LnmK also represents an emerging family of novel AT/DC enzymes.

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Supporting Information Available: Full experimental details, Figures S1 and S2, and Table S1. This material is available free of charge via the Internet at http://pubs.acs.org.

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