Stereospecificity of the Dehydratase Domain of the Erythromycin Polyketide Synthase

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Stereospecificity of the Dehydratase Domain of the Erythromycin Polyketide Synthase

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Abstract: The dehydratase (DH) domain of module 4 of the 6-deoxyerythronolide B synthase (DEBS) has been shown to catalyze an exclusive *syn* elimination/*syn* addition of water. Incubation of recombinant DH4 with chemoenzymatically prepared *anti*-(2*R*,3*R*)-2-methyl-3-hydroxypentanoyl-ACP (**2a-ACP**) gave the dehydration product **3-ACP**. Similarly, incubation of DH4 with synthetic **3-ACP** resulted in the reverse enzyme-catalyzed hydration reaction, giving an ~3:1 equilbrium mixture of **2a-ACP** and **3-ACP**. Incubation of a mixture of propionyl-SNAC (**4**), methylmalonyl-CoA, and NADPH with the DEBS β-ketoacyl synthase-acyl transferase [KS6][AT6] didomain, DEBS ACP6, and the ketoreductase domain from tylactone synthase module 1 (TYLS KR1) generated *in situ* *anti*-**2a-ACP** that underwent DH4-catalyzed *syn* dehydration to give **3-ACP**. DH4 did not dehydrate *syn*-(2*S*,3*R*)-**2b-ACP**, *syn*-(2*R*,3*S*)-**2c-ACP**, or *anti*-(2*S*,3*S*)-**2d-ACP** generated *in situ* by DEBS KR1, DEBS KR6, or the rifamycin synthase KR7 (RIFS KR7), respectively. Similarly, incubation of a mixture of (2*S*,3*R*)-2-methyl-3-hydroxypentanoyl-*N*-acetylcysteamine thioester (**2b-SNAC**), methylmalonyl-CoA, and NADPH with DEBS [KS6][AT6], DEBS ACP6, and TYLS KR1 gave *anti*-(2*R*,3*R*)-**6-ACP** that underwent *syn* dehydration catalyzed by DEBS DH4 to give (4*R*,5*R*)-(*E*)-2,4-dimethyl-5-hydroxy-hept-2-enoyl-ACP (**7-ACP**). The structure and stereochemistry of **7** were established by GC-MS and LC-MS comparison of the derived methyl ester **7-Me** to a synthetic sample of **7-Me**.

Of the more than 2000 nonaromatic polyketides, the vast majority contain one or more disubstituted or trisubstituted double bonds, most of which have *E* (*trans*) geometry.[1] Moreover, essentially all polyketides that do not themselves display a double bond are biosynthesized by way of one or more unsaturated polyketide chain elongation intermediates. Thus although 6-deoxyerythronolide B (**1**, 6-dEB), the parent aglycone of the erythromycin family of antibiotics, does not have any double bonds in the final macrolactone, the responsible modular polyketide synthase (PKS), 6-dEB synthase (DEBS), does in fact harbor a dehydratase domain in module 4, termed DEBS DH4 (Figure 1).[2,3]

Direct evidence for the intermediacy of an unsaturated polyketide in erythromycin biosynthesis first came from disruption of the NADPH-binding motif of the ER4 domain, resulting in accumulation of a derivative of the corresponding (*E*)-$\Delta^{6,7}$-anhydro-6-dEB by mutants of the erythromycin producer *Saccharopolyspora erythraea*.[4] Although the stereochemistry of the substrate for the DEBS DH4 dehydratase is not known, the responsible ketoreductase, DEBS KR4, is predicted to generate the (3*R*)-diastereomer of the 2-methyl-3-hydroxyacyl-ACP pentaketide, as deduced from the presence of a Leu-Ala-Asp triad closely correlated with the formation of (3*R*)-3-hydroxyacyl-ACP polyketide intermediates.[5] Indeed, the vast majority of KR domains that are paired with a DH domain appear to harbor a conserved "Leu-Asp-Asp" motif.[5a,b] DEBS KR4 is also predicted to belong to the class of nonepimerizing ketoreductases, which would give rise to a (2*R*)-methyl group in the reduced product.[5c]

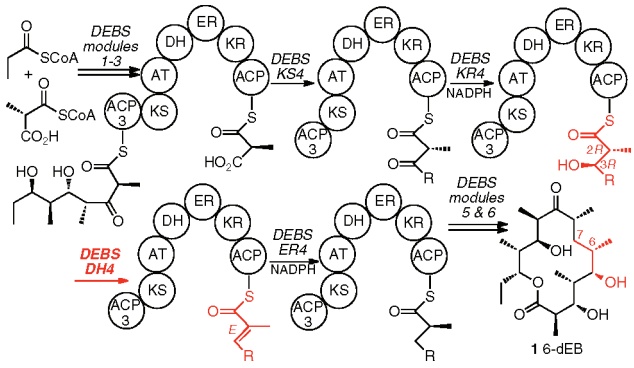

Figure 1. Proposed tetraketide substrate and pentaketide intermediates of DEBS module 4. The module has a KR, a DH, and an ER domain in addition to the obligate KS, AT, and ACP domains.

To establish the substrate specificity and stereochemical course of the DEBS DH4-catalyzed dehydration we used a chemoenzymatic strategy to prepare the requisite ACP-bound substrate and product analogues, **2a-ACP** and **3-ACP**. To this end the free acids **2a** and **3** were each converted to the corresponding -SCoA thioesters, **2a-SCoA** and **3-SCoA**, and thence to *anti*-(2*R*,3*R*)-2-methyl-3-hydroxypentanoyl-ACP6 (**2a-ACP**) and the expected dehydration product, (*E*)-2-methylpent-2-enoyl-ACP (**3-ACP**), from DEBS *apo*-ACP6 using the phosphopantetheinyl transferase Sfp (Scheme 1A).[6] The two ACP derivatives, which were readily distinguished by reversed-phase LC-ESI(+)-MS, both exhibited the expected molecular weights.[7] The structures were each confirmed by the MS^2 phosphopantetheinate (PPant) ejection method which gave **2a-pant**, *m*/*z* 375.33, and **3-pant**, *m*/*z* 357.3, each with the predicted MW, as well as MS^3 analysis of each of the characteristic PPant ejection fragments.[8]

Incubation of recombinant DEBS DH4[9] with **2a-ACP** resulted in formation of the predicted dehydration product **3-ACP**, as

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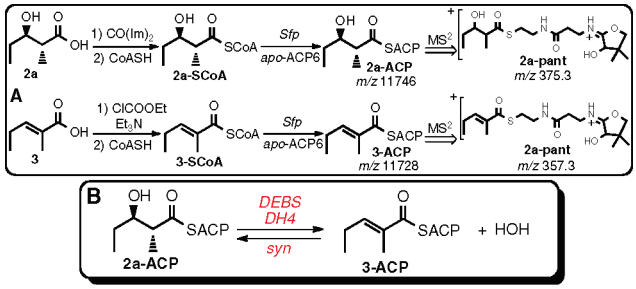
Scheme 1. (A) Synthesis and Analysis of ACP-Bound Substrates and (B) DEBS DH4-Catalyzed Interconversion of **2a-ACP** and **3-ACP**

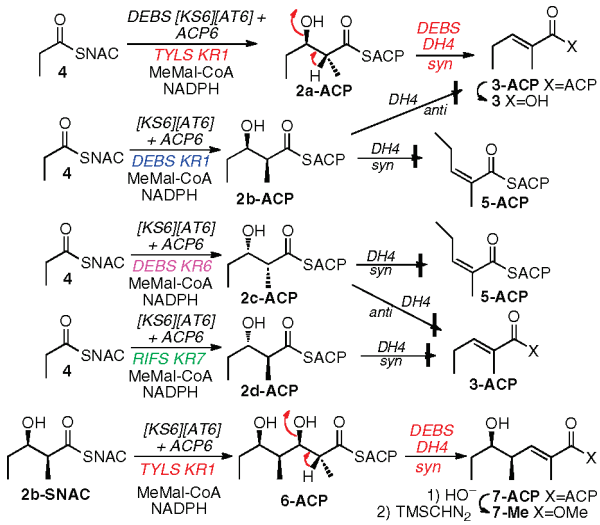


established by direct monitoring by LC-ESI(+)-MS^3, including detection of the corresponding intact acyl-ACP and PPant ejection fragments for both **2a-ACP** and **3-ACP** (Scheme 1B). Similarly, incubation of DEBS DH4 with **3-ACP** resulted in the reverse enzyme-catalyzed hydration reaction, giving an ~3:1 equilibrium mixture of **2a-ACP** and **3-ACP**.[10]

We also carried out combinatorial incubations using mixtures of recombinant PKS domains in order to generate *in situ* each of the four diastereomers of **2a**−**2d-ACP** (Scheme 2).[11] In this manner, a mixture of the DEBS [KS6][AT6] didomain, DEBS ACP6, and TYLS KR1, the ketoreductase domain from module 1 of the tylactone synthase, was incubated with propionyl-SNAC (**4**), methylmalonyl-CoA, and NADPH to produce *anti*-(2*R*,3*R*)-**2a-ACP**.[11b] Addition of recombinant DEBS DH4, either simultaneously with or subsequent to the formation of **2a-ACP**, resulted in dehydration to yield exclusively the predicted (*E*)-2-methylpent-2-enoyl-ACP (**3-ACP**), as confirmed by GC-MS analysis of the corresponding acid **3** and comparison with synthetic **3**.[12] By contrast, DEBS DH4 did not dehydrate either *syn*-(2*S*,3*R*)-**2b-ACP** or *syn*-(2*R*,3*S*)-**2c-ACP** generated by DEBS KR1 or KR6, respectively,[11a,c] to either *E*-**3**-ACP or the corresponding *Z*-isomer **5-ACP**, nor did DEBS DH4 dehydrate *anti*-(2*S*,3*S*)-**2d-ACP** produced by recombinant RIFS KR7,[13] the KR domain from module 7 of the rifamycin synthase.

In further confirmation of the stereochemistry of the dehydration reaction, incubation of DEBS DH4 with *anti*-(2*R*,3*R*,4*S*,5*R*)-2,4-dimethyl-3,5-dihydroxyheptanoyl-ACP (**6-ACP**) generated *in situ* from **2b-SNAC**, methylmalonyl-CoA, and NADPH by DEBS [KS6][AT6] + ACP6 + TYLS KR1, as previously described,[11b] gave exclusively *E*-**7-ACP** (Scheme 2). The structure and stereochemistry of **7-ACP** were determined by chiral GC-MS and LC-MS analysis of the derived methyl ester **7-Me**, obtained by basic hydrolysis and treatment of the liberated acid with TMS-diazomethane, and comparison with an authentic synthetic standard of **7-Me**.[14]

Scheme 2. Stereochemistry of DEBS DH4-Catalyzed Dehydration



Sequence alignments of the DEBS DH4 domain with numerous PKS and FAS DH domains reveal conserved ^{2409}**H**XXXGXXXX**P** and ^{2571}**D**(A/V)(V/A)(A/L)(**Q**/H) motifs.[2] Site-directed mutagenesis of the conserved active site His2409 of the DEBS DH4 domain abolished DEBS activity in *Sac. erythraea*[15a] while the analogous His mutation also inactivates the homologous DH2 domain of the picromycin synthase.[15b] Together the conserved His and Asp residues comprise the catalytic dyad of the dehydratase, in which the active site His acts as a general base while the Asp2571, located 4.1 Å from H2409 at the base of the substrate tunnel, is thought to serve as a general acid.[9,16,17]

Our results establish definitively that the DEBS DH4 domain catalyzes a *syn* elimination of water during erythromycin biosynthesis. The prototype dehydration catalyzed by the DH domain of the yeast FAS to give the characteristic disubstituted (*E*)-enoyl-ACP intermediates of fatty acid biosynthesis also takes place with net *syn* stereochemistry,[18] as do the dehydrations catalyzed by the DH domains of module 2 of nanchangmycin synthase[19] and module 2 of tylactone synthase.[11b] Indeed, the significant levels of overall sequence identity (>40%) and similarity (>55%) and the presence of the conserved motifs containing the catalytic dyad in more than 50 DH domains from a wide range of modular PKS systems strongly suggest that the formation of all (*E*)-unsaturated polyketide intermediates involves a common *syn* dehydration mechanism.

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Supporting Information Available: Experimental procedures, LC-ESI(+)-MS^3, and GC-MS data. This material is available free of charge via the Internet at http://pubs.acs.org.

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(12) The *E*-isomer **3** was cleanly resolved from the *Z*-isomer **5**, and the two compounds were not interconverted under the conditions of the reaction.
(13) You, Y.-O. Cane, D. E., unpublished observations.
(14) Although DH4 processed both **2a-ACP** and **6-ACP**, DEBS DH4 does not dehydrate the corresponding SNAC thioester analog, *anti*-(2*R*,3*R*)-**2a-SNAC** (ref 9). This observation is consistent with the presence of a presumptive ACP-binding region on the DH surface adjacent to the entrance to the substrate binding tunnel, a feature also found in bacterial FabZ proteins (ref 17).
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