

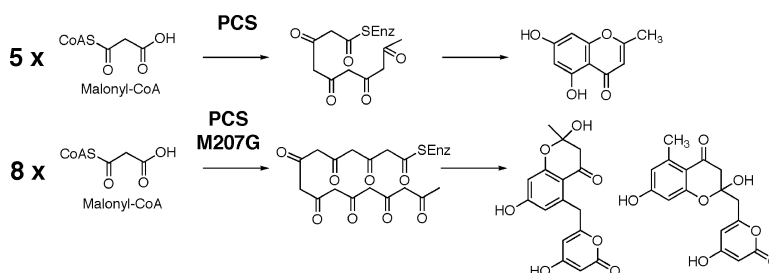
Communication

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## A Plant Type III Polyketide Synthase that Produces Pentaketide Chromone

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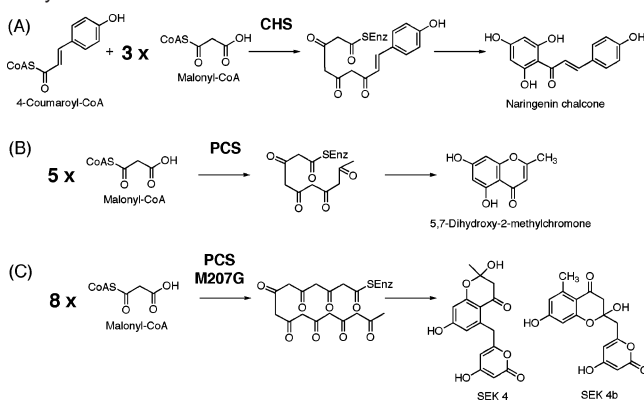
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A growing number of functionally diverse type III polyketide synthases (PKSs), the chalcone synthase (CHS) (EC 2.3.1.74) superfamily enzymes, have been cloned and sequenced from various plants,<sup>1</sup> which include recently reported a diketide (benzalacetone)<sup>2a,b</sup> and a heptaketide (aloesone) synthase (ALS)<sup>2c</sup> from *Rheum palmatum*. In addition, bacterial type III PKSs, such as a pentaketide 1,3,6,8-tetrahydroxynaphthalene-producing enzyme, have been also reported.<sup>3,4</sup> The CHS-superfamily enzymes are structurally and mechanistically distinct from the type I (modular type) and type II (subunit type) PKSs, using free CoA thioesters as substrates without the involvement of acyl carrier protein, to carry out a complete series of decarboxylation, condensation, cyclization, and aromatization reactions with a single active site. The homodimer of 40–45 kDa proteins typically selects 4-coumaroyl-CoA as a starter and performs up to three condensations with malonyl-CoA to produce naringenin chalcone, (4,2',4',6'-tetrahydroxychalcone), which is the biosynthetic precursor of flavonoids (Scheme 1A). Recent crystallographic and site-directed mutagenesis studies have revealed structural and functional details of the plant and bacterial type III PKSs.<sup>1–6</sup>

Here we report a novel plant-specific type III PKS that catalyzes formation of a pentaketide chromone, 5,7-dihydroxy-2-methylchromone, from five molecules of malonyl-CoA (Scheme 1B). Remarkably, replacement of a single amino acid residue Met207 (corresponding to the *Medicago sativa* CHS active-site residue Thr197) yielded a mutant enzyme that efficiently produces aromatic octaketides, SEK4 and SEK4b, the products of the minimal PKS for the benzoisochromanquinone actinorhodin (*act* from *Streptomyces coelicolor*)<sup>7</sup> (Scheme 1C). A cDNA encoding the pentaketide chromone synthase (PCS) (the GenBank accession no. AY823626) was cloned and sequenced from young roots of aloe (*Aloe arborescens*), a medicinal plant rich in aromatic polyketides including chromones and anthraquinones, by RT-PCR using degenerate primers based on the conserved sequences of known CHSs as described before.<sup>2</sup> A 1212-bp open reading frame encoded a  $M_r$  44,568 protein with 403 amino acids. The deduced amino acid sequence showed 50–60% identity to those of CHS-superfamily enzymes from other plants (58% identity (232/403) with *M. sativa* CHS,<sup>5a</sup> and 50% identity (206/403) with *R. palmatum* ALS<sup>2c</sup> that catalyzes formation of a heptaketide, aloesone (2-acetyl-7-hydroxy-5-methylchromone), from acetyl-CoA and six molecules of malonyl-CoA). *A. arborescens* PCS maintains an almost identical CoA binding site, and the catalytic triad of Cys164, His303, and Asn336 (numbering in *M. sativa* CHS) is absolutely conserved in all type III PKSs. Furthermore, most of the active-site residues including Met137, Gly211, Gly216, Pro375, as well as Phe215, and Phe265,<sup>1</sup> are conserved in PCS (Figure 1). The CHS-based homology modeling predicted that *A. arborescens* PCS has the same three-dimensional overall fold as *M. sativa* CHS,<sup>5a</sup> with the total cavity volume (1124 Å<sup>3</sup>) slightly larger than that of CHS (1019 Å<sup>3</sup>) and almost as large as that of *R. palmatum* ALS (1173 Å<sup>3</sup>).<sup>2c</sup>

**Scheme 1.** Formation of Polyketides by CHS-Superfamily Enzymes



Recombinant PCS was heterologously expressed in *Escherichia coli* BL21(DE3)pLysS as fusion protein with GST at the N-terminal (pET vector). After cleavage of the GST-tag, the purified enzyme gave a single band with molecular mass of 44 kDa on SDS-PAGE, while the native PCS appeared to be a homodimer since it had molecular mass of 88 kDa as determined by gel filtration. *A. arborescens* PCS efficiently accepted malonyl-CoA as a sole substrate to yield a single product with a parent ion peak  $[M + H]^+$  at  $m/z$  193 on LC-ESIMS. Spectroscopic data (<sup>1</sup>H NMR, LC-MS, and UV) of the product obtained from a large-scale enzyme reaction (1.0 mg from 20 mg of malonyl-CoA) are completely identical with those of an authentic 5,7-dihydroxy-2-methylchromone. The aromatic pentaketide has been isolated from several plants and is known to be a biosynthetic precursor of khellin and visnagin, the anti-asthmatic furochromones found in *Ammi visnaga*.<sup>8</sup> Interestingly, acetyl-CoA, resulting from decarboxylation of malonyl-CoA, was also accepted as a starter substrate but not so efficiently as in the case of *R. palmatum* ALS.<sup>2c</sup> This was confirmed by the <sup>14</sup>C incorporation rate from [<sup>14</sup>C]acetyl CoA in the presence of cold malonyl-CoA, while the yield of the pentaketide from [<sup>14</sup>C]malonyl-CoA was almost at the same level in the presence or absence of cold acetyl-CoA in the reaction mixture. The recombinant PCS showed the  $K_M = 71.0 \mu\text{M}$  and  $k_{\text{cat}} = 445 \times 10^{-3} \text{ min}^{-1}$ , with a broad pH optimum within a range of 6.0–8.0. On the other hand, like other type III PKSs,<sup>1,9</sup> *A. arborescens* PCS showed the promiscuous substrate specificity; the enzyme also accepted aromatic (4-coumaroyl, cinnamoyl, and benzoyl) and aliphatic (*n*-hexanoyl, *n*-octanoyl, and *n*-decanoyl) CoA esters as a starter substrate; however, it yielded only triketide and tetra- and pentaketide products.

One of the characteristic features of *A. arborescens* PCS is that the CHS active-site residues, Thr197, Gly256, and Ser338 (numbering in *M. sativa* CHS),<sup>5a</sup> are uniquely replaced with Met, Leu, and Val, respectively. Interestingly, the three residues are also missing in the heptaketide-forming *R. palmatum* ALS<sup>2c</sup> (T197A/G256L/S338T), and in *Gerbera hybrida* 2-pyrone synthase (2PS)<sup>6</sup> (T197L/

M.s CHS	1	-----	<b>M</b> VSVSEIRKA	ORAE <sup>+</sup> GPATIL	AIGTAN <sup>+</sup> PENC	VEOSTY <sup>+</sup> PDVY	FRV <sup>+</sup> INSEHMT	ELK <sup>+</sup> KKFORIC	DKSMIR <sup>+</sup> FRYM	YLTEEILKEN	PNMCEYMAPS	90			
A.h STS	1	-----	<b>M</b> VSVSGIRRV	ORAE <sup>+</sup> GPATVL	AIGTANPPNC	IIOSTVADLY	FRV <sup>+</sup> INSEHMT	DLKKKFORIC	ERT <sup>+</sup> IKRRFL	YLTEEILKEN	PNMCEYMAPS	90			
G.h 2PS	1	-----	<b>M</b> GSYS	SDI <sup>+</sup> VEVERIA	GRAG <sup>+</sup> GIATIL	AIGTANPPNC	VADYADLY	FRV <sup>+</sup> INSEHMT	ELK <sup>+</sup> KKFORIC	EKT <sup>+</sup> IKRRFL	ALTEEYLLEN	PNMCEYMAPS	95		
R.p ALS	1	-----	<b>M</b> ADVLCERNS	GRAG <sup>+</sup> GPATVL	AIGTAP <sup>+</sup> PHIC	YROADY <sup>+</sup> PDVY	FRV <sup>+</sup> INSEHMT	DLKKKFORIC	DFSC <sup>+</sup> IKRRFL	FHTEEILKEN	PNMCEYMAPS	91			
A.a PCS	1	-----	<b>M</b> SLSLSLPL	ME <sup>+</sup> LVGIRKA	GRAD <sup>+</sup> GIATVM	AIGTAP <sup>+</sup> PHI	PHO <sup>+</sup> TADLY	FRV <sup>+</sup> INSEHMT	ELK <sup>+</sup> KKFORIC	KRM <sup>+</sup> IKRRYF	NYTEEFLKY	PNMITSYDEPS	100		
M.s CHS	91	LA	AROD <sup>+</sup> LVV	EVPR <sup>+</sup> LGEKAA	VKA <sup>+</sup> IKEWGQF	KSKI <sup>+</sup> THLIPC	TTSG <sup>+</sup> VDMPGA	DYQ <sup>+</sup> LTKLLGL	RYV <sup>+</sup> KRYMY	YQCG <sup>+</sup> FAGGTV	LR <sup>+</sup> LAKDLAEN	NKGARV <sup>+</sup> LVVC	190		
A.h STS	91	LA	ARE <sup>+</sup> DMIR	EVPR <sup>+</sup> LGEKAA	TKA <sup>+</sup> IKEWGQF	KSKI <sup>+</sup> THLIPC	TTSG <sup>+</sup> VADPGV	DYE <sup>+</sup> IVLVLGL	RYV <sup>+</sup> KRYMY	YQCG <sup>+</sup> FAGGTV	LR <sup>+</sup> LAKDLAEN	NKGARV <sup>+</sup> LVVC	190		
G.h 2PS	96	LN	AROD <sup>+</sup> LVV	GVPL <sup>+</sup> LGEKAA	VKA <sup>+</sup> IKEWGQF	KSKI <sup>+</sup> THLIPC	TTAG <sup>+</sup> VDMPGA	DYQ <sup>+</sup> LTKLLGL	SPS <sup>+</sup> VKRYMY	YQCG <sup>+</sup> FAGGTV	LR <sup>+</sup> LAKDLAEN	NKGARV <sup>+</sup> LVVC	195		
R.p ALS	92	LN	AROD <sup>+</sup> LVV	EVPR <sup>+</sup> LGEKAA	VKA <sup>+</sup> IKEWGQF	KSKI <sup>+</sup> THLIPC	TTSG <sup>+</sup> VDMPGA	DYQ <sup>+</sup> LTKLLGL	RYV <sup>+</sup> KRYMY	YQCG <sup>+</sup> FAGGTV	LR <sup>+</sup> LAKDLAEN	NKGARV <sup>+</sup> LVVC	191		
A.a PCS	101	LN	RODIC <sup>+</sup> VP	GVPL <sup>+</sup> LGEKAA	VKA <sup>+</sup> IKEWGQF	KSE <sup>+</sup> ITHLIPC	TTSG <sup>+</sup> VDMHSA	DE <sup>+</sup> CKALLGL	HAN <sup>+</sup> VNTCYM	YQCG <sup>+</sup> FAGGTV	MR <sup>+</sup> LAKDLAEN	NKGARV <sup>+</sup> LVVC	200		
M.s CHS	191	SE	IVAV <sup>+</sup> FRG	PS <sup>+</sup> THLDSLV	GOAL <sup>+</sup> FDGAA	ALIV <sup>+</sup> GSDFVP	E <sup>+</sup> ENPIPELV	W <sup>+</sup> LACTIAPDS	EGA <sup>+</sup> IGHLRE	AGL <sup>+</sup> TFHLIKD	VP <sup>+</sup> GISVKNIT	NAL <sup>+</sup> VEAPEPI	290		
A.h STS	191	SE	IVAV <sup>+</sup> FRG	PS <sup>+</sup> ETDDBLV	GOAL <sup>+</sup> FDGAA	ALIV <sup>+</sup> GSDFVP	E <sup>+</sup> ENPIPELV	ST <sup>+</sup> CKLVEES	HGA <sup>+</sup> IGHLRE	VGL <sup>+</sup> TFHLIKD	VP <sup>+</sup> DISCNIN	DAL <sup>+</sup> NFAE <sup>+</sup> PI	290		
G.h 2PS	196	SE	IVAV <sup>+</sup> FRG	PS <sup>+</sup> THLDSLV	GOAL <sup>+</sup> FDGAA	ALIV <sup>+</sup> GSDFVP	E <sup>+</sup> ENPIPELV	ST <sup>+</sup> CKLVEES	ERA <sup>+</sup> VKHLRE	GGL <sup>+</sup> TFHLIKD	VP <sup>+</sup> LVVSNIT	NAL <sup>+</sup> VEAPEPI	295		
R.p ALS	192	SE	IVAV <sup>+</sup> FRG	PS <sup>+</sup> THLDSLV	GOAL <sup>+</sup> FDGAA	ALIV <sup>+</sup> GSDFVP	E <sup>+</sup> ENPIPELV	S <sup>+</sup> AGIATPDS	LHT <sup>+</sup> MAHLRE	AGL <sup>+</sup> TFHLIKD	VP <sup>+</sup> LVVSNIT	NAL <sup>+</sup> VEAPEPI	291		
A.a PCS	201	SE	IVAV <sup>+</sup> FRG	PS <sup>+</sup> THLDSLV	GOAL <sup>+</sup> FDGAA	ALIV <sup>+</sup> GSDFVP	E <sup>+</sup> ENPIPELV	CR <sup>+</sup> CVIEN	EDV <sup>+</sup> HLHLRE	AGM <sup>+</sup> TFHLIKD	SP <sup>+</sup> GISVKNIT	ACL <sup>+</sup> IDVFKSV	300		
M.s CHS	291	GIS	-----	<b>D</b> WNS	IF <sup>+</sup> WTAHPGGR	A <sup>+</sup> ILDOVEKIL	EL <sup>+</sup> KPEKNAI	RF <sup>+</sup> VLSEYGM	SS <sup>+</sup> ACVLFILD	EM <sup>+</sup> RKSTONG	EL <sup>+</sup> TTGEGLEW	GV <sup>+</sup> LPFGPGI	TV <sup>+</sup> ETVLRV	41	389
A.h STS	291	GIS	-----	<b>D</b> WNS	IF <sup>+</sup> WTAHPGGR	A <sup>+</sup> ILDOVEKIL	N <sup>+</sup> LKPEKNAI	RF <sup>+</sup> VLSEYGM	SS <sup>+</sup> ACVLFILD	EM <sup>+</sup> RKRSIEG	EL <sup>+</sup> TTGEGLEW	GV <sup>+</sup> LPFGPGI	TV <sup>+</sup> ETVLRV	41	389
G.h 2PS	296	GIS	-----	<b>D</b> WNS	IF <sup>+</sup> WTAHPGGR	A <sup>+</sup> ILDOVEKIL	N <sup>+</sup> LKPEKNAI	RF <sup>+</sup> VLSEYGM	IS <sup>+</sup> ACVLFILD	EM <sup>+</sup> RKRSIAG	EL <sup>+</sup> TTGEGIDC	GV <sup>+</sup> LPFGPGI	TV <sup>+</sup> ETVLRV	41	389
R.p ALS	292	GIS	-----	<b>D</b> WNS	IF <sup>+</sup> WTAHPGGR	A <sup>+</sup> ILDOVEKIL	EL <sup>+</sup> KPKMRS	RF <sup>+</sup> VLSEYGM	IS <sup>+</sup> ACVLFILD	EM <sup>+</sup> RKRSFREG	EL <sup>+</sup> TTGEGLEW	GV <sup>+</sup> LPFGPGI	TV <sup>+</sup> ETVLRV	41	391
A.a PCS	301	GIS	-----	<b>D</b> WNS	IF <sup>+</sup> WTAHPGGR	A <sup>+</sup> ILDOVEKIL	EL <sup>+</sup> PKPEKNAI	RF <sup>+</sup> VLSEYGM	VS <sup>+</sup> ASVLFILD	EM <sup>+</sup> RKRSIAG	EL <sup>+</sup> TTGEGLEW	GV <sup>+</sup> LPFGPGI	TV <sup>+</sup> ETVLRV	41	403

**Figure 1.** Comparison of primary sequences of *A. arborescens* PCS and other CHS-superfamily enzymes. M.s CHS, *M. sativa* CHS; A.h STS, *Arachis hypogaea* stilbene synthase; G.h 2PS, *G. hybrida* 2PS; R.p ALS, *R. palmatum* ALS. The active-site residues conserved in the CHS-superfamily enzymes (Cys164, Phe215, His303, and Asn336, numbering in *M. sativa* CHS) are marked with #, and residues for the CoA binding, with +.

G256L/S338I) that also selects acetyl-CoA as a starter to produce a triketide pyrone. A CHS triple mutant (T197L/G256L/S338I) has been shown to yield an enzyme that was functionally identical to 2PS, suggesting the substitutions are responsible for the starter substrate specificity of the enzymes.<sup>6b</sup> To test the hypothesis, a mutant enzyme was constructed in which Met207 (corresponding to Thr197 in CHS) was replaced by Thr. However, the point mutation did not significantly affect the enzyme activity; PCS M207T mutant was functionally almost identical to the wild-type PCS. In contrast, when Met207 was substituted with Gly, there was a dramatic change in the enzyme activity; PCS M207G mutant efficiently afforded two new products with a parent ion peak [M + H]<sup>+</sup> at *m/z* 319 on LC-ESIMS, which were identified as aromatic octaketides SEK4 and SEK4b (ratio 1:4), the shunt products of the minimal type II PKS for actinorhodin,<sup>7</sup> by direct comparison with authentic compounds. Here formation of only a trace amount of 5,7-dihydroxy-2-methylchromone was detected by LC-MS. The pentaketide-forming PCS was thus transformed into an octaketide-producing enzyme by the single amino acid mutation. This is the first demonstration of a type III PKS catalyzing seven successive polyketide chain elongation reactions.

In conclusion, *A. arborescens* PCS is a novel plant-specific type III PKS that produces an aromatic pentaketide from five molecules of malonyl-CoA. Site-directed mutagenesis revealed that Met207 determines the polyketide chain length and the product specificity; PCS M207G mutant yielded SEK4 and SEK4b from eight molecules of malonyl-CoA.<sup>10</sup> This provided new insights into the catalytic functions and specificities of type III PKSs. Further characterization of the enzymes including their three-dimensional structure will be reported in due course.

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**Supporting Information Available:** Materials and methods. This material is available free of charge via the Internet at <http://pubs.acs.org>.

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