Type II thioesterase from *Streptomyces coelicolor* A3(2)

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Type I polyketide synthases (PKSs) are complexes of large, multimodular enzymes that catalyse biosynthesis of polyketide compounds via repetitive reaction sequences, during which each step is catalysed by a separate enzymic domain. Many type I PKSs, and also non-ribosomal peptide synthetase clusters, contain additional thioesterase genes located adjacent to PKS genes. These are discrete proteins called type II thioesterases (TE IIs) to distinguish them from chain-terminating thioesterase (TE I) domains that are usually fused to the terminal PKS module. A gene of a new TE II, *scoT*, associated with the cluster of putative type I PKS genes from *Streptomyces coelicolor* A3(2), was found. The deduced amino acid sequence of the gene product shows extensive similarity to other authentic thioesterase enzymes, including conservation of characteristic motifs and residues involved in catalysis. When expressed in the heterologous host *Streptomyces fradiae*, *scoT* successfully complemented the resident TE II gene (*tylO*), and, by restoring a significant level of macrolide production, proved to be catalytically equivalent to the TylO protein. *S¹* nuclease mapping of *scoT* revealed a single potential transcription start point with expression being switched on for a short period of time during a transition phase of growth.

**Keywords:** thioesterase type II, *Streptomyces fradiae*, disruption mutant complementation, *S¹* nuclease mapping

INTRODUCTION

Polyketides are a large and structurally a diverse group of compounds, many of which exhibit biological activity as antibiotics, immunosuppressants or anticancer drugs. Polyketides are synthesized by a common mode of condensation and reduction reactions similar to that of fatty acid biosynthesis. Nascent polyketides are processed by large multienzyme complexes, polyketide synthases (PKSs). In the type I PKSs, involved in production of macrolide antibiotics such as erythromycin, reactions of the biosynthetic cycle are catalysed sequentially by separate enzymic domains housed in large multifunctional polypeptides. Each complete cycle of condensation and reduction reactions is catalysed by a module, a functional unit of the PKS. The substrate acyl chains which undergo successive reactions are tethered as thioesters by acyl carrier domains of the PKS polypeptides. A terminal thioesterase domain (TE) catalyses release and cyclization of the full-length (fully processed) polyketide chain (Katz & Donadio, 1993).

Many type I PKSs, and also non-ribosomal peptide synthetase clusters, contain additional TE genes located adjacent to the PKS genes within the cluster of antibiotic biosynthetic genes (Weissman et al., 1998; Schneider & Marahiel, 1998; Shaw-Reid et al., 1999; August et al., 1998; Xue et al., 1998; Heathcote et al., 2001). The products of such genes are discrete proteins called type II thioesterases (TE IIs) to distinguish them from chain-terminating thioesterase (TE I) domains (Gokhale et al., 1999). In fatty acid synthase complexes, TE IIs are alternative chain-terminating enzymes exhibiting hydrolase activity towards medium-chain-length acyl thioesters (Smith, 1994). There is no obvious role for the TE IIs associated with multienzyme PKS complexes, nor is the mechanism of their action known.

Abbreviations: PKS, polyketide synthase; TE, thioesterase.

The GenBank accession number for the sequence reported in this paper is AF109727.
The function of TE IIs is predicted from gene-disruption analysis, complementation studies, and determination of their substrate specificities (Weissman et al., 1998; Butler et al., 1999; Heathcote et al., 2001). Polyketide production is drastically reduced, by 90% or more, in strains with a deleted TE II gene (Xue et al., 1998; Butler et al., 1999; Doi-Katayama et al., 2000), indicating an important function, proposed to involve editing of aberrant intermediates (Butler et al., 1999) during the course of polyketide biosynthesis. More recently, this hypothesis has been confirmed and the mechanism clarified. Thus, the TyLO protein displayed hydrolytic activity in vitro towards short-chain acyl-CoAs, indicating that the enzyme could remove aberrantly decarboxylated (and, therefore, non-reactive) extender acyl chains from the PKSs during polyketide biosynthesis (Heathcote et al., 2001). By hydrolytic release of such aberrant acyl groups, TE II was proposed to unblock PKS modules and restore overall efficiency of the complex enzyme.

The proposed common role for TE IIs in PKS multienzyme systems raises the question of whether specific TE IIs might be replaceable by other TE IIs normally associated with other PKS complexes. Based on the TE II substrate-specificity studies published to date (Weissman et al., 1998; Heathcote et al., 2001), such enzymes do not seem to select the structure of the acyl substrates.

Genetic engineering studies allow assembly of novel polyketide chains following fusion, swapping or repositioning of catalytic domains, modules or whole peptides within PKS polypeptides (Hutchinson & Fujii, 1995; Ranganathan et al., 1999; Tang et al., 2000). In engineered PKSs, co-expression of TE IIs in addition to other PKS proteins might help in achieving elevated levels of the polyketide products.

We were studying a gene cluster for the new PKS type I in Streptomyces coelicolor A3(2) (Kuczek et al., 1997; K. Pawlik, M. Kotowska & K. Kuczek, unpublished data; GenBank accession numbers U88833, AF109727 and AF 202898) located in a previously unmapped region of the chromosome, between cosmids 2H4 and 10H5 (Redenbach et al., 1996), now covered by cosmids 2C4, 1G7, BAC8D1 and IF3 (http://www.sanger.ac.uk/Projects/S_coelicolor/). During our studies, we found a new gene, encoding a putative TE II (ScoT). The gene is located within the putative polyketide biosynthetic gene cluster. In this paper, we describe this gene.

When expressed in the heterologous host, Streptomyces fradiae, scoT functionally complemented disruption of the native TE II gene, tyLO.

**METHODS**

**Bacterial strains, cosmid clones, plasmids and growth media.** The Streptomyces strains used are listed in Table 1. S. fradiae and its mutants were maintained and propagated at 37 °C on AS1 agar (Wilson & Cundliffe, 1998) or at 30 °C in Difco tryptic soy broth. S. coelicolor A3(2) was maintained and propagated at 30 °C on 79 agar medium (IMET Catalogue of Strains [Jena] 1987) or SMM agar (Kieser et al., 2000). Escherichia coli SURE strain [e14 (McrA) Δ(mcrCB−hsdSMR−mrr)171 endA1 supE44 thi-1 gyrA96 relA1 lac recB recF sbcC unnuC::Tn5 (Kan) wucC (F′ proAB lacZAM15 Tn10 (Tet)) was a host for cosmid clone 1G7 of S. coelicolor A3(2) genomic DNA in SuperCos vector (Stratagene), which was kindly provided by H. M. Kieser (John Innes Institute, Norwich, UK). pBluescript SK(+) and SK(−) phagemid vectors (Stratagene) were used for cloning of restriction fragments from the cosmid and for their sequencing. E. coli K-12 strain DH5α was used for routine plasmid manipulation and was grown in standard media (Sambrook et al., 1989). DNA was introduced into S. fradiae via conjugal transfer from E. coli S17-1 (Simon et al., 1983).

**DNA and RNA isolation, hybridization and sequencing.** Plasmids propagated in E. coli were isolated according to standard procedures (Sambrook et al., 1989). Cosmid DNA was purified by the procedure for high-molecular-mass plasmid DNA preparation and was used for restriction analysis and cloning of scoT by standard genetic procedures (Sambrook et al., 1989). The hybridization probe was random-prime labelled with DIG-11-DUTP. Labelling, hybridization (at 68 °C) and detection of hybrids were carried out according to the manufacturer’s recommended procedure (The DIG System User’s Guide for Filter Hybridization; Boehringer) with CSPD (Tropix) as a substrate for the luminescent reaction. The sequence of the S. coelicolor DNA was determined both manually (Kuczek et al., 1998), by using the chain-termination method with the Sequenase version 2.0 sequencing kit of Amersham, and by automated sequencing (performed by Qiagen Sequencing Services, Hilden, Germany). The sequence was determined on both strands and was submitted to GenBank (accession no. AF109727). Comparisons of the nucleotide and amino acid sequences with the databases were performed with the BLAST and CLUSTAL W programs. RNA was isolated as described by Strauch et al. (1991).
Fermentation and analysis of its products. Strains of *S. fradiae* were fermented in media described elsewhere, and fermentation products were extracted and analysed by reverse-phase HPLC, with absorbance measurement at 282 nm, also as described elsewhere (Butler et al., 1999). Desmycosin was used as an internal standard to identify fermentation products in tyLO-disrupted strains.

*S* nuclease mapping. For each *S* nuclease reaction, 30 or 40 μg RNA was hybridized in NaTCA buffer (Murray, 1986; solid NaTCA (Aldrich) dissolved to 3 M final concentration in 50 mM PIPES, 5 mM EDTA, pH 7·0) to about 0·002 pmol (approx. 10^4 Cerenkov c.p.m.) of the probe. The oligonucleotide 5'-GTCGAACCTCGGCGTACGTC-3' was uniquely labelled at its 5' end with [γ^32]P ATP using T4 polynucleotide kinase, and was used in the PCR with the unlabelled oligonucleotide 5'-CCTCGCAGCGCGGAGAG-AAT-3', which anneals upstream of the *scoT* promoter, to generate a 430 bp probe. The PCR used M145 total DNA as a template. Subsequent steps were as described by Strauch et al. (1991).

**RESULTS**

**TE II gene scoT**

We investigated cosmid 1G7 from the library of chromosomal DNA of *S. coelicolor* A3(2). The cosmid is located between cosmids 2C4 and BAC8D1 (http://www.sanger.ac.uk/Projects/S_coelicolor/). DNA of cosmid 1G7, digested with DraI and BamHI, was screened with a probe having a sequence characteristic of acyltransferase active sites (Kuczek et al., 1997). Under non-stringent conditions, six fragments were found to hybridize with the probe. These hybridizing fragments were cloned for sequence determination which, with the aid of CODONPREFERENCE analysis, revealed an ORF of 807 bp, located on two fragments and ending 265 bp from the T3 end of the 1G7 cosmid (Fig. 1a–c). The ORF, designated *scoT*, was deduced to encode a protein of 268 amino acid residues (molecular mass 28686 Da; pI 6·17), of which about 53% were predicted to be hydrophobic.

Comparison of the *scoT* sequence (GenBank AF109727) with others in the databases revealed extensive simi-
Fig. 3. HPLC analysis of fermentation products of *S. fradiae*. (a) Wild-type; (b) *tylO*-disrupted strain; (c) *tylO*-disrupted strain, complemented with *scoT*.

Fig. 4. S1 nuclease transcript mapping of *scoT*. (a) S1 nuclease mapping of the transcriptional start sites of *scoT*. A 430 bp PCR product (nt) labelled uniquely at the 5′ end position was used as a probe for *scoT* mRNAs. Asterisks indicate the probable transcription start points; the sequences shown are those of the template strand. Lanes T, G, C and A are sequence ladders derived from the same labelled primer that was used to generate the PCR product. (b) The promoter region of *scoT*. Possible -10- and -35-region sequences are underlined. A possible RBS is shown shaded. Transcriptional start points are indicated by asterisks, and the direction of transcription is indicated by an arrow. The translation start codon is shown boxed. The numbers are nucleotide positions as denoted in GenBank accession no. AF109727. (c) Analysis of the *scoT* transcript, using RNA isolated from a liquid SMM-grown culture of *S. coelicolor* A3(2) strain M145. 'EXP', 'TRANSITION' and 'STAT' indicate the exponential, transition and stationary phases of growth, respectively. The shaded box labelled ‘RED’ denotes the presence of undecylprodigiosin in the mycelium.

Fig. 4 illustrates the transcriptional mapping of the *scoT* gene in *S. fradiae*. The mapping reveals the transcriptional start sites of the *scoT* transcript, which are indicated by asterisks. The promoter region of *scoT* is shown, with possible -10- and -35-region sequences underlined. A possible ribosome binding site (RBS) is shown shaded. The direction of transcription is indicated by an arrow. The translation start codon is shown boxed. The numbers are nucleotide positions as denoted in GenBank accession no. AF109727. 'EXP', 'TRANSITION' and 'STAT' indicate the exponential, transition and stationary phases of growth, respectively. The shaded box labelled ‘RED’ denotes the presence of undecylprodigiosin in the mycelium.

The ATG start codon of the *scoT* gene is preceded by a potential RBS sequence (AAGGGG) ending 8 bp before the start (nucleotides complementary to the 3′ end of the 16S rRNA from *Streptomyces lividans* are underlined) (Strohl, 1992) (see Fig. 4b). The ORF ends with a TGA stop codon. The amino acid motif GxSxG (x=any amino acid) characteristic of acyltransferases and TEs, with Ser-90 as the active-site residue, is present within the deduced sequence of the ScoT protein. The ATG start codon of the *scoT* gene is preceded by a potential RBS sequence (AAGGGG) ending 8 bp before the start (nucleotides complementary to the 3′ end of the 16S rRNA from *Streptomyces lividans* are underlined) (Strohl, 1992) (see Fig. 4b). The ORF ends with a TGA stop codon. The amino acid motif GxSxG (x=any amino acid) characteristic of acyltransferases and TEs, with Ser-90 as the active-site residue, is present within the deduced sequence of the ScoT protein. A second conserved amino acid which might also be involved in catalysis is His-224 (Fig. 2). Usage of AGC as the codon for the active-site serine is typical of TE IIs [AGY for TE

Similarities with TEs from various actinomycetes and other bacteria, and also with rat S-acyl fatty acid synthase complex. The greatest similarity was found with TE IIs (Pfam00975), i.e. 43% identity with a TE II (AF040570) from the rifamycin biosynthetic gene cluster of *Amycolatopsis mediterranei*, 43% identity with a TE II (X60379) associated with 6-deoxyerythronolide B synthase from *Saccharopolyspora erythraea*, and 40% identity with TyIO (U08223), the TE II involved in tylosin biosynthesis in *Streptomyces fradiae*. ScoT is predicted to belong to the well-known alpha/beta hydrolase family (Pfam00975).
II and TCN for TE I, where \(Y = (C, T), N = (A, C, G, T)\) (Smith, 1994).

**Biological activity of TE II**

We attempted to determine whether the product of \(scoT\) has TE II activity. This was examined by studying whether it could functionally replace the native TE II (i.e. TylO) in the tylosin producer, *S. fradiae*. ScoT and TylO show extensive amino acid sequence similarity, and the complementation system for the TE II gene-disrupted *S. fradiae* strain was constructed (Butler et al., 1999). Therefore, \(scoT\) was cloned in a conjugal expression vector, plST9828 (Fig. 1d), and integrated into the chromosome, at the \(attB\) site, of a tylO-disrupted strain of *S. fradiae* under the control of the strong, constitutive promoter \(ermEp^+\) (Butler et al., 1999). This was done via conjugal transfer from *E. coli*, and three resultant transconjugant strains were subjected to fermentation analysis using quadruplicate cultures of each strain. Since TylO is co-expressed with the downstream gene, tylCVI (which encodes an enzyme involved in synthesis of the deoxyhexose sugar mycarose), disruption of tylO results in a polar effect on tylCVI expression, such that the tylO-disrupted strain produces demycarosyl-tylosin (desmycosin), as do strains in which the disruption is successfully complemented by cloned DNA (Butler et al., 1999).

Thus, the tylO disruptant was complemented by \(scoT\), as measured by the yield of desmycosin in fermentations analysed by HPLC with desmycosin as the internal standard (Fig. 3a–c). Desmycosin production was restored to up to 48% of the level of macrolide produced by the wild-type strain (Fig. 3c). Because of the close similarity in the molar absorbance coefficients of tylosin and desmycosin, the amount of desmycosin produced as a fermentation product by a mutant strain was directly compared with the amount of tylosin produced by the wild-type strain. Control fermentation of the non-complemented, tylO-disrupted strain yielded only minimal amounts of desmycosin (Fig. 3b). These results showed that the TE II gene, \(scoT\), from *S. coelicolor* A3(2) could, by complementation, restore macrolide production to a significant level in the *S. fradiae* strain. Expression of \(scoT\) was induced at the 19th hour of growth, i.e. in late transition phase, and was quickly shut down in stationary phase (Fig. 4c).

**DISCUSSION**

**ScoT is TE II protein**

The translated sequence of \(scoT\) displayed extensive similarity to the deduced sequences of TE IIs associated with type I PKS complexes. Such similarity extended to several characteristics: (1) the overall amino acid sequence similarity; (2) the conservation of characteristic amino acid motifs; (3) the molecular mass of the peptide; (4) the distance from the amino terminus of the protein to the active-site serine (usually about 100 residues); (5) the position of the conserved histidine residue; (6) active-site serine codon AGC (Smith, 1994).

The amino acid sequences of all the known TE IIs are strongly conserved, especially in implicated catalytically active sites. The sequence data suggest that \(scoT\) encodes a TE II which, presumably, is catalytically active. However, in the absence of data relating to its substrate specificity, the probability that ScoT might be capable of functioning in association with a heterologous PKS system could not be predicted.

**ScoT complements the natural function of TE II in *S. fradiae***

ScoT was able to replace TylO, the TE II of the tylosin pathway, by restoring the efficiency of macrolide biosynthesis in the tylO-disrupted strain. The two enzymes appear, therefore, to be equivalent in their catalytic function. Interestingly, in their natural context, these enzymes are apparently associated with PKS enzymes that differ in module number and in the nature of the extender acyl units incorporated by the respective modules. The primary product of the tylosin PKS in *S. fradiae*, a linear polyketide derived from condensation of five propionate units, two acetate units and one butyrate unit (Baltz & Seno, 1988), undergoes cyclization into a 16-atom lactone ring, tylactone. This means that in tylactone biosynthesis, malonyl-CoA, methylmalonyl-CoA and ethylmalonyl-CoA are used as extender units. Although the polyketide product of the modular PKS with which ScoT putatively associates has not yet been determined, the sequences of the acyltransferase domains in each of the five extension modules of the PKS (Kuczek et al., 1997; K. Pawlik, M. Kotowska & K. Kuczek, unpublished data) suggest that all five should use malonyl-CoA extender units according to the consensus sequence motifs correlated
with the substrate specificity of the acyltransferase domains (Haydock et al., 1995).

In any event, if ScoT is active as an editing enzyme with both the tylosin PKS and its natural PKS partner, it must be able to hydrolyse thioester bonds irrespective of the length of the extender units employed or the size of the nascent polyketide intermediates, since ScoT can apparently cooperate in the biosynthesis of a product longer than that of its native PKS partner.

We suggest that a mechanism other than substrate selectivity, probably based on differences in kinetic rates of hydrolysis by ScoT and polyketide condensation, is involved in competition between these two reactions. To clarify this, however, further studies which involve kinetic measurements of the enzyme activity are needed.

Transcription of scoT occurs in a growth-phase-dependent manner

S. nuclease mapping of the scoT promoter region in S. coelicolor A3(2) showed that transcription was growth-phase dependent. It was detectable only during late transition phase, indicating the operation of a regulatory system that prevents expression of the gene throughout most of the growth cycle. Since production of secondary metabolites by Streptomyces is commonly initiated during transition phase, onset of scoT expression might be correlated with expression of the gene cluster encoding type I PKS, located close to scoT. Our results on this will be published in due course.

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Type II thioesterase


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