Three tuf-like genes in the kirromycin producer Streptomyces ramocissimus
Vijgenboom, E.; Woudt, L.P.; Heinstra, P.W.H.; Rietveld, K.; Haarlem, J. van; Wezel, G.P. van; ...; Bosch, L.

Citation

Version: Publisher's Version
License: Licensed under Article 25fa Copyright Act/Law (Amendment Taverne)
Downloaded from: https://hdl.handle.net/1887/3217538

Note: To cite this publication please use the final published version (if applicable).
Three \textit{tuf}-like genes in the kirromycin producer \textit{Streptomyces ramocissimus}


Author for correspondence: E. Vijgenboom. Tel: +31 71 274278. Fax: +31 71 274340.

We have identified, cloned and sequenced three \textit{tuf}-like genes from \textit{Streptomyces ramocissimus} (Sr.), the producer of the antibiotic kirromycin which inhibits protein synthesis by binding the polypeptide chain elongation factor EF-Tu. The \textit{tuf-1} gene encodes a protein with 71\% amino acid residues identical to the well characterized elongation factor Tu of \textit{Escherichia coli} (Ec.EF-Tu). The genetic location of \textit{tuf-1} downstream of a \textit{fus} homologue and the \textit{in vitro} activity of Sr.EF-Tu1 show that \textit{tuf-1} encodes a genuine EF-Tu. The putative Sr.EF-Tu2 and Sr.EF-Tu3 proteins are 69\% and 63\% identical to Ec.EF-Tu. Homologues of \textit{tuf-1} and \textit{tuf-3} were detected in all five \textit{Streptomyces} strains investigated, but \textit{tuf-2} was found in \textit{S. ramocissimus} only. The three \textit{tuf} genes were expressed in \textit{E. coli} and used to produce polyclonal antibodies. Western blot analysis showed that Sr.EF-Tu1 was present at all times under kirromycin production conditions in submerged and surface-grown cultures of \textit{S. ramocissimus} and in germinating spores. The expression of \textit{tuf-2} and \textit{tuf-3} was, however, below the detection level. Surprisingly, Sr.EF-Tu1 was kirromycin sensitive, which excludes the possibility that EF-Tu is involved in the kirromycin resistance of \textit{S. ramocissimus}.

\textbf{Keywords:} \textit{Streptomyces ramocissimus}, \textit{tuf} genes, EF-Tu, kirromycin

\textbf{INTRODUCTION}

The polypeptide chain elongation factor EF-Tu of \textit{E. coli} is one of the most abundant proteins in the bacterial cell and fulfils an essential function in protein synthesis. The factor is encoded by two \textit{tuf} genes (Jaskunas \textit{et al.}, 1975; Yokota \textit{et al.}, 1980; An & Friesen, 1980), which are well separated on the chromosome and are located in completely different genetic contexts (Lindahl \textit{et al.}, 1977; Lee \textit{et al.}, 1981). The gene products differ in one single amino acid at the C-terminus. The functional significance of this \textit{tuf} gene ‘duplication’ is not well understood. The two genes in \textit{E. coli}, \textit{tuf-A} and \textit{tuf-B}, are coordinately expressed in an 1:1 ratio throughout growth, indicating that the organism sets value on the presence of both genes (van der Meide \textit{et al.}, 1983a, b).

The initial findings in \textit{E. coli} led to studies of the \textit{tuf} gene organization in various eubacteria (Sela \textit{et al.}, 1989; Filer & Furano, 1981; Ludwig \textit{et al.}, 1990) and an archaeobacterium (Lechner & Böck, 1987). Southern blot analysis revealed that the gene ‘duplication’ is widespread among Gram-negative bacteria (Filer & Furano, 1981). By contrast, the two \textit{Gram-positive} bacteria, \textit{Bacillus subtilis} and \textit{Micrococcus luteus}, studied by these authors have only one \textit{tuf} gene. These and later experiments led to the proposal that the difference in \textit{tuf} gene number is characteristic for these two groups of bacteria. Similar studies, performed more recently and covering representatives of various phyla within the eubacterial kingdom, showed that there are exceptions to the rule. The fastidious Gram-negative bacterium \textit{Chlamydia trachomatis} contains only one \textit{tuf} gene (Goldstein \textit{et al.}, 1989), as is also true for the extreme thermophilic bacterium \textit{Thermatoga maritima} (Bachleitner \textit{et al.}, 1989). One may even argue that \textit{E. coli} does not meet the rule, since it harbours the \textit{seB} gene encoding an additional EF-Tu, albeit a highly specialized one of strongly deviating size (Forchhammer \textit{et al.}, 1989). Exceptions are also found in the group of Gram-positive eubacteria. Several strains of the
genus *Clostridium* were shown to contain more than one *tuf* gene (Sela et al., 1989).

The antibiotic kirromycin inhibits protein synthesis by binding to EF-Tu which causes retention of the factor on the ribosome and immobilization of the latter on the mRNA (Wolf et al., 1977). Kirromycin belongs to the group of elfamycins, antibiotics with polyene structures (Edwards et al., 1992) which are produced by the Gram-positive streptomycetes *S. ramoecissimus* and *S. collinus* and a few others (Parmeggiani & Swart, 1985; Cundliffe, 1989).

Streptomycetes are representatives of the morphologically more complex genera of the Gram-positive bacteria. The life-cycle of the streptomycetes starts with germinated spores converting into chains of spores. When mature, these spores forming branched vegetative mycelia. From these aerial hyphae, streptomycetes produce secondary metabolites such as a wide variety of antibiotics.

Various mechanisms are exploited by antibiotic-producing organisms to protect themselves against their own product (Cundliffe, 1989). The mechanism used by kirromycin producers, like *S. ramoecissimus*, is essentially unknown (Glöckner & Wolf, 1984). Here we investigate the possibility that protection is achieved through the expression of a kirromycin-resistant EF-Tu species. Analysis of the *tuf* genes and their expression is a prerequisite. Much to our surprise we identified three rather divergent *tuf*-like genes, an unprecedented finding in prokaryotes. As a primary step towards identification of the products of the three *tuf*-like genes, we were heterologously expressed in *E. coli* using the lac promoter. With antibodies raised against two of the *tuf* gene products we studied the temporal expression of the three *tuf* genes in *S. ramoecissimus*. In both liquid cultures during kirromycin production and in surface-grown cultures when complete development takes place, only *tuf-1* is abundantly expressed but *tuf-2* and *tuf-3* expression is below the detection level.

**METHODS**

**Bacterial strains and plasmids.** Cloning was done in *E. coli* strains 490, JM101 or JM109 (Messing, 1979; Yanisch-Perron et al., 1985), using the plasmid pUC8 (Vieira & Messing, 1982) for *tuf-1*, and pAT153 (Twiang & Sherratt, 1980) for *tuf-2* and *tuf-3*. Subclones were made in pUC18 or pUC19 (Yanisch-Perron et al., 1985). In the heterologous expression studies strain KA797 [ara (lac-proAB) thi F' (proAB' lacT')], collection of the Department of Molecular Genetics, Leiden University, The Netherlands] was sometimes used instead of JM101. *S. ramoecissimus* was obtained from Gist-brocades NV, The Netherlands.

**Cloning strategy.** Both *tuf-1* and *tuf-2* were isolated by a combination of Southern hybridization and a sub-selection procedure. For cloning of *tuf-1*, chromosomal DNA of *S. ramoecissimus* was digested with BgII and ligated in *Bam*HI-digested pUC8. After transformation to *E. coli*, plasmid DNA was isolated from transformant pools, each pool representing about 300 colonies. This DNA was screened by Southern hybridization with a *HpaI*- *NruI* fragment of the *E. coli* *tufA* gene as probe. The positive pools were subsequently reduced in size until the clone harbouring *tuf-1* (pUSRT1) was isolated. In order to identify the position of *tuf-1* on the BgII insert of pUSRT1, DNasel deletion derivatives were generated essentially as described by Hong (1982). The location of *tuf-1* could be derived from the length of the insert, the *SalI* restriction pattern and Southern analysis which showed whether the *SalI* fragments that contain *tuf* sequences were still present. By this approach *tuf-1* was localized in the middle of the 2.8 kb BgII fragment.

For cloning of *tuf-2*, *BamHI*-digested chromosomal DNA was fractionated on a 1% agarose gel and fragments with a length corresponding to the signal in a Southern blot probed with the *tuf-1* internal 330 bp and 240 bp *SalI* fragments were ligated in pAT153. Clones were screened again by hybridization, using the sib-selection procedure. *tuf-2* was mapped on the positive clones (pASRT2) by digestion with various enzymes, such as *SalI*, *SmaI* and *PstI*, and identification of the fragments carrying *tuf*-like sequences by Southern hybridization. The *tuf-2* gene was thus localized at one end of the 2.8 kb *BamHI* fragment.

Cloning of *tuf-3* was achieved in a one-step screening. The gene was localized on a 12 kb *BamHI* fragment and a 9 kb *BamHI*–*EcoRI* fragment by Southern hybridization using a 330 bp internal fragment from the *tuf-1* gene. *BamHI* fragments with a length of 12 kb were isolated from an 1% agarose gel, digested with *EcoRI* and ligated in *EcoRI* and *BamHI*-digested pAT153. Since *EcoRI* sites are very rare in *Streptomyces* DNA this approach should yield a high percentage of positive clones. DNA isolated from *E. coli* transformants was analysed directly by Southern hybridization. The *tuf-3* gene was localized on the 9 kb *BamHI*–*EcoRI* fragment (pASRT3) as described for *tuf-2*.

**Southern hybridization.** Chromosomal DNA was isolated as described by Hopwood et al. (1988). DNA from 1% agarose gels was blotted to Hybond-N. Filters were hybridized with 32P-labelled probes in 6× SSC, 0.1% SDS, 1mM EDTA, 2× Denhardt’s solution [0.04% Ficoll (M, 400000), 0.04% polyvinyl pyrrolidone (M, 360000), 0.1% pyrophosphate, 200 μg calf thymus DNA ml⁻¹] for 16 h at 65 °C. When 50% formamide was used in the hybridization buffer, the incubation was done at 42 °C. Filters were washed in 6× SSC at 65 °C and 2× SSC at 65 °C for homologous hybridizations and 0.5× SSC or 0.2× SSC at 65 °C for homologous hybridizations.

Diphosphorylated DNA probes were labelled with [32P]ATP and T4 polynucleotide kinase, essentially as described by Maniatis et al. (1982), or labelled with the random prime method (Feinberg & Vogelstein, 1983, 1984).

**DNA sequencing.** Sequencing was done by the dideoxynucleotide method of Sanger et al. (1977) and M13mp18 or mp19 as vector (Yanisch-Perron et al., 1985). 7-Deaza-2'-deoxyguanosine triphosphate was used to minimize band compression due to GC-rich regions.

**Growth of cultures.** The *E. coli* strains were grown and transformed with the indicated plasmids and cultured in LB medium at 37 °C. Media were supplemented with 100 μg ampicillin ml⁻¹ and transcription from the lac promoter was induced by adding 0.5 mM IPTG. *Streptomyces* strains were cultured at 30 °C in baffled flasks in various liquid media: S medium (4 g peptone, 4 g yeast extract, 10 g glucose, 0.5 g MgSO₄, 7H₂O, 2 g KH₂PO₄ and 2 g K₂HPO₄ per litre of water), TSB + 1% Casamino acids, YE or YMG (for details on media see Hopwood et al., 1985). Solid media for surface-grown material
RESULTS

Isolation of three tuf-like genes from S. ramocissimus

A Southern blot of S. ramocissimus chromosomal DNA digested with either BamHI, BglII or PsiI revealed three bands ranging from 2.8 to 15 kb when hybridized with an E. coli tufA probe (Fig. 1). Two bands can be explained by a restriction site within a tuf gene with an expected size of about 1200 bp but three bands cannot. Apparently, at least two separate tuf-like genes are present on the S. ramocissimus genome. Fragments were therefore cloned and sequenced for further identification.

Using a fragment completely internal to the E. coli tufA coding sequence (Hpal–NruI) as a probe and E. coli as the host for cloning, a high background from the chromosomal genes was too be expected when screening libraries by colony hybridization. Therefore we applied a sib-selection procedure in which Southern hybridization was used to screen plasmid DNA isolated from transformant pools. By successively reducing the pool size the 2.8 kb BglII fragment, which hybridizes strongly with the tufA probe (cf. Fig. 1), was cloned. The DNA sequence was determined and analysed by computer with the Wisconsin

---

**Fig. 1.** Southern blot of S. ramocissimus chromosomal DNA. DNA was digested with BamHI, BglII or PsiI and probed with the Hpal–NruI fragment of E. coli tufA. The tuf gene identified on each of the signals is indicated with the corresponding number. The signal for tuf-3 is not visible in the BglII lane but its position was identified on a Southern blot probed with the tuf-1 gene of S. ramocissimus (data not shown).

Three tuf-like genes in *Streptomyces ramocissimus*
Fig. 2. DNA sequences of (a) tuf-1, (b) tuf-2 and (c) tuf-3 from *S. ramocissimus*. The deduced amino acid sequences are indicated below the DNA sequence and the putative ribosome binding sites (AGGAGG for both tuf-1 and tuf-2, and GAGG for tuf-3) are underlined. Nucleotides 1-1026 in (a) code for the C-terminal part of EF-G. The nucleotide sequences are deposited in the EMBL Data Library, accession nos X67057 (tuf-1), X67058 (tuf-2) and X67059 (tuf-3).

GCG programs Translate and Codonpreference (Deveraux *et al.*, 1984) which revealed two open reading frames (ORFs) (Fig. 2a). One ORF displayed a high degree of identity with the C-terminal part of the *E. coli ftsA* gene, encoding EF-G (*Zengel et al.*, 1984) and the other with *tufA* (*Yokota et al.*, 1980). The latter ORF codes for a
protein of 396 amino acids, designated (Sr)EF-Tu1 (see Fig. 3). A probe derived from the C-terminal part of the \( f u s \) gene present on the cloned \( B g I I \) fragment gave a single signal in the Southern blot. This probing also showed that the 2.8 kb \( B g I I \) fragment is part of the 5.2 kb \( B a m H I \) and of the 6.2 kb \( P s t I \) fragment (data not shown). Partial sequencing of the 6.2 kb \( P s t I \) fragment and hybridization studies suggest that the gene organization on this part of the \( S. r a m o c i s s i m u s \) genome is \( r p s L-r p s G-f u s-t t f \), identical to that of \( E. c o l i \) (Post et al., 1980), Spirulina platensis (Buttarelli et al., 1989), Micrococcus luteus (Ohama et al., 1987) and Anacystis nidulans (Meng et al., 1989) (data not shown). To gain more insight into the nature of the fragments that hybridized more weakly with the \( E. c o l i \) \( t u f A \) probe (\( B a m H I \) fragments of 2.8 and 12 kb and \( P s t I \) fragments of 4.3 and 15 kb), the Southern hybridization experiment was repeated with probes from the N-terminal and C-terminal part of the \( S. r a m o c i s s i m u s \) \( t u f-1 \) gene. Both probes hybridized with each of the four fragments, indicating that they contain complete \( t u f \)-like genes.

A \( t u f-1 \) probe that gave a stronger signal in the Southern analysis than the \( E. c o l i \) \( t u f A \) probe was used to clone the 2.8 kb \( B a m H I \) fragment and a 9 kb \( E c o R I-B a m H I \) fragment. The 2.8 kb \( B a m H I \) fragment carries an ORF corresponding to a protein of 396 amino acids, whereas the 9 kb \( B a m H I-E c o R I \) fragment carries an ORF corresponding to a protein of 388 amino acids (Figs 2b, c, 3). The genes were designated \( t u f-2 \) and \( t u f-3 \) and their products \( S r.EF-Tu2 \) and \( S r.EF-Tu3 \), respectively, although we do not know whether they encode genuine EF-Tus.

The nucleotide and amino acid sequence comparisons

Degrees of nucleotide sequence identity of the three \( S. r a m o c i s s i m u s \) \( t u f \)-like genes and \( E. c o l i \) \( t u f A \) are listed in Table 1. Most strikingly, the \( S. r a m o c i s s i m u s \) \( t u f \) genes display a much lower degree of similarity than do the two \( E. c o l i \) \( t u f \) genes (99%), which differ at four base positions only. The nucleotide sequence of \( t u f-3 \), encoding the GDP-binding domain (amino acids 1-200), has 76% identity with the corresponding sequences of \( t u f-1 \) and \( t u f-2 \). This identity drops to 63%, however, for the sequence encoding the C-terminal part of the protein. This drop in identity coincides with a change in the codon usage towards favouring codons with \( A \) or \( T \) in the third position, which is unusual for \( S t r e p t o m y c e s \). Obvious deviations from the codon usage often found in genes with a high level of expression (Wright & Bibb, 1992) are not observed in \( t u f-1 \) and \( t u f-2 \). However, it is noteworthy that \( t u f-1 \), but not \( t u f-2 \) and \( t u f-3 \), has a high percentage of GGT codons for Gly, as has also been observed for the ribosomal protein \( L 7 / L 12 \) of \( S. a n t i b i o t i c u s \) (Parra et al., 1992).

Both \( t u f-1 \) and \( t u f-2 \) are preceded by putative ribosome binding sites with 6/6 homology to the 3' end of known 16S rRNA sequences (van Wezel et al., 1991, and references therein). In the case of \( t u f-3 \) this is fit only 4/6 (Fig. 2c). A search for promoter sequences upstream of the three \( t u f \) genes using the \( S t r e p t o m y c e s \) promoter consensus sequence described by Strohl (1992) was unsuccessful. Sequences upstream and downstream of the genes were analysed for identity with known sequences in the databases. A positive result was obtained only in the case of the \( t u f-1 \) upstream region where the \( f u s \) gene, encoding EF-G, was localized.

In Fig. 3 the deduced amino acid sequences are compared with the \( E. c o l i \) EF-Tu sequence since most of the data regarding structure/function relationships concern the \( E. c o l i \) protein. All three \( S t r e p t o m y c e s \) proteins contain the consensus sequence typical for GDP-binding proteins (Dever et al., 1987) and show a 100% fit with the P-loop motif (Saraste et al., 1990). The Ec.EF-Tu amino acid residues His-66, Lys-208 and Lys-237 (underlined in Fig. 3) that have been cross-linked to tRNA (Duffy et al., 1981; van Noort et al., 1984) are conserved in EF-Tu1 but not in EF-Tu2 or EF-Tu3. Lys-56 of Ec.EF-Tu, which has been found to be methylated in the late exponential phase and stationary phase (van Noort et al., 1986), is not present at that position in any of the three. All amino acid residues known to be altered in kirromycin-resistant mutants are conserved in the three \( S r . E F - T u s \) (see Discussion). On the other hand, Lys-357 of Ec.EF-Tu, previously cross-linked to kirromycin (van Noort et al., 1984) is not conserved.

The results of a comparison between the deduced amino acid sequences of the three \( S r . E F - T u s \) and some of the known EF-Tu sequences of almost all the phyla in the eubacterial kingdom, one representative of the archaeabacteria and two eukaryotes are shown in Table 2. \( S r . E F - T u 1 \) and \( S r . E F - T u 2 \) are more closely related to each other than to any of the other sequences listed in Table 2. This suggests that the genes were derived relatively recently from a common ancestral gene. In contrast, the similarity between EF-Tu3 and EF-Tu1 or EF-Tu2 is only slightly higher than with any of the other eubacterial EF-Tus. The degree of identity of EF-Tu3 to each of these other eubacterial EF-Tus is about the same, but much higher than to the archaeabacterial or eukaryotic EF-1\( \alpha \) species. So, although a relationship of EF-Tu3 with the EF-Tus from the same organism is not apparent, EF-Tu3 clearly belongs to the eubacterial lineage. This is consistent with the finding that the three \( S r . E F - T u s \) show the same degree of identity/similarity with the EF-1\( \alpha \) species of \( R b i z o m y c o r r a c e m o s u s \) and \( X e n o p o s t a l a e n s \). Interestingly, EF-Tu3 shows a somewhat closer relationship with \( T h e r m o -
Three tuf-like genes in Streptomyces ramocissimus

EF-Tu1  1  AKAKFERTKPHVINIGTGIDHGKTTLAATKVLHDAYPDNLNEATPFDN  Q RF PF Q
EF-Tu2  2  S TAYV L M V  . . ERGSGTEV R
EF-Tu3  3  S E V V T AKT GG . A RA Q
EF-TuA  4  51 101 151 201 251 301 351

51  IDKAPERQGITISIAHVEYQTEARHYAHVDCPGHA Q ADYIKMNITGAAQM
R AA N E DT M V V L
N KA NTS D PT V

101  DGAILVVAATDGPMPOQTEHVLLARQVGVPYIVVA LNKA D VMDD DEIMEL
T L S L I A DH . . AG LTD
R I G I F C L L

151  VELEVRELLSEYEFPPGDLPVVRVSALKALEGDAQWQTSVDMKAVDES
T V K R PR R E L D F
D HGYG GA G PK A IEA LD TY
M Q D T I G E E A K I E A G FL SY

201  IPEPERDVDPFPLMPIEDVFTITGRGTVMGRERGLKVNQNETVIDIGIK
V V R V V Y A L V N L AV TVR GNR E VL AG
A I L S S V I I G E V E

251  TEKTITTVGTIEFMKRLLDECGPAGENVGLLLRGIKRDEVERGQVIKPGS
EQR R R V Q V R
L . . V L T G PM A D A VP DA R H VAA
. TQKS C V R V E I LA T

301  VTPHTEFEAQAYILSKDEGGRHTPFFNYRPFYFRTTDVTGVVHLEPGT
Q E T K
V RSR S V V AR T VTSG I A V D D G . V
IK K SEV KG TIE V

351  EMVMNPDNTEMVLEIQPYAMEEGLKFIAIREGGRTVGAGQVTKIVK 396
A H Q I R 396
GVAR ETVS I GRE PL P G T AL 388
IK V T HI DD R V A VLG 393

Fig. 3. Amino acid sequences of EF-Tu1, 2 and 3 from S. ramocissimus and EF-TuA from E. coli aligned with the GAP program of the Wisconsin GCG sequence analysis package (Devereux et al., 1984). The GDP binding consensus sequence is underlined and in bold. The residues corresponding to the Ec.EF-Tu amino acids involved in tRNA interaction are underlined in the EF-Tu1 sequence. The amino acids changed in kirromycin-resistant E. coli EF-Tus are indicated in bold. The residues Lys-56 and Lys-357 which are sometimes methylated in EF-TuA are printed in italic and underlined.

coccus celer EF-Tu than do EF-Tu1 and EF-Tu2. The unusual sequence data of EF-Tu3 prompted a search for tuf-3 homologues in Streptomyces spp. and other bacteria.

Number of tuf-like genes in other Streptomyces species

The presence of three tuf-like genes in S. ramocissimus raised the question whether this is a particular feature of this species or a more general gene arrangement of Streptomyces. We therefore analysed chromosomal DNA of several Streptomyces species digested with PstI and BamHI by probing the Southern blot with a fragment internal to the coding sequence of tuf-1 (Fig. 4a), of tuf-2 (Fig. 4b) and of tuf-3 (Fig. 4c). The signals in (a) correspond to tuf-1 homologues in the various strains. The signals in (c) are tuf-1 [cf. (a)] and tuf-3 homologues. In addition some weaker signals can be observed which have not been characterized further. The tuf-2 probe in (b) does not reveal tuf-2 homologues in any of the strains except for S. ramocissimus. The stronger signals correspond to tuf-1 [cf. (a)] and the weaker signals to tuf-3 [cf. (c)].

Heterologous expression of the tuf-like genes in E. coli

Expression of tuf-1. Transformation of E. coli with pUSRT1-1 (Fig. 5a) did not result in good heterologous
expression of $tuf-1$ in cells during exponential growth (i.e. 1 and 2 h after induction). Highest expression was observed 16 h after induction, when the cells were in the stationary phase (Fig. 6). Further analyses were then performed with immunoblotting using antibodies raised against EF-Tu isolated from $S$. ramocissimut. The Western blot of Fig. 7 (lanes 1 and 2) shows that this EF-Tu migrates to the same electrophoretic position as the product of $tuf-1$, isolated from stationary phase $E$. coli cells after heterologous $tuf-1$ expression. Therefore, we conclude that the EF-Tu species isolated from $S$. ramocissimut is the product of $tuf-1$. Both EF-Tu isolated from $S$. ramocissimut and the product of $tuf-1$, heterologously expressed in $E$. coli are able to participate in poly(Phe) synthesis in vitro and are inhibited by kirromycin (Fig. 8a, b). Kirromycin sensitivity (EF-Tu1) was dominant over kirromycin resistance (EF-Tu of $E$. coli strain PM1455) and therefore inhibition of poly(Phe) synthesis was observed (Fig. 8b).

**Expression of $tuf-2$.** For the expression of $tuf-2$ in $E$. coli two recombinant plasmids were constructed, pUSRT2-1 and pUSRT2-3 (Fig. 5b). Expression of $tuf-2$ in JM101 transformed with pUSRT2-1 could not be demonstrated (Fig. 7, lane 3). In overnight cultures of JM101 transformed with pUSRT2-3 which has part of the $tuf-2$ upstream sequence deleted, $tuf-2$ expression was detectable (Fig. 7, lane 4). The heterologous expression of $tuf-2$ was substantially lower than that of $tuf-1$. It could only be detected on Western blots and not in Coomassie Brilliant Blue stained gels. Moreover, about 80% of the $tuf-2$ product was found in so-called inclusion bodies, which are spun down at 30000g (data not shown). The expression was too low for purification, functional characterization and immunization. Although EF-Tu2 has the same number of amino acids (396) as EF-Tu1, it cannot be demonstrated in JM101 cells transformed with pUSRT3-1 (Fig. 5c). Sequences immediately upstream of the putative ribosome binding site (GAGG, nt 1111-1114, Fig. 2c) of the $tuf-3$ gene were deleted to remove potential transcriptional termination signals. This did not result in appreciable expression either. The ribosomal binding site of $tuf-1$ was then cloned upstream of $tuf-3$, yielding the plasmid pUSRT3-3 (Fig. 5d). This resulted in very high expression of $tuf-3$ in the $E$. coli strain KA797 (Fig. 9, lanes 2, 4 and 5), which made distinction between the two factors in $S$. ramocissimut extracts possible.

**Expression of $tuf-3$.** Expression of the $tuf-3$ gene could not be demonstrated in JM101 cells transformed with pUSRT3-1 (Fig. 5c). Sequences immediately upstream of the putative ribosome binding site (GAGG, nt 1111-1114, Fig. 2c) of the $tuf-3$ gene were deleted to remove potential transcriptional termination signals. This did not result in appreciable expression either. The ribosomal binding site of $tuf-1$ was then cloned upstream of $tuf-3$, yielding the plasmid pUSRT3-3 (Fig. 5d). This resulted in very high expression of $tuf-3$ in the $E$. coli strain KA797 (Fig. 9, lanes 2, 4 and 5), which made distinction between the two factors in $S$. ramocissimut extracts possible.

Table 2. Amino acid sequence comparison of the three $tuf$ gene products of $S$. ramocissimut with representatives of the various kingdoms.

<table>
<thead>
<tr>
<th>Kingdom</th>
<th>$S$. ramocissimut $tuf$-1</th>
<th>$S$. ramocissimut $tuf$-2</th>
<th>$S$. ramocissimut $tuf$-3</th>
</tr>
</thead>
<tbody>
<tr>
<td><strong>Eubacteria</strong></td>
<td></td>
<td></td>
<td></td>
</tr>
<tr>
<td>$S$. ramocissimut</td>
<td>100</td>
<td>88; 94</td>
<td>65; 78</td>
</tr>
<tr>
<td>$S$. ramocissimut</td>
<td>100</td>
<td>88; 94</td>
<td>65; 78</td>
</tr>
<tr>
<td>Micrococcus luteus</td>
<td>79; 87</td>
<td>77; 87</td>
<td>61; 76</td>
</tr>
<tr>
<td>E. coli (purple bacteria)</td>
<td>74; 85</td>
<td>72; 84</td>
<td>60; 77</td>
</tr>
<tr>
<td>Thermus aquaticus (thermophiles)</td>
<td>71; 84</td>
<td>71; 84</td>
<td>63; 77</td>
</tr>
<tr>
<td>Thermatoga maritima (6)</td>
<td>70; 84</td>
<td>69; 84</td>
<td>63; 80</td>
</tr>
<tr>
<td>Anaocystis nidulans (cyanobacteria)</td>
<td>70; 83</td>
<td>67; 82</td>
<td>60; 75</td>
</tr>
<tr>
<td>Spirulina platensis (cyanobacteria)</td>
<td>70; 82</td>
<td>67; 80</td>
<td>59; 75</td>
</tr>
<tr>
<td>Mycoplasma genitalium (Gram-pos., low GC)</td>
<td>69; 82</td>
<td>67; 80</td>
<td>60; 74</td>
</tr>
<tr>
<td>Cyanophora paradoxa (cyanelle)</td>
<td>68; 81</td>
<td>65; 80</td>
<td>59; 75</td>
</tr>
<tr>
<td><strong>Archaeobacteria</strong></td>
<td></td>
<td></td>
<td></td>
</tr>
<tr>
<td>Thermococcus celer (11)</td>
<td>39; 61</td>
<td>38; 60</td>
<td>40; 63</td>
</tr>
<tr>
<td><strong>Eukaryotes</strong></td>
<td></td>
<td></td>
<td></td>
</tr>
<tr>
<td>Rhizomucor racemous (12)</td>
<td>33; 57</td>
<td>33; 57</td>
<td>35; 57</td>
</tr>
<tr>
<td>Xenopus laevis, 42Sp50 (13,14)</td>
<td>33; 52</td>
<td>33; 52</td>
<td>34; 54</td>
</tr>
<tr>
<td>Xenopus laevis, EF-1αS and EF-1αO (13,14)</td>
<td>33; 57</td>
<td>32; 57</td>
<td>34; 55</td>
</tr>
</tbody>
</table>
Three tuf-like genes in Streptomyces ramocissimus

Fig. 4. Southern blot of chromosomal DNA isolated from (1) E. coli, (2) S. ramocissimus, (3) S. coelicolor, (4) S. ambofaciens, (5) S. lividans, (6) S. glaucescens and digested with BamHI plus PstI. The blots were probed with (a) 243 bp SmaI fragment of tuf-1 (nt 1435–1678, Fig. 2a), (b) 1000 bp NarI fragment of tuf-2 (nt 483–1483, Fig. 2b), (c) 633 bp SalI fragment of tuf-3 (nt 1503–2136, Fig. 2c). The blot in (a) was washed under more stringent conditions (0.3 x SSC) than those in (b) and (c) (1.5 x SSC) in order to identify the signal corresponding to the tuf-1 homologues in the various chromosomal DNAs.

this subcellular distribution of the product by varying the culturing conditions, such as lowering temperatures and shortening growth and periods of induction by IPTG. To solubilize the tuf-3 gene product pellets were treated with 4 M urea and 100 μg lysozyme ml⁻¹ according to Frankel et al. (1990) and centrifuged at 30000 g. The tuf-3 gene product now appeared in the S30 supernatant and remained soluble after removal of urea by passing the supernatant through Sephadex G-25 (PD10 column, Pharmacia). The eluate of this column was submitted to agarose gel electrophoresis and the tuf-3 gene product isolated by freeze-sweeping. The tuf-3 product thus obtained was homogeneous as judged by SDS-PAGE (Fig. 9, lane 4) and migrated slightly faster than E. coli EF-Tu (Fig. 9, lane 5) but significantly faster than EF-Tu1 (Fig. 9, lanes 3 and 4). Activity of the protein, however, could not be demonstrated with in vitro assays. Polyclonal antibodies raised against the tuf-3 product showed cross-reactivity towards EF-Tu1 and heterologously expressed tuf-2 product. The tuf-3 product, however, is not recognized by anti-EF-Tu1 (data not shown).

Homologous expression

The availability of antibodies raised against EF-Tu1 enabled us to study its synthesis and that of EF-Tu2 under various conditions in S. ramocissimus. The antibodies raised against the tuf-3 product enable the detection of all three EF-Tus. That they also recognize EF-Tu3 produced in Streptomyces was demonstrated by putting tuf-3 behind the constitutive ermE promoter on the plasmid pIJ4090 (J. White & M. J. Bibb, unpublished), resulting in pISRT3-1. Over-expression had to be studied in S. coelicolor M145 since a suitable transformation system for S. ramocissimus was not found. Submerged cultures of pISRT3-1 transformants of S. coelicolor were grown in TSB medium for 24 h. S30 extracts were then submitted to immunoblotting, using the antibodies against the tuf-3...
Fig. 5. Construction of plasmids for heterologous expression. (a) pUSRT1-1. A 1.8 kb NruI(1006)-EcoRI(2836) fragment containing the entire tuf-1 gene was subcloned from the 2.8 kb BglII fragment of pUSRT1 in SmaI- and EcoRI-digested pUC19 (Yanisch-Perron et al., 1985). The NruI site is located 180 bp upstream of the GTG start codon of tuf-1 and the EcoRI site is from pUC19, adjacent to the BglII/BamHI ligation site. (b) pUSRT2-1. From the 2.8 kb BamHI fragment containing the entire tuf-2 gene, a BamHI(B)-EcoRI(2100) subclone was constructed in pUC19. pUSRT2-3. pUSRT-2 was digested with MluI(200) and the protruding 3' ends were converted to blunt ends by T4 DNA polymerase. After digestion with EcoRI, the fragment harbouring tuf-2 was cloned in SmaI-EcoRI-digested pUC19 resulting in pUSRT2-2. In order to ensure that translation, starting at the ATG of lacZ in pUC19, did not continue into tuf-2, the 5' protruding ends of HindIII (site in the polylinker of pUC19 and upstream of the tuf-2 fragment) -digested pUSRT2-2 were filled and ligated. The plasmid pUSRT2-3 contains a stop codon (TAG) located at the position of the original HindIII site and in frame with the lacZ start. (c) pURST3-1. This was constructed by partially digesting pASRT3 with SstI and with PstI. The SstI(348)-PstI(4300) fragment was subcloned in pUC18. (d) pURST3-3. In order to replace the ATG upstream region of tuf-3 by that of the tuf-1 GTG upstream region, EcoRI sites were constructed immediately in front of the translation start codons (steps 1 and 3). The final construct pURST3-3 was isolated after a three fragment ligation: BamHI–EcoRI (tuf-1 upstream region), EcoRI–PstI (containing tuf-3), and BamHI–PstI-digested pUC18 (steps 2, 4 and 5). All base changes were made by oligonucleotide-directed mutagenesis according to Kunkel et al. (1990) and confirmed by sequencing.
Three tuf-like genes in Streptomyces ramocissimus

Fig. 6. Temporal expression of tuf-1 in E. coli JM101 studied with SDS-PAGE. E. coli JM101 transformed with pUSRT1-1 was grown in LB broth at 37 °C. The expression of tuf-1 was induced by the addition of 0.5 mM IPTG at OD₆₀₀ 0.2. The indicated times are relative to the addition of IPTG (= 0 h). Total cell extracts were subjected to SDS-PAGE. The gel was stained with Coomassie Brilliant Blue. The sample in lane 0 was taken immediately before the addition of IPTG. The positions of Ec.EF-Tu and Sr.EF-Tu1, as indicated in the figure, were identified in Western blots with antibodies raised against Sr.EF-Tu.

Fig. 7. Expression of tuf-1 and tuf-2 in E. coli JM101 (16 h induced with IPTG) studied with immunoblotting using antibodies raised against EF-Tu1 isolated from S. ramocissimus. The tuf gene products observed in each lane are, from top to bottom. Lane 1, EF-Tu1 purified from S. ramocissimus; lane 2, EF-Tu1 and Ec.EF-Tu, total extract of E. coli JM101 pUSRT1-1; lane 3, Ec.EF-Tu, total extract of E. coli JM101 pUSRT2-1; lane 4, EF-Tu2 and Ec.EF-Tu, total extract of E. coli JM101 pUSRT2-3; lane 5, EF-Tu1, EF-Tu2 and Ec.EF-Tu, mixture (1:1) of samples applied in lane 1 and 4.

Fig. 8. EF-Tu1 is kirromycin sensitive. (a) Poly(U)-directed incorporation of [14C]phenylalanine into trichloroacetic acid precipitable material was studied as a function of the kirromycin concentration in an in vitro translation system dependent on EF-Tu. Reactions were carried out with ribosomes and EF-G isolated from E. coli. Incorporation of 14C-label observed with Ec.EF-Tu (isolated from LBE1001, a wild-type E. coli strain) in the absence of kirromycin, normalized to 100%. ○, EF-Tu1, isolated from S. ramocissimus. For experimental details see van der Meide (1982). (b) Poly(U)-directed poly(Phe) synthesis was measured with and without 30 pg kirromycin ml⁻¹ in S30 supernatants of the kirromycin-resistant E. coli strain PM1455 and in PM1455 transformed with pUSRT1-1. The S30 supernatants were fractionated over Sephadex G-25 and the first four fractions with an absorbance at 260 nm were combined. An aliquot was incubated with tRNA, [³H]Phe and poly(U) at 37 °C (for experimental details see Luiten et al., 1991). Samples were taken at the indicated times and in vitro translation of poly(U) was measured as trichloroacetic acid precipitable ³H-labelled product.
Fig. 9. Expression of \textit{tuf-3} in \textit{E. coli} studied with SDS-PAGE. Proteins were stained with Coomassie Brilliant Blue. Lane 1, total extract of KA797 cultured for 8 h in LB medium; lane 2, total extract of KA797(pUSRT3-3) cultured for 8 h in LB medium and induced with IPTG during the last 2 h; lane 3, EF-Tu1 purified from \textit{S. ramocissimus}; lane 4, purified EF-Tu3; lane 5, Ec.EF-Tu.

Fig. 10. Western blot analysis of EF-Tu1 and EF-Tu3 probed with antibodies against Sr.EF-Tu3. Lane 1, Sc.EF-Tu1 – S30 supernatant fraction of liquid grown \textit{S. coelicolor} M145; lane 2, Sc.EF-Tu1 and EF-Tu3 – S30 supernatant fraction of liquid-grown \textit{S. coelicolor} M145 pSRT3-1; lane 3, EF-Tu3 purified from \textit{E. coli} JM101(pUSRT3-3); lane 4, EF-Tu1 isolated from \textit{S. ramocissimus}.

Fig. 11. Temporal expression of \textit{tuf} genes in submerged cultures of \textit{S. ramocissimus}, studied with Western blotting using anti-EF-Tu1 (a) and anti-EF-Tu3 (b). Lane 1, purified EF-Tu1; lane 2, S30 pellet fraction after 20 h culturing; lane 3, S30 supernatant fraction after 20 h culturing; lane 4, S30 pellet fraction after 44 h; lane 5, S30 supernatant fraction after 44 h; lane 6, S30 pellet fraction after 68 h; lane 7, S30 supernatant fraction after 68 h; lane 8, EF-Tu2 and Ec.EF-Tu, total extract of \textit{E. coli} JM101(pUSRT2-3); lane 9, EF-Tu3 purified from \textit{E. coli} JM101(pUSRT3-3).

Fig. 12. Western blot of extracts from surface-grown \textit{S. ramocissimus}. The blot was incubated with antibodies raised against the \textit{tuf-3} product. In lanes 1 to 6 equal amounts of protein were loaded. \textit{S. ramocissimus} was grown on minimal medium. The bars above the Western blot indicate the presence of aerial hyphae (42–80 h) and of spores (58–80 h) as observed by phase-contrast microscopy. S30 supernatant fractions were prepared after 18 h (lane 1), 27 h (lane 2), 42 h (lane 3), 51 h (lane 4), 66 h (lane 5), and 80 h (lane 6) of growth. Lane 7, Sc.EF-Tu1 and EF-Tu3 – S30 supernatant of liquid-grown \textit{S. coelicolor} M145(pSRT3-1); lane 8, EF-Tu2 and Ec.EF-Tu – S30 supernatant of \textit{E. coli} JM101(pUSRT2-3).

The Western blot of Fig. 10 revealed the presence of both EF-Tu3 and \textit{S. coelicolor} EF-Tu1 (Sc.EF-Tu1) in the transformed cells (Fig. 10, lane 2) and that of solely Sc.EF-Tu1 in the parental cells (Fig. 10, lane 1). This demonstrated that Sc.EF-Tu1 is recognized by the antibodies raised against the \textit{tuf-3} product and that it has
the same migration rate as EF-Tu1 of S. ramocissimus (Fig. 10, lanes 1, 2 and 4). EF-Tu3 obtained from pISRT3-1 expression in S. coelicolor migrated at the same rate as does the product of heterologously expressed tuf-3. Therefore we suppose that EF-Tu3, when synthesized in S. ramocissimus, behaves similarly during SDS-PAGE. Overexpression of tuf-2 in S. coelicolor has not yet been achieved. But assuming that EF-Tu2 is recognized by both types of antibodies and that it migrates as demonstrated for the product of tuf-2 expressed in E. coli, EF-Tu2 can be detected as well.

Temporal tuf gene expression in S. ramocissimus

Submerged mycelium of S. ramocissimus was cultured for various periods of time in S medium, whereafter the mycelium was sonicated and the resulting suspensions were centrifuged at 30000 g. Under these culture conditions kirromycin is produced. This was demonstrated by extraction of the antibiotic from the medium and analysis with thin-layer chromatography (data not shown). S30 pellets and S30 supernatants were then submitted to SDS-PAGE and immunoblotting using anti-EF-Tu1 (Fig. 11a) and anti-EF-Tu3 (Fig. 11b). EF-Tu1 is clearly present in S30 supernatants (but not in S30 pellets) of exponentially growing cells (20 h cultures, lanes 2 and 3). Larger amounts can be seen, both in the pellet and in the supernatant fractions of cells cultured for 44 h (lanes 4 and 5) and 68 h (lanes 6 and 7). A very faint band is visible at the position of EF-Tu2 but its appearance was not reproducible and degradation of EF-Tu1 cannot be excluded. A signal corresponding to EF-Tu3 was not observed.

Surface-grown cultures of Streptomyces show complete morphological differentiation. It was of interest to investigate whether or not expression of tuf genes coincides with one or more of the differentiation stages. Surface-grown cells from S. ramocissimus were therefore cultured on minimal medium for various periods of time. S30 supernatant fractions, analysed by Western blotting using anti-EF-Tu3 (Fig. 12, lanes 1–6), showed the presence of EF-Tu1 only. A similar analysis of S30 supernatant fractions from pre-germinated spores and aerial hyphae also revealed the presence solely of EF-Tu1 (not shown).

The presence of three tuf-like genes in the mycelial bacterium S. ramocissimus is intriguing. As outlined in the Introduction, the group of Gram-positive bacteria was assumed to harbour only one tuf gene. Our results indicate that this is not so in the case of S. ramocissimus and most likely not in that of more, if not all, Streptomyces spp. (Fig. 4). The location of tuf-1, i.e. downstream of fks, is similar to that of E. coli tufA in the str operon and is in line with tuf-1 encoding a genuine EF-Tu. This is confirmed by the characterization of the tuf-1 product in vitro (Fig. 8). Evidence for a gene organization like that of the E. coli tufB operon (four tRNA genes preceding tufB) was not obtained for either tuf-2 or tuf-3.

A further striking finding is that the amino acid sequences of EF-Tu1, 2 and 3 from S. ramocissimus are not as similar as those of EF-TuA and B from E. coli. In the fungus Rhizomucor racemosus, the products of the three genes coding for EF-1a show 99% identity. On the other hand, the eukaryote Xenopus laevis has three genes encoding EF-1α which do not show the strong sequence conservation of their products as observed in other organisms (Djé et al., 1990). Two EF-1α genes, one expressed in embryos and adult cells (EF-1αS), the other in oocytes (EF-1αO), have a high product identity (91%). The EF-1α (42Sp50) encoded by the third gene has an identity of only 69% compared to the other two (Deschamps et al., 1991). It is found in so-called storage particles as a complex with 5S RNA and various tRNAs (Djé et al., 1990, and references therein). The possibility may be envisaged, therefore, that EF-Tu3 from S. ramocissimus has a specialized function. In this context, it is worth mentioning that the identity between EF-Tu1 and EF-Tu2 is 88%, whereas that between EF-Tu3 and the other EF-Tus from the streptomycete is only 65%.

The sequence data do not provide any indication that one of the streptomycete EF-Tus might be kirromycin resistant. Amino acid residues (indicated in bold type in Fig. 3) known to be altered in kirromycin-resistant E. coli EF-Tu mutants, i.e. residues 375, 316, 222, 124 (Duisterwinkel et al., 1984; Zeef & Bosch, 1993) and 329 (Abdulkarim et al., 1991) are conserved in all three S. ramocissimus EF-Tus. Kirromycin resistance due to residues elsewhere in the molecule cannot be excluded. We, therefore, expressed the three tuf-like genes in E. coli and studied their temporal expression in S. ramocissimus. After heterologous expression of tuf-1 most of the product can be recovered from E. coli in a soluble form. By contrast, heterologous expression of tuf-2 and tuf-3 yields inactive products, deposited in inclusion bodies. We do not know what determines the different fate of the three tuf products. Incorrect folding of the nascent chain has been invoked to explain this phenomenon, observed after overexpression of foreign genes. If so, it is unclear why the products of tuf-2 and tuf-3 should not fold properly during de novo synthesis in E. coli, whereas the tuf-1 product folds correctly. Functional differences between the gene products may be considered in this context.

Although functional characterization of only the tuf-1 gene product has been achieved, heterologous gene expression of all three genes in E. coli enabled the identification of each protein and the production of antibodies. A larger difference in molecular mass was observed in the Western blots than expected on the basis of the amino acid sequence derived from the nucleotide sequence (maximally eight amino acid residues). Post-translational modification seems an unlikely explanation since both the tuf-1 and tuf-3 products, either homologously or heterologously expressed, displayed the same electrophoretic migration rate.

One of the questions of interest is whether kirromycin production coincides with the expression of one or more of the tuf genes. It has been shown in E. coli that kirromycin sensitivity is dominant over kirromycin re-
sistance (van de Klundert et al., 1978). Provided that this rule applies to S. ramocissimus and that either tuf-2 or tuf-3 encodes a kirromycin-resistant EF-Tu, we would expect a clear reduction of the amount of EF-Tu1, which is kirromycin sensitive, and a simultaneous increase in concentration of EF-Tu2 or EF-Tu3. We could only identify unambiguously one tuf product, EF-Tu1, in submerged cultures of S. ramocissimus under conditions when kirromycin is produced. Surface-grown cultures also produced EF-Tu1 only. If present in S. ramocissimus, the intracellular amount of EF-Tu2 and EF-Tu3 is less than a few percent of that of EF-Tu1. These data suggest that protection of S. ramocissimus against its own product, kirromycin, is not provided by alteration of EF-Tu. Protection must therefore be achieved by mechanisms such as efficient transport of the antibiotic out of the cell, deposition of it in an intracellular compartment or intracellular modification (for a review see Cundliffe, 1989).

The absence of detectable tuf-2 and tuf-3 expression raises the question whether they are silent genes or expressed at very low levels. We opt for the latter and suggest that they have specialized functions not requiring the high concentration normally found for elongation factor Tu. An obvious experimental approach to investigate whether tuf-2 and/or tuf-3 are essential would be gene inactivation. Up till now we have been unable to transform S. ramocissimus. Other Streptomyces spp. such as S. coelicolor and S. lividans can be transformed readily (Hopwood et al., 1985). Therefore the perspective of studying tuf-3 inactivation in one of these strains is much more promising.

ACKNOWLEDGEMENTS

We thank Drs R. G. M. Luiten, J. A. van den Berg, R. F. Beudeker, B. Kraal and R. H. Cool for helpful discussions, and Drs P. H. van der Meide and P. van Solingen for some of the data presented in Fig. 8. This research was supported by Gist-brocades NV, The Netherlands and the Technology Foundation (STW) which is subsidized by the Netherlands Organization for Scientific Research (NWO).

REFERENCES


Received 8 September 1993; revised 17 October 1993; accepted 26 October 1993.