The \textit{tuf3} gene of \textit{Streptomyces coelicolor} A3(2) encodes an inessential elongation factor Tu that is apparently subject to positive stringent control

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\textbf{INTRODUCTION}

The polypeptide chain elongation factor Tu (EF-Tu), responsible for delivering amino-acyl tRNAs to the translating ribosome, is one of the most abundant proteins in micro-organisms: it can constitute up to 10\% of total cell protein in rapidly growing \textit{Escherichia coli} cells (van der Meide \textit{et al.}, 1983). Two \textit{tuf} genes, \textit{tufA} and \textit{tufB}, encode EF-Tu in \textit{E. coli}, and are very similar in nucleotide sequence. The Gram-positive actinomycete \textit{Streptomycyes ramosissimus} produces the antibiotic kirromycin, which binds specifically to EF-Tu, and possesses three \textit{tuf} genes, designated \textit{tuf1}, \textit{tuf2} and \textit{tuf3}. EF-Tu1 and EF-Tu2 show 85\% amino acid sequence identity, and both of them share about 65\% amino acid sequence identity with EF-Tu3 (Vijgenboom \textit{et al.}, 1994). While \textit{tuf1} encodes the major elongation factor EF-Tu1, the roles of \textit{tuf2} and \textit{tuf3} are unknown: polyclonal antibodies raised against EF-Tu2 and EF-Tu3 that had been produced in \textit{E. coli} failed to detect either protein in extracts of \textit{S. ramosissimus} cultures grown under a variety of conditions (Vijgenboom \textit{et al.}, 1994). While \textit{tuf2} appears to be absent

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\textbf{Abbreviations}: 2-dog, 2-deoxyglucose; EF-Tu, elongation factor Tu; SHX, serine hydroxamate; Spc, spectinomycin; Str, streptomycin; Thio, thio-estrepton.

The GenBank accession number for the \textit{tuf3} sequence reported in this paper is X77040.
from most *Streptomyces* species, *Streptomyces coelicolor* A3(2) and many other streptomycetes contain close homologues of both *tuf*1 and *tuf*3 (van Wezel, 1994). Like *tuf*A of *E. coli*, *tuf*1 of *S. coelicolor* is located in the *str* operon (van Wezel et al., 1994a, 1995), and is well-separated from *tuf*3 on the physical map of the *S. coelicolor* chromosome (van Wezel et al., 1995). While EF-Tu1 is abundant in *S. coelicolor*, EF-Tu3 could not be detected (van Wezel et al., 1994a).

The stringent response, which was first characterized as a rapid reduction in stable RNA synthesis upon amino acid starvation, is a pleiotropic response to the accumulation of uncharged tRNAs, and there is considerable evidence to suggest that the highly phosphorylated nucleotide ppGpp plays a key role in mediating stringent control (Casbel & Rudd, 1987). *E. coli* *tuf*A and *tuf*B are subject to negative stringent control in response to amino acid starvation, with enhanced ppGpp levels coinciding with severely reduced levels of transcription of both genes (Reeh et al., 1976). *S. coelicolor* also undergoes the stringent response (Takano & Bibb, 1994), which can be elicited either by nutritional shiftdown or by addition of serine hydroxamate (SHX; a competitive inhibitor of seryl-tRNA synthetase), and is characterized by ppGpp synthesis and a rapid decrease in the level of transcription of rRNA genes (Strauch et al., 1991). Although the role of ppGpp in mediating the growth rate control of gene expression remains controversial (Hernandez & Bremer, 1990, 1993; Gaal & Gourse, 1990), recent evidence has implicated the highly phosphorylated nucleotide in stationary phase gene expression in *E. coli* (Gentry et al., 1993). Interestingly, antibiotic production in streptomycetes is generally limited to stationary phase, and mutants of a number of *Streptomyces* species that are deficient in ppGpp synthesis are also deficient in antibiotic production, leading to the suggestion that ppGpp might serve as a general trigger for antibiotic biosynthesis (Ochi, 1986, 1987; Takano & Bibb, 1994, and references therein). Furthermore, there is a reasonably good correlation in *S. coelicolor* between ppGpp synthesis and the transcription of antibiotic pathway-specific regulatory genes (Takano & Bibb, 1994).

In an attempt to determine the role of *tuf*3 in *S. coelicolor*, we have inactivated the gene by replacing part of it with an antibiotic resistance determinant. The transcription start site of *tuf*3 was identified by *in vitro* and *in vivo* analyses, and transcription of *tuf*3 was monitored during growth in liquid culture and after induction of the stringent response, either by nutritional shiftdown or by addition of SHX. The results suggest that *tuf*3 is an essential gene that is subject to positive stringent control.

**METHODS**

**Bacterial strains and plasmids.** *S. coelicolor* strains M145 (prototrophic, SCP1 SCP2; Hopwood et al., 1985), J1501 (hisA1 uraA1 strA1 Pgl1; SCP1 SCP2; Chater et al., 1982), J1501ΔglkA (E. Viijenboom, unpublished data) and J1681 (J1501Δ블다A; Leskiw et al., 1993) were obtained from the John Innes Centre strain collection. *E. coli* JM101 (Messing et al., 1981) was the host for pUC18 (Yanisch-Perron et al., 1985) and constructs derived from it.

pLSCT3-1, pLSCT3-2 and pLSCT3-U1 were made by cloning fragments of the *S. coelicolor* *tuf*3-containing plasmid pBSCT1-3 (van Wezel et al., 1994a) via pUC18 into the xyE-based promoter-probe vector pJ14083 (Clayton & Bibb, 1990). Plasmid inserts were: *PswI-MluI* (−500/+1700) in pLSCT3-1, *KpnI-MluI* (−260/+1700) in pLSCT3-2 and *PstI-KpnI* (−1900/−5) in pLSCT3-U1 (Fig. 2). In each construct, *tuf*3 or its upstream region was inserted in pJ14083 in the same orientation as xyE (Zukowski et al., 1983). However, since the constructs pLSCT3-1 and pLSCT3-2 also contain 500 bp of sequence downstream of *tuf*3, these constructs were not used for promoter probing.

The strain used for *tuf*3 inactivation was *S. coelicolor* J1501ΔglkA, and the gene replacement vector was pJ12559, a 12.2 kb construct derived from pBR329 (Covarrubias & Bolivar, 1982) that is unable to replicate in *Streptomyces* since it lacks an appropriate origin of replication (Fig. 1). In this construct the *add*A gene (Prenkti & Krisch, 1984), which confers spectinomycin (Spc) and streptomycin (Str) resistance on both *E. coli* and *Streptomyces*, is flanked on one side by the −1900/−260 *tuf*3 upstream region and on the other by the 3.6 kb fragment containing the second half of *tuf*3 and 3 kb of downstream sequence. Thus a double recombination event will replace the −260/+600 segment of *tuf*3 by *add*A. Additional selectable markers on pJ12559 are *trr* [conferring thiostrepton (Thio) resistance in *Streptomyces*], cloned as a 1 kb *Bgl*II fragment from pJ14083, and *glkA* encoding glucose kinase, which was available as a 1.3 kb *Pst*I fragment on the plasmid pJ2423 (Angell et al., 1994). J1501ΔglkA is resistant to 2-deoxyglucose (2-dog), but the presence of the pJ12559-derived glkA renders this strain 2-dog-sensitive. Successful inactivation of *tuf*3 by the required double crossover results in loss of both *trr* and *glkA*, yielding a Thio<sup>+</sup> 2-dog<sup>+</sup> phenotype.

**Culture conditions.** Surface-grown cultures were cultivated on R2YE or on minimal medium (MM) agar plates, using glucose or mannitol as the carbon source (Hopwood et al., 1985). Liquid cultures were grown in a minimal medium supplemented with Casamino acids (SMM; Takano et al., 1992), or in yeast extract/malt extract medium (YEME) with 0.5 % glycine (Hopwood et al., 1985), and were inoculated at a density of 5 x 10<sup>5</sup> c.f.u. ml<sup>−1</sup> and grown at 30 °C with vigorous shaking (300 r.p.m. min<sup>−1</sup>). Reproducibly dispersed growth was obtained, with a doubling time of 2.2 h in SMM and 1.9 h in YEME. In SMM, rapid transition into stationary phase occurred approximately 14 h after inoculation (Strauch et al., 1991). Nutritional shiftdown and treatment with 25 mM SHX was performed as described byStrauch et al. (1991).

**Promoter-probe experiments.** The xyE gene from *Pseudomonas putida* (Zukowski et al., 1983) present in pJ14083 (Clayton & Bibb, 1990) was used as a reporter gene for *in vivo* promoter activity. Transformants containing pLSCT3-U1 were grown on R2YE and MM (Hopwood et al., 1985) in the presence of 10 μg Thio ml<sup>−1</sup> (a gift from Bristol-Meyers Squibb). Plates were sprayed with 0.5 M catechol after 1, 2, 3 and 4 d growth and the amount of catechol converted into yellow 2-hydroxymuconic semialdehyde by catechol 2,3-dioxygenase was assessed visually.

**In vitro transcription analysis.** RNA polymerase was isolated from a culture of *S. coelicolor* M145 in the transition between exponential growth and stationary phase, as described previously by Buttner & Brown (1985), and partially separated into different holoenzyme forms by Superose-6 FPLC. In *vitro* run-off
transcription experiments were performed as described by Buttner & Brown (1985). Products were analysed on denaturing 6% (w/v) polyacrylamide gels using 32P-end-labelled HpaII fragments of pBR322 as size markers. The 600 bp PvuII-Styl (−500/+100) fragment and the 360 bp KpnI-Styl (−260/+100) fragment were isolated from pISCT3-1 and pISCT3-2, respectively (Fig. 2), and used as templates.

RNA isolation. RNA was isolated from M145, J1501 or J1681 according to Hopwood et al. (1985). To remove residual DNA, the RNA was salt-precipitated in 3 M NaOAc (pH 6.0). The RNA samples were then treated with DNaseI (1 h at 37 °C with 0.1 U DNaseI per 50 ml initial culture sample), extracted with a 1:1 mixture of phenol/chloroform (saturated with 100 mM Tris, pH 7.0) and precipitated in 0.4 M NaOAc (pH 6.0) with 2-propanol. The RNA was resuspended in water and the concentration was determined spectrophotometrically.

Nuclease S1 mapping. Hybridization of 10 µg RNA with the appropriate DNA probe was performed according to Murray (1986) in NaTCA buffer (Summerton et al., 1983). All subsequent steps were carried out as described previously by Strauch et al. (1991), using an excess of probe. The 600 bp PvuII–Styl fragment from pISCT3-1 (Fig. 2), 32P-labelled at the 5′ end of the Styl site, was used for mapping tuf3 transcripts; the 25 bp non-homologous extension upstream of the PvuII site allowed discrimination between DNA–RNA hybrids and reannealed probe. The 525 bp SmaI–XhoI (−70/+460) fragment from pASCT1-1 (van Wezel et al., 1994a; Fig. 2), 32P-labelled at the 5′ end of the XhoI site, was used for mapping tufl transcripts. The 558 bp FspI–HincII fragment, corresponding to nt positions −708 to −151 with respect to the 5′ end of the 16S RNA coding sequence and 32P-labelled at the 5′ end of the HinclII site, was used for mapping rrnA transcripts (van Wezel et al., 1994b).

ppGpp measurements. ppGpp levels were determined as described by Strauch et al. (1991).

RESULTS

Inactivation of tuf3 by gene replacement

To study the role of tuf3 in S. coelicolor we inactivated the gene by replacing the segment of tuf3 that extends from −260 to +600 (with respect to the translation start site of

\[\text{tuf3}\]
**Fig. 3.** In vitro transcription analysis of *S. coelicolor* tuf3. P, Run-off transcript originating at P_{tuf3}; RNAP fraction, RNA polymerase fractions eluting from a Superose-6 FPLC column. The right-hand side of the figure shows a DNA size marker (denatured HpaI-digested pBR322) in nt. GATC, tuf3 nt sequence ladder generated using a 19 nt primer whose 5' end corresponds precisely to the 5' end of the labelled probe used for 5'll nuclease mapping (see Methods).

tuf3 with an antibiotic resistance gene (*aad*) that confers resistance to Spc and Str. This resulted in the deletion of the tuf3 promoter (see later) and ribosome-binding site, and of protein-coding sequences essential for EF-TU function (van Wezel et al., 1994a). Protoplasts of *S. coelicolor* J1501ΔgkA (gkA encodes glucose kinase which confers sensitivity to 2-dog) were transformed with the tuf3 disruption construct pJ2559 (see Methods and Fig. 1), selecting for resistance to Thio, Spc and Str. Resistant colonies were likely to have arisen from single-crossover integration of the plasmid into the tuf3 region of the chromosome. Spores from five of the 20 independent pJ2559 transformants obtained were plated on MM containing 2-dog and Spc to select for the second crossover event, which removed gkA and *irr*, and resulted in replacement of the 5' half of tuf3 by *aad*A. Five putative tuf3 mutants were screened by three Southern hybridizations, with probes recognizing *aad*A (Fig. 1), the N-terminal part of tuf3 that should have been deleted, and the part of tuf3 that should have remained. All five isolates did indeed lack the 5'-half of the tuf3 gene and gave the expected hybridization patterns with all three probes. Since they also had all of the expected genetic markers (resistant to 2-dog and Spc, sensitive to Thio and unable to grow on glucose as a carbon source), they were considered to be tuf3 deletion mutants. The mutants were indistinguishable from the parental strain J1501ΔgkA in their growth rates, colony morphology and ability to produce the pigmented secondary metabolites actinorhodin and undecylprodigiosin, and no morphological abnormalities could be detected at the microscopic level.

**Expression of the tuf3 promoter occurs in surface-grown cultures when present on a high-copy-number plasmid**

M145 transformants containing the multi-copy plasmid pISCT3-U1, which has the −1900/−5 region (relative to the translation start site) of tuf3 in front of *xylE* (Fig. 2), gave colonies that rapidly became yellow when sprayed with catechol after 2 d growth on solid MM containing mannitol as carbon source. After 4 d, spraying with catechol produced bright-yellow aerial hyphae. This suggests that catechol dioxygenase production (i.e. *xylE* transcription) takes place in both vegetative and aerial mycelium, although the pigmentation of the aerial hyphae might have been the result of diffusion of the yellow compound from the vegetative mycelium (diffusion of the product of XylE activity, the yellow compound 2-hydroxymuconic semialdehyde, into the agar was also clearly apparent). Interestingly, pISCT3-U1 transformants produced neither aerial mycelium nor the pigmented antibiotics actinorhodin and undecylprodigiosin on MM with glucose or on R2YE plates, even
after prolonged incubation at 30 °C, a phenotype comparable to that of an *S. coelicolor* bldA mutant (Lawlor et al., 1987). M145 transformants containing pISCT3-1 or pISCT3-2 displayed normal growth and differentiation, regardless of the medium used.

**In vitro transcription of tuf3**

RNA polymerase from a transition phase culture of *S. coelicolor* M145, partially fractionated into different holoenzyme forms by Superose-6 FPLC, was used in *in vitro* run-off transcription assays to identify promoters in the tuf3 upstream region. The *PvuI*-StyI (−500/+100) and the *KpnI*-StyI (−260/+100) fragments were used as templates. Since both fragments gave identical results, only those obtained with the *KpnI*-StyI template are shown (Fig. 3). In each case, two major transcripts were observed. One corresponded to the size of the template and was probably the result of end-to-end transcription. The second band (designated P in Fig. 3) corresponded to a transcript of approximately 295 nt and suggests a transcription start site around nt position −195 (with respect to the translation start site), which was confirmed by nuclease S1 mapping (see below). The putative transcription start site is preceded by the sequences TCGACG and GATGAT, separated by 17 bp (Fig. 4), which resemble the consensus −35 and −10 sequences, respectively, for the major class of eubacterial promoters.

In *S. coelicolor*, such sequences appear to be recognized by ρ^hbdB* (Brown et al., 1992), whose activity was most abundant in RNA polymerase fraction 28 (data not shown), the one that gave the strongest signal for P_{tufS} (Fig. 3).

**Transcription of tuf1 and tuf3 during liquid culture**

To establish the level and timing of tuf3 transcription *in vivo*, RNA from M145 and J1501 cultures grown in SMM was analysed by nuclease S1 mapping using the 620 bp *PvuI*-Styl fragment as probe. Growth of, and ppGpp production by, the M145 culture used for RNA isolation are shown in Fig. 5(a). No protection of the tuf3 probe was observed. We also analysed the transcription of tuf1 in the *S. coelicolor* M145 culture, using the same RNA preparations. tuf1 lies in the S12 ribosomal protein operon (van Wezel et al., 1994a, 1995) and, by analogy to *E. coli* (Lindahl & Zengel, 1986, and references therein), is likely to be transcribed from a promoter upstream of *rpsL* (encoding S12). For mapping of tuf1 transcripts we used the 530 bp *SmaI*-XhoI (−70/+460) fragment from pASCT1-1 (van Wezel et al., 1994a), uniquely end-labelled at the XhoI site, as probe (Fig. 2), and therefore expected full-length protection of the probe. Since different probes were used, strict quantitative comparisons are not possible, but it is interesting to note that
the levels of the *ttf1* transcripts, which reflect rates of synthesis and degradation, were considerably higher than those derived from the *rrnA* P1 and P2 promoters (Fig. 5b), even though P2 is the strongest promoter of the *rrnA* operon (van Wezel et al., 1994b). The control, 30 µg tRNA, failed to protect the probe, indicating that the full-length protection was not due to probe reannealing. Transcripts corresponding to *ttf1* and *rrnA* were barely detectable approximately 16 h after inoculation, corresponding to early stationary phase. Thus, transcription of *ttf1* shows the same growth-phase dependence as *rrnA*.

**tuf3** transcription in the *bldA* deletion mutant J1681

Interestingly, nuclease S1 mapping using RNA from J1681, a *bldA* deletion mutant of J1501 defective in the formation of aerial mycelium and spores, showed *tuf3* transcripts in this strain (Fig. 6), but only after prolonged exposure of the autoradiograms. While no signal was detected during exponential phase (Fig. 6, J1681, lane 1), a band was detected in RNA isolated from late-exponential-phase and stationary-phase cultures. The 295 nt protected fragment corresponds in size to the transcript observed in the *in vitro* run-off transcription assays (Fig. 3). The transcription initiation site for the corresponding promoter is around nt position -195 relative to the *tuf3* translation start site. We failed to detect *tuf3* transcripts during transition phase in the congenic *bldA*+ strain J1501 (Fig. 6, J1501, lanes 1 and 2, respectively), consistent with the data obtained for M145.

**tuf3** is transcribed after nutritional shiftdown and after addition of SHX

Since transcription of *E. coli tufA* and *tufB* is negatively stringently controlled (Reeh et al., 1976), we analysed how *ttf1* and *tuf3* transcription responded to amino acid starvation provoked by either nutritional shiftdown or by addition of SHX. Nutritional shiftdown of an *S. coelicolor* M145 culture at an OD450 of 0.6 led to a marked increase in the level of ppGpp, with a maximum of about 200 pmol (mg dry weight)-1 15 min after shiftdown (Fig. 7a), falling to 45 pmol (mg dry weight)-1 2 h after shiftdown. The culture continued growing (albeit at a slow rate) and reached stationary phase 6–7 h after shiftdown. *ttf1* transcripts were barely detectable 30 min after shiftdown (Fig. 7b), suggesting that expression of the major EF-Tu gene of *S. coelicolor* is also subject to negative stringent control. Reappearance of *ttf1* transcripts 4-8 h after amino acid depletion presumably reflects adaptation to the new growth rate and the turnover of excess EF-Tu1 present after shiftdown.

In contrast, *tuf3* transcripts appeared within 30 min of shiftdown, and reached a maximum after 1 h (Fig. 7c). The amount of *tuf3* transcript under these conditions was about ten times higher than that in transition-phase and stationary-phase cultures of J1681 (comparable amounts of RNA were used in each experiment, and autoradiogram exposure times were typically ten times longer for identification of the *tuf3* transcripts in J1681 than after nutritional shiftdown of M145). *tuf3* transcripts were barely detectable 3 h after shiftdown of M145.

The stringent response can also be elicited by treatment with SHX, although lower levels of ppGpp are induced than after nutritional shiftdown [75 and 200 pmol (mg dry weight)-1, respectively; Fig. 8a]. While addition of SHX leads to a marked reduction in the level of rRNA transcripts (Strauch et al., 1991), addition of SHX to a final concentration of 50 mM led to the appearance, within 30 min, of low-abundance *tuf3* transcripts (Fig. 8b).

**DISCUSSION**

*tuf3* deletion mutants were not noticeably affected in growth or differentiation, demonstrating that EF-Tu3 does not play an essential role in the *Streptomyces* life-cycle. Western blotting using antibodies raised against the highly homologous *S. ramosissimus* EF-Tu3 failed to identify the *tuf3* gene product in total protein extracts isolated from M145 after nutritional shiftdown (van Wezel, 1994). This suggests that TF-Eu3, if present at all in *S. coelicolor*, occurs only in trace amounts, even when *tuf3* transcripts can be detected.

The XyIE+ phenotype of pISCT3-U1 revealed a promoter within 1900 bp of the *tuf3* translation start site. Earlier work (van Wezel, 1994) had shown that M145 containing pISCT3-2, which has only 260 bp of sequence upstream of *tuf3*, produces EF-Tu3 in the absence of any additional
promoter. Therefore it is possible that the strong xylE expression observed with pSCT3-U1 may be entirely due to a promoter located within 260 bp of the tuf3 translation start site.

In vitro run-off transcription assays with S. coelicolor RNA polymerase revealed a transcription initiation site at approximately nt position −195 relative to the tuf3 translation start site. The sequence of the putative tuf3 promoter (TCGACG−17 bp−GATGAT; Fig. 4) shows an 8 out of 12 nt match with the consensus sequences for the major class of eubacterial promoters (TTGACA−17 bp−TATAAT; Hawley & McClure, 1983). The RNA polymerase fraction that yielded the highest level of tuf3 transcription in vitro (Fig. 3) was enriched in RNA polymerase containing σ^rnb^, consistent with recognition by σ^rnb^ in vivo. The tuf3 promoter is preceded by a stretch of seven As and one T (Fig. 4), a very unusual sequence in the G+C-rich streptomycetes. Similar A+T-rich sequences found approximately 45 bp upstream of the transcription start site of various E. coli promoters were shown to interact with the α subunit of RNA polymerase, resulting in a stimulation of transcription (Ross et al., 1993). The A+T-rich stretch near the tuf3 promoter lies at a similar position, and it is possible that this sequence is involved in α-dependent transcriptional activation.

tuf3 transcripts appeared immediately after invoking the stringent response, either after nutritional shiftdown or after addition of SHX, suggesting that transcription of tuf3 may be subject to positive stringent control, which may also be true for the histidine biosynthetic operon of Salmonella typhimurium (Rudd et al., 1985; Cashel & Rudd, 1987). Another gene that may be subject to positive stringent control in S. coelicolor is actII-ORF4 (Fernández-Moreno et al., 1991), the putative activator gene for the actinorhodin biosynthetic pathway (Takano & Bibb, 1994). However, in contrast to tuf3, actII-ORF4 transcripts can be detected in stationary-phase cultures of M145. Whether ppGpp plays a causal role in triggering the expression of these genes remains an open question. Interestingly, expression of rpoS, which encodes the stationary-phase-specific σ factor σ^s^ of E. coli (reviewed by

![Fig. 7. Transcription of tuf1 and tuf3 after nutritional shiftdown of S. coelicolor M145. (a) Growth curve (△, ○) and ppGpp production (□) of a SMM-grown culture, with (△) and without (○) nutritional shiftdown (SD) at an OD<sub>450</sub> of 0.6. (b) Transcription of tuf1 after nutritional shiftdown. (c) Transcription of tuf3 after shiftdown. P, tuf3 transcripts initiated at the tuf3 promoter around nt position −195; M, DNA size marker as in Fig. 3; C, control lane (30 μg tRNA).](image)
Fig. 8. (a) Growth curve (O, △) and ppGpp production (□) by S. coelicolor M145 in SMM, in the absence (O) or presence (△) of 25 mM SHX. ‘SHX’ indicates time point of addition of SHX (OD₆₀₀ 0.6). ppGpp levels were only measured in the SHX-treated culture. (b) Transcription of tuf3 after addition of 25 mM SHX. M, DNA size marker as in Fig. 3.

Hengge-Aronis, 1993), appears to be positively regulated by increased levels of ppGpp (Gentry et al., 1993; Takayanagi et al., 1994; Lange & Hengge-Aronis, 1994). Is there a σS-like σ factor present in S. coelicolor that is responsible for ppGpp-dependent transcription of tuf3 and actII-ORF4? Although the experiments performed in this study suggest that P₉₃₄ is a σbrain-type promoter, E. coli σS and σ70 (the major σ factor of E. coli) show overlapping promoter specificities (Tanaka et al., 1993).

A low level of tuf3 transcription was observed in late-exponential and stationary-phase cultures of the bldA deletion mutant 51681, but not in its bldA⁺ progenitor J1501. If ppGpp does play a role in activating tuf3 transcription, perhaps the sensitivity of the tuf3 promoter to ppGpp is enhanced in the bldA mutant; alternatively, perhaps bldA mutants have elevated levels of ppGpp, reducing the incremental increase required to activate tuf3 transcription.

While tuf1 transcripts were abundant during exponential growth, roughly coinciding with transcription from the rrnA P1 and P2 promoters, transcription of tuf3 was not observed in unstressed cultures. However, the tuf3 upstream region gave a high level of xylE expression when cloned in a multi-copy promoter-probe plasmid, and high levels of EF-Tu3 had been observed previously in transformants containing either pISCT3-1 or pISCT3-2 (van Wezel, 1994). These multi-copy effects might reflect repression of tuf3 by a protein that is readily titrated out when tuf3 is present at high-copy-number. Alternatively, differences in the extent of DNA supercoiling of the chromosomally and plasmid-located tuf3 promoters may (partly) explain the discrepancy in their activity: the degree of DNA supercoiling is known to influence the effect of ppGpp on transcription initiation in vitro, suggesting that ppGpp regulation may be affected by DNA supercoiling in vivo (Ohlsen & Gralla, 1992).

The bald phenotype observed on R2YE plates after introduction of the -1900/-5 segment of the tuf3 upstream region on a multi-copy vector (pISCT3-U1) into M145 might reflect the titration of a transcription factor required for differentiation by a regulatory element contained in the cloned fragment. Other DNA fragments have been cloned that inhibit or prevent differentiation when present in S. coelicolor in multiple copies, most of which probably sequester proteins involved in development of aerial hyphae or spores (Champness & Chater, 1994). Examples are the putative σwhiC-dependent promoters P₉₃₄ and P₉₅, which probably titrate out this σ factor, leading to absence of sporulation (Tan & Chater, 1993). pISCT3-U1 overlaps pISCT3-1 by 500 bp at the tuf3-proximal end, and pISCT3-1 displayed normal growth and differentiation on R2YE; thus the putative regulatory element cannot be located near the tuf3 promoter, and hence it seems unlikely that it is involved in regulation of tuf3 transcription.

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