Disruption of sblA in Streptomyces lividans permits expression of a heterologous α-amylase gene in the presence of glucose

Josette Gagnat, Hichem Chouayekh, Claude Gerbaud, François Francou and Marie-Joelle Virolle

Author for correspondence: Marie-Joelle Virolle. Tel: +33 169156913. Fax: +33 169156678.
e-mail: virolle@igmors.u-psud.fr

In a transposition mutant of Streptomyces lividans TK24, the usually glucose-repressible expression of a heterologous α-amylase gene (aml) became resistant to glucose repression. The transposon had inserted into an ORF called sblA which encodes a 274 aa product sharing significant sequence similarities with various phosphatases that act on small phosphorylated substrates. sblA was transcribed as a monocistronic mRNA and its transcription was enhanced at the transition phase. Because its transcriptional and putative translational start points coincide, sblA is likely to be translated in the absence of a conventional RBS. The sblA-disrupted mutant is characterized by early growth arrest in glucose-grown cultures and by partial relief of glucose repression of aml expression.

Keywords: glucose repression, induction, inositol monophosphatase, transition phase

INTRODUCTION

Streptomyces are saprophytic Gram-positive bacteria living in the soil. Their saprophytic life style is made possible by their ability to degrade many kinds of organic molecules, thanks to their extremely large and diverse range of hydrolytic enzymes, including proteases, nucleases, lipases and enzymes hydrolysing polysaccharides (Williams et al., 1983). We are currently studying the regulation of one of these hydrolytic enzymes, an α-amylase from Streptomyces limosus encoded by aml and stably integrated as one copy in the chromosome of Streptomyces lividans TK24 via the attachment site of the integrative vector pSAM2. In that strain, called S. lividans TK24(pTS6000), expression of aml was shown to be under the control of a LacI-like negative transcriptional regulator encoded by reg1 (Nguyen et al., 1997). Reg1 is a homologue of the malR gene product of Streptomyces coelicolor. In S. coelicolor, MalR negatively regulates transcription of the maltose transport operon encoded by malEFG (van Wezel et al., 1997). Interruption of reg1 in S. lividans, and of malR in S. coelicolor, concomitantly abolishes both malto- and dextrin induction and glucose repression of aml (Nguyen et al., 1997) and malEFG expression (van Wezel et al., 1997), respectively. In the streptomycetes, as in Escherichia coli, the genes encoding the secreted α-amylase and those encoding elements of the maltose transport system are in the same regulon. However, this regulon is controlled by the positive transcriptional regulator MalT in E. coli (Boos & Shuman, 1998), whereas in the streptomycetes it is controlled by a LacI-like negative transcriptional regulator.

When cultures of S. lividans TK24(pTS6000) are grown in the presence of a ‘non-repressive’ carbon source such as glycerol or mannitol, expression of aml is switched on at a low level at the end of the exponential phase of growth, even in the absence of exogenous inducer. Adding a low level of exogenous inducer (10−4 M maltotriose) to cultures growing exponentially in a glycerol medium does not induce aml expression, whereas adding the exogenous inducer after the growth-phase-dependent aml expression has started clearly enhances aml expression. Both growth-phase-related and maltotriose-inducible aml expression are strongly repressed in the presence of glucose (Virolle & Gagnat, 1994). The molecular mechanisms responsible for growth-phase-dependent aml expression are not yet elucidated, but could be related to growth-phase-dependent degradation of the internal storage compound glycogen. This degradation might provide the

Abbreviations: Amp, ampicillin; Apr, apramycin; CBS, Cibachron blue starch; IMP, inositol monophosphatase; Nos, nosiheptide.

The EMBL accession number for the sequence reported in this paper is AJ223365.
maltodextrins inducing, at a low level, the different components of the maltose regulon. Low level induction of the maltose transport system, and thus the transport of external inducer, could account for the growth-phase-related pattern of *aml* inducibility.

For more insight into the molecular mechanisms involved in glucose repression of *aml* expression, we developed a transposon mutagenesis procedure yielding *S. lividans* mutants in which *aml* expression had become insensitive to glucose repression. In this paper, we report the characterization of one such mutant. The interrupted gene, called *sblA*, was cloned and sequenced and its transcription was investigated. Effects of the *sblA* null mutation on growth and *aml* expression in different culture conditions are reported.

**METHODS**

**Bacterial strains and plasmids.** The strains and plasmids used in this study are listed in Table 1.

**Table 1.** Strains and plasmids used

<table>
<thead>
<tr>
<th>Strains</th>
<th>Description</th>
<th>Insert</th>
<th>References</th>
</tr>
</thead>
<tbody>
<tr>
<td><em>S. lividans</em> TK24(pTS6000)</td>
<td>Wild-type strain with one copy of the <em>aml</em> gene from <em>S. limosus</em> present on a 5.85 kb <em>Bcl</em>I fragment and integrated into the chromosome via a derivative of the integrative plasmid pSAM2</td>
<td></td>
<td>Virolle &amp; Gagnat (1994)</td>
</tr>
<tr>
<td><em>S. lividans</em> TK24(pTS6000)</td>
<td>Derivative of <em>S. lividans</em> TK24(pTS6000) where <em>sblA</em> was interrupted with the <em>Ωaac</em> cassette</td>
<td></td>
<td>This study</td>
</tr>
</tbody>
</table>

<table>
<thead>
<tr>
<th>Plasmids</th>
<th>Relevant characteristics</th>
<th>Insert</th>
<th>References</th>
</tr>
</thead>
<tbody>
<tr>
<td>pBR322 derivatives</td>
<td></td>
<td></td>
<td></td>
</tr>
<tr>
<td>pH45Ωaac</td>
<td>Amp&lt;sup&gt;R&lt;/sup&gt; Apr&lt;sup&gt;R&lt;/sup&gt;</td>
<td>The <em>Ωaac</em> cassette conferring resistance to Apr</td>
<td>Blondelet-Rouault <em>et al.</em> (1997)</td>
</tr>
<tr>
<td>p6998</td>
<td>Amp&lt;sup&gt;R&lt;/sup&gt; Apr&lt;sup&gt;R&lt;/sup&gt;</td>
<td>The <em>BamHI</em>–<em>BglII</em> fragment (Fig. 1a) carrying part of Tn5096 and flanking chromosomal DNA</td>
<td>This study</td>
</tr>
<tr>
<td>pIJ2925 derivatives&lt;sup&gt;a&lt;/sup&gt;</td>
<td></td>
<td></td>
<td></td>
</tr>
<tr>
<td>p7000</td>
<td>Amp&lt;sup&gt;R&lt;/sup&gt;</td>
<td>The 2 kb <em>SpfI</em>–<em>BglII</em> chromosomal DNA fragment from <em>S. lividans</em> carrying <em>sblA</em> (Fig. 1b)</td>
<td>This study</td>
</tr>
<tr>
<td>p7001</td>
<td>Amp&lt;sup&gt;R&lt;/sup&gt; Apr&lt;sup&gt;R&lt;/sup&gt;</td>
<td>Insert of p7000 bearing the <em>Ωaac</em> cassette cloned into the <em>BamHI</em> site of <em>sblA</em></td>
<td>This study</td>
</tr>
<tr>
<td>pGM160&lt;sup&gt;b&lt;/sup&gt; derivatives&lt;sup&gt;+&lt;/sup&gt;</td>
<td></td>
<td></td>
<td></td>
</tr>
<tr>
<td>pCZA168 (used in transposition mutagenesis)</td>
<td>Amp&lt;sup&gt;R&lt;/sup&gt; Apr&lt;sup&gt;R&lt;/sup&gt; in <em>E. coli</em>, Nos&lt;sup&gt;R&lt;/sup&gt; Apr&lt;sup&gt;R&lt;/sup&gt; in <em>Streptomyces</em></td>
<td>Tn5096</td>
<td>Solenberg &amp; Baltz (1991)</td>
</tr>
<tr>
<td>p7002 (used in gene replacement)</td>
<td>Amp&lt;sup&gt;R&lt;/sup&gt; Apr&lt;sup&gt;R&lt;/sup&gt; in <em>E. coli</em>, Nos&lt;sup&gt;R&lt;/sup&gt; Apr&lt;sup&gt;R&lt;/sup&gt; in <em>Streptomyces</em></td>
<td>Same insert as p7001</td>
<td>This study</td>
</tr>
</tbody>
</table>

<sup>a</sup>Plasmid derived from pUC18 (Janssen & Bibb, 1985).

<sup>b</sup>-*E. coli*/*Streptomyces* shuttle vectors derived from pGM160 (Muth *et al.*., 1989) by deletion of the *HindIII*–*HindIII* fragment carrying the *aacC4* gene (a generous gift of J.-L. Pernodet, Université Paris-Sud, France); thermosensitive replication in *Streptomyces*.

**Culture conditions.** All physiological studies of regulation were carried out in triplicate in modified liquid minimal medium (NMMP; Hopwood *et al.*, 1985). Spores were pregerminated as described by Hopwood *et al.* (1985) and used at 10<sup>6</sup> ml<sup>−1</sup> to inoculate 20 ml NMMP supplemented at 1% (w/v) with glucose or glycerol. The cultures were grown in 150 ml Erlenmeyer flasks with four indents; each flask contained 12–14 g 4 mm diameter glass beads to achieve dispersed growth. Cultures were grown at 30°C under constant agitation (160 r.p.m.) on a Braun Certomat R orbital shaker. Growth and α-amylase production were measured every 3 h. In the induction studies, maltotriose was added at 10<sup>−4</sup> M to one of a set of two glucose- and glycerol-grown cultures as soon as Aml was detected in culture supernatants. The theoretical basis and methodology of the turbidimetric assay used to follow Aml production were described by Virolle *et al.* (1990).

**Transposon mutagenesis.** The delivery plasmid pCZA168 (Solenberg & Baltz, 1991), carrying the *tsr* gene that confers resistance to nosiheptide (Nos) in *Streptomyces* and the transposon Tn5096 harbouring the *aacC4* gene that confers resistance to geneticin (G418) in both streptomycetes and *E.*
coli, was used in transposon mutagenesis. Protoplasts of strain TK24(pTS6000) were transformed by pCZA168, plated on R2YE medium (Hopwood et al., 1985) and overlaid with SNA (Hopwood et al., 1985) containing Nos (50 μg ml⁻¹). Spores from the transformants were spread on solid defined agar to obtain separate colonies. This minimal agar consisted of a basal layer (20 ml) of minimal agar (Hopwood et al., 1985) containing 1% glucose, 0.25% (w/v) Casamino acids and G418 (15 μg ml⁻¹) to maintain selective pressure for the presence of Tn5096, and a top layer (5 ml) of the same medium containing 2% (w/v) Cibachron blue starch (CBS), as a chromogenic substrate for α-amylase (Klein et al., 1969). These cultures, called ‘CBS plates’, were incubated for 3 at 30 °C (no haloes were seen), then for 2–3 weeks at 40 °C. At this non-permissive temperature for pCZA168 replication, colonies stopped growing uniformly in diameter, but after 1 week, most of them had grown sectors (a mean of four per colony), 1–2% of which were surrounded by white haloes of CBS hydrolysis and were considered to be potentially interesting mutants. Mycelium from these sectors was streaked on the same medium to confirm their phenotype.

**Chemicals and enzymes.** G418 was purchased from Sigma and Nos was a generous gift from Rhône-Poulenc. Restriction enzymes, DNA ligase and T4 polynucleotide kinase were used according to the recommendations of the suppliers (Boehringer Mannheim and Biolab).

**DNA manipulation.** Total genomic DNA and plasmid DNA were isolated from *S. lividans* TK24(pTS6000) as described by Hopwood et al. (1985). Methods for plasmid isolation from *E. coli*, purification of DNA fragments, preparation of DNA probes, Southern blotting or colony hybridization were as described by Sambrook et al. (1989).

**Procedure used to clone the transposon bordering sequences.** Total DNA of the chosen mutant was cut by BamHI [a BamHI site is located downstream of the 3' end of the aacC4 gene of Tn5096] and BglII (this site is absent in Tn5096). Fragments were ligated into the BamHI site of pBR322 (Bolivar et al., 1977) and the ligation mix was used to transform competent *E. coli* DH5α cells. Transformant colonies were selected on agar media containing G418 (30 μg ml⁻¹). Plasmid DNA was extracted from 24 independent transformants and was digested with PstI (site located near one end of Tn5096, Fig. 1a) and Smal or SalI (two enzymes that cut streptomyctene DNA frequently). Analysis of restriction patterns by agarose gel electrophoresis revealed two different types of bordering sequences. They were sequenced using the oligonucleotide OTN 1 (5'-TCAAGTCTGGCCGACCTCCTTGCAGCCT-CCGTTGCTGAC-3'), which is complementary to the sequence downstream of the NruI site of Tn5096 (Fig. 1a). One type of bordering sequence was shown to be pCZA168 DNA whereas the other was bona fide chromosomal DNA. The pBR322 derivative carrying the chromosomal DNA was called p6998 (Fig. 1a). To clone the gene interrupted by the transposon, a mini-library of the approximately 2 kb SalI–BglII chromosomal DNA fragments from *S. lividans* was constructed in pIJ2925 (Janssen & Bibb, 1985) and probed with the 440 bp SalI–SalI fragment I of p6998.

**DNase I treatment was used in addition to salt precipitation.** RNA used for Northern blot analysis was prepared from transition-phase cultures grown in NMM with 1% (w/v) mannitol as the carbon source. RNA used for high-resolution nucleic acid S1 mapping was kindly provided by Eriko Takano (John Innes Institute, Norwich, UK). It was prepared from cultures grown in SMM medium (Takano et al., 1992) and sampled at intervals during the exponential, transition and stationary phases.

For Northern blot analysis, total RNA was denatured with glyoxal/dimethylsulfoxide (DMSO), fractionated on 1% agarose gels, transferred to Hybond-N membrane and hybridized at 65 °C with the 563 bp BclI no. 3–NoI no. 10 fragment labelled with [α-32P]dCTP using the T7 quick prime kit (Pharmacia). Molecular mass standards from BRL were treated in the same way as the RNA samples and labelled as DNA probes.

The DNA fragment used in high-resolution nucleic acid S1 mapping was the PCR fragment synthesized using the −180 reverse primer (5'-ATGCAACTTGGCACAGGATTG-3') showing complementarity to pUC18, and the 5'-CATCAGC- GACTCTTGTGGGTTTGCAG-3' oligonucleotide showing complementarity to the sblA region boxed in Fig. 2. It was phosphorylated at its 5' end with [γ-32P]ATP; 40 μg total RNA was hybridized with 50 nmol labelled probe (corresponding to approximately 10⁴ Cerenkov counts min⁻¹) in NaTCA buffer (Murray, 1986) at 45 °C overnight after denaturation at 70 °C for 10 min. All subsequent steps were carried out as described by Strauch et al. (1991) using S1 nuclease from Pharmacia. As a sequencing template, p7000 double-stranded DNA was used with the oligonucleotide mentioned above phosphorylated at its 5' end with [γ-32P]ATP. The sequence ladders were run in parallel with the S1 protected products. The resulting poly-

---

**Fig. 1.** (a) Restriction map of the 3.5 kb BamHI–BglII chromosomal fragment cloned from the chosen transposition mutant of *S. lividans* TK24(pTS6000) including part of Tn5096 (white box) and chromosomal flanking sequences. (b) Restriction map of the 2 kb SphI–BglII chromosomal fragment carrying sblA and a truncated downstream ORF (ORFX). The arrows indicate the transcriptional directions of the two ORFs. OTN1 is the 40 nt long oligonucleotide showing complementarity to a region located downstream of the NruI ORFs. The 440 bp SalI–SalI fragment I was used to probe the mini-library of the approximately 2 kb SphI–BglII chromosomal DNA fragments from *S. lividans* TK24.
acrylamide gel was dried, exposed for 72 h and scanned with a phosphor imager.

**sblA gene disruption.** To replace sblA with its disrupted allele, we used p7002, a derivative of the thermosensitive vector pGM160 (Muth et al., 1989) carrying the sblA gene interrupted by the Ωaac cassette (Blondelet-Rouault et al., 1997) conferring resistance to G418. The Nos° colonies of *S. lividans* TK24 and TK24(pTS6000) transformed with p7002 were grown for 24 h at 30 °C in TS medium (Hopwood et al., 1985) containing G418 (15 µg ml⁻¹). Mycelium was then harvested and homogenized for use as a low-density inoculum in the same medium. These cultures were grown for 72 h at 40 °C to eliminate the autonomously replicating plasmid. Mycelium was harvested, homogenized and sonicated to obtain small mycelial fragments. These were plated on HT agar (Pridham, 1957) containing G418 (30 µg ml⁻¹). Well-separated, sporulating colonies were replica-plated on HT agar containing G418 (30 µg ml⁻¹) as controls and on HT agar containing Nos (50 µg ml⁻¹) to screen for G418® Nos° colonies. Twenty-five per cent of the G418® colonies were Nos°. These had lost the replicative plasmid and had arisen from double crossover events between sequences carried by p7002 and homologous chromosomal sequences. Chromosomal DNA was isolated from two independent G418® Nos° colonies of each strain and the presence of the Ωaac cassette confirmed by cutting with NcoI or SphI followed by Southern blot analysis.

**Determination of the chromosomal location of sblA by PFGE.** Chromosomal DNAs of *S. lividans* TK24(pTS6000) and *S. lividans* TK24(pTS6000) sblA:Ωaac were digested with *AseI* or *Dral* as described by Leblond et al. (1990). The DNA fragments were separated on 1 or 1.3% agarose gels by PFGE. Electrophoresis buffer contained 20 mM triethanolamine (Fluka), 8.75 mM acetic acid and 1.5 mM EDTA. Electrophoresis was carried out for 30 h with pulse times of 60 s for *AseI* digests and 200 s for the *Dral* digests.

**RESULTS**

**Isolation of mutants of *S. lividans* TK24(pTS6000) producing α-amylase in the presence of glucose**

In *S. lividans* TK24(pTS6000), the regulatory features of *aml* expression (Virolle & Gagnat, 1994) described in the Introduction were established in liquid minimal medium (NMMP, Hopwood et al., 1985) and observed on solid minimal medium plates in the presence of CBS. With glycerol as the carbon source, *S. lividans* TK24(pTS6000) colonies were surrounded by large haloes of CBS hydrolysis, indicating α-amylase production, whereas much smaller haloes were seen with glucose-containing medium.

Mutants of TK24(pTS6000) producing α-amylase on glucose plates were isolated by transposon mutagenesis using Tn5096 carried by pCZA168 (Solenberg & Baltz, 1991). Tn5096 is derived from the insertion sequence IS493 (Solenberg et al., 1989) present at three copies in the *S. lividans* TK24 chromosome. All the mutants isolated were apramycin (Apr)-resistant (Tn5096 marker) and NosR (plasmid marker), suggesting that, besides true transposition events, integration of pCZA168 into the chromosome via homologous recombination between Tn5096 and one of the three chromosomal copies of IS493 had occurred.

**Cloning of the gene interrupted by Tn5096:** nucleotide sequence and similarities between the deduced protein and database proteins

For the chosen mutant, the Tn5096 bordering sequences were first cloned into pBR322 by taking advantage of the presence of *aacC4* in the transposon. Of the two types of bordering sequences obtained, one was, as expected, pCZA168 DNA, whereas the other was bona fide chromosomal DNA. The pBR322 derivative carrying the chromosomal sequences flanking the Tn5096 insertion on one side was called p6998 (Fig. 1a). The 440 bp Sall–SalII insert was used as a probe to screen an *E. coli* mini-library of the approximately 2 kb SphI–BglII chromosomal DNA fragments from *S. lividans*. Two positive clones with the same 2 kb SphI–BglII insert were isolated. The restriction map of the insert is shown in Fig. 1b. The resulting plasmid was called p7000 and its insertion was sequenced.

The sequence of the ORF interrupted by Tn5096 is shown in Fig. 2. Comparison of this sequence with the transposon flanking sequence identified the exact insertion point (position 540) of Tn5096. The interrupted ORF starts with a GTG in position 259 and ends with a TGA in position 1080. No typical *Streptomyces* RBS could be found in the vicinity of the putative GTG start codon. The 72% G+C content of this ORF is in good
α-Amylase expression in an S. lividans sblA mutant

Fig. 3. Alignment of the amino acid sequences of the five proteins giving the highest BLAST scores with SblA. These enzymes belong to the IMP family. sblA, Streptomyces lividans sblA (EMBL accession no. AJ223365); ImpA, Mycobacterium smegmatis impA (EMBL accession no. AF005905); SUHB, Escherichia coli suhB (SWISS-PROT accession no. P22783); strO, Streptomyces griseus strO (SWISS-PROT accession no. P29785); pur3, Streptomyces alboniger pur3 (EMBL accession no. X92429). Consensus symbols: %, either F or Y; g, any one of N, D, Q, E, B or Z. In the consensus line, upper case letters are highly conserved residues (>90%); lower case letters are less conserved residues (50–90%).

The ORF encodes 274 amino acids. Searches using the GAP-BLAST program (Altschul et al., 1997) indicated that the sequence shared similarities with proteins belonging to the inositol monophosphatase (IMP) family (Fig. 3). The greatest similarity was to the product of the suhB gene of E. coli (Yano et al., 1990) (30–8% identity and 48–8% similarity). This ORF was thus called sblA for suhB-like. SuhB has IMP activity but exhibits quite a broad range of substrate specificity (Matsuhisa et al., 1995) and its biological role is not yet clearly understood. Furthermore, SblA shared significant similarity (29–7% identity and 48–2% similarity) with the product of the impA gene of Mycobacterium smegmatis encoding an IMP (Parish et al., 1997), and with three proteins from various Streptomyces species. These three proteins are encoded by genes belonging to two different antibiotic biosynthetic pathways. One is encoded by pur3 (29–8% identity and 48–6% similarity), a gene belonging to the puromycin biosynthetic cluster of Streptomyces alboniger and thought to be a phosphatase acting on one of the precursors of puromycin (Tercero et al., 1996). The other two are encoded by strO, a gene belonging to the streptomycin biosynthetic cluster of Streptomyces griseus (30–2% identity and 53% similarity) or Streptomyces griseus (28% identity and 51% similarity) and thought to encode an N-amidino-scyllo-inosamine-4-phosphate phosphatase (Ahlert et al., 1997).

Proteins belonging to the IMP family are thought to be involved in the degradation (or the synthesis) of small phosphorylated molecules. These proteins usually share agreement with the mean G+C content of Streptomyces DNA. Codon usage is extremely biased toward G or C (93–8%) at the third position of the triplet (Bibb et al., 1984).

Fig. 4. Northern blot analysis of the sblA transcript. Lane 1, molecular mass markers; lane 2, 20 µg RNA isolated from cultures of S. lividans TK24 grown in NMMP supplemented with 1% (w/v) mannitol, stopped at the transition phase and hybridized with the 563 bp BclI No. 3–NotI No. 10 fragment internal to sblA giving an approximately 840 bp hybridizing band.

two conserved regions, I and II. Region I (96 aa) contains IMP signature I: [FWV]-x(0,1)-[LIVM]-D-P-[LIVM]-x-[SG]-[ST]-x(2)-[FY]-x-[HKRNSTY] and region II (55 aa) contains IMP signature II: [WV]-D-x-[AC]-[GSA]-[GSAPV]-x-[LIVACP]-[LIV]-[LIVAC]-x(3)-[GH]-[GA].
The IMP I signature would comprise residues involved in binding metallic ions such as Mg$^{2+}$ whereas the IMP II signature would be more specifically involved in substrate binding (Neuwald et al., 1991). Fig. 3 shows that IMP signature I (from residue 92 to 105) is fairly well conserved in SblA whereas IMP signature II (from residue 227 to 244) is not.

Transcriptional regulation of sblA expression

Northern blot analysis indicated that sblA was transcribed as unique monocistronic mRNA of approximately 840 bp (Fig. 4). Therefore, the mutant phenotype linked to the interruption of sblA was likely to be due to the inactivation of the gene itself and not to a polar effect on downstream sequences.

Furthermore, S1 nuclease protection studies (Fig. 5) showed that sblA was weakly transcribed throughout growth, but with a net increase at the transition phase, indicating growth-phase-dependent regulation. Taking into account the occurrence of small differences in migration of the S1-protected products depending on the volume of the samples loaded, the transcript was thought to start in the close vicinity of the GTG translational start codon. Transcriptional and translational start points are usually very close for proteins translated in the absence of a conventional RBS (Strohl, 1992). From the existence of this leaderless transcript, $-35$ (GAGGCC) and $-10$ (TACCCG) promoter sequences with a spacing of 17 bp could be proposed. Noteworthy is the presence of eight direct repeats of the sequence 5’-C/C/GGGG(T/C)-3’ upstream of the $-35$ region, with the last copy overlapping the putative $-35$ region. Moreover, a 23 bp sequence with dyad symmetry and including an RBS-like sequence is present within the coding sequence, 167 bp downstream of the GTG start codon.

Disruption and chromosomal localization of sblA

In S. lividans, a convenient way to map genes on the circular chromosome is to interrupt them by introducing a cassette that contains rare restriction sites. Disruption of sblA was achieved by cloning the aac cassette conferring resistance to Apr (Blondelet-Rouault et al., 1997) into the BamHI site no. 4 close to the insertion point of Tn5096. The wild-type chromosomal copy of sblA was replaced by this interrupted derivative. Southern blot analysis confirmed that the wild-type copy of sblA was replaced by the interrupted derivative. Southern blot analysis confirmed that the wild-type copy of sblA has been replaced by the interrupted copy (data not shown). The S. lividans TK24(pTS6000) sblA::Ωaac mutant strain (Fig. 6b) had the same phenotype as the initial transposition mutant (Fig. 6a).

The presence in the resistance cassette of sites for Asel and Dral, enzymes cutting Streptomyces DNA rarely, allowed the approximate location of the interrupted
gene on the \( S. \) lividans TK24 chromosome to be determined by PFGE. When the chromosomal DNA of \( S. \) lividans TK24(pTS6000) \( \text{sblA::Ωaac} \) was digested with AseI, the original 615 kb AseI fragment D (Leblond et al., 1993) was split into two fragments of 355 kb (co-migrating with the AseI fragment F) and 260 kb (data not shown). When a DraI digestion was carried out, the original 1700 kb DraI fragment III (Leblond et al., 1993) was split into two fragments of 450 kb and 1250 kb (data not shown). \( \text{sblA} \) is thus located at approximately 450 kb from a chromosomal end at roughly 150 kb on the left of AUDI in a chromosome region known for its high genetic instability (Vollf et al., 1996). Disruption of this gene did not lead to any detectable chromosomal rearrangements. Recently a BLAST search carried out at the Sanger centre (http://www.Sanger.ac.uk) revealed the presence of a protein bearing over 95% amino acid sequence identity with SblA on the overlapping cosmids \( \text{Stf}80 \) and \( \text{Stf}76 \). These cosmids are located on the AseI-F fragment of the chromosome of \( \text{S. coelicolor} \) (Redenbach et al., 1996) close to a chromosomal end.

**Effects of sblA disruption on growth**

\( S. \) lividans TK24(pTS6000) \( \text{sblA::Ωaac} \) had the same mutant phenotype as the initial transposition mutant (Fig. 6). Colonies of TK24(pTS6000) \( \text{sblA::Ωaac} \) were smaller on glucose plates than those of the corresponding wild-type strain, whereas no such growth difference was seen on glycerol plates (data not shown). Growth curves of \( S. \) lividans TK24(pTS6000) and TK24(pTS6000) \( \text{sblA::Ωaac} \) were established in NMMP (Hopwood et al., 1985) in the presence of 1% glucose or glycerol as carbon sources (Fig. 7). Glucose-grown cultures of the wild-type strain showed higher biomass production than glycerol-grown cultures. Growth rates of glycerol- or glucose-grown cultures of the mutant were comparable to those of the wild-type during exponential growth. However, glucose-grown cultures of the \( \text{sblA} \) mutant reproducibly entered earlier into stationary phase than the glucose-grown wild-type cultures. This premature growth arrest led to a 25% deficit in biomass compared with the wild-type strain.

**Effects of sblA disruption on the heterologous aml gene and on expression of the endogenous amylolytic genes**

To assess more precisely the way the regulatory characteristics of \( \text{aml} \) were changed in the \( \text{sblA} \) mutant, cultures of \( S. \) lividans TK24(pTS6000) and TK24(pTS6000) \( \text{sblA::Ωaac} \) were grown in NMMP containing glycerol or glucose as carbon sources. Growth and Aml activity were measured every 3 h. Aml activity was detectable in the supernatant of glycerol- and glucose-grown cultures of both strains at the end of exponential growth in the absence of any exogenous inducer. In glycerol-grown cultures of the wild-type strain, maximal Aml activity was approximately 0.045 IU (mg protein)\(^{-1}\), and the \( \text{sblA} \) mutant reproducibly contained 1.3–1.5-fold more Aml than the wild-type (Fig. 8a). In glucose-grown cultures of the wild-type strain, maximal Aml activity was extremely low [approx. 0.01 IU (mg protein)\(^{-1}\)] and the \( \text{sblA} \) mutant reproducibly contained 2.5–3-fold more Aml than the wild-type strain (Fig. 8a). The relative enhancement of growth-phase-related \( \text{aml} \) expression, in the absence of exogenous inducer, was more pronounced for the \( \text{sblA} \) mutant in the glucose- than in the glycerol-grown cultures.

It was previously shown that \( \text{aml} \) expression is not inducible by maltotriose in glucose-grown cultures of TK24(pTS6000) (Virolle & Gagnat, 1994); therefore, the inducibility of \( \text{aml} \) expression in glucose-grown cultures of the \( \text{sblA::Ωaac} \) mutant was tested. Two sets of two cultures of TK24(pTS6000) and two cultures of TK24(pTS6000) \( \text{sblA::Ωaac} \) were grown in the same conditions as above. When Aml activity was just detectable in culture supernatants, \( 10^{-4} \) M maltotriose was added to one set of glycerol- and glucose-grown cultures. Aml activity was assayed in the culture.
sequence 5

sequence is not. Eight direct repeats of the gene interrupted by the transposon Tn
holoenzyme of streptomycetes whereas the (TAGAPuT) recognized by the major RNA polymerase toward the end of the exponential phase of growth. Its unique promoter and its transcription is enhanced
sblA
S
seen on the CBS plates in Fig. 6.

This paper describes the isolation of an S. lividans strain, the extremely low
respectively. In glucose-grown cultures of the wild-type
aml
supernatants 1 h after maltotriose addition (Fig. 8b).
aml
expression proved to be maltotriose-inducible in glycerol-grown cultures of the wild-type and the mutant strains with rather similar induction ratios of 7 and 8, respectively. In glycerol-grown cultures of the wild-type strain, the extremely low aml expression was not increased upon maltotriose addition, whereas the enhanced aml expression of the sblA mutant strain was further inducible upon maltotriose addition (induction ratio of 3). These results were consistent with the phenotype of the TK24(pTS6000) sblA::Ωaac mutant seen on the CBS plates in Fig. 6.

Similarly, the very weak amylolytic activity of S. lividans TK24 was clearly enhanced in S. lividans TK24 sblA::Ωaac on the CBS plates in the presence of glucose (Fig. 6). The interruption of sblA thus had a similar effect on the expression of endogenous amylolytic genes of S. lividans to that on the heterologous aml gene.

**DISCUSSION**

This paper describes the isolation of an S. lividans transposition mutant in which a usually strongly glucose-repressed gene, the heterologous aml gene from S. limosus encoding an α-amylase (Virolle & Gagnat, 1994), was expressed in the presence of glucose. The gene interrupted by the transposon Tn5096 was called sblA. It is transcribed as a monocistronic RNA from a unique promoter and its transcription is enhanced toward the end of the exponential phase of growth. Its putative –10 region is similar to the consensus sequence (TAGApuT) recognized by the major RNA polymerase holoenzyme of streptomycetes whereas the –35 (TTGACN) sequence is not. Eight direct repeats of the sequence 5′-C(C/G)GGAGG(C/T)-3′ are found up-stream of the sblA promoter region, the last copy overlapping the putative –35 sequence. These repeats exhibit similarities to the operator site (5′-GGGGGA-(T/G)GGAGG-3′) recognized by MalT, the activator of the maltose regulon in E. coli (Boos & Shuman, 1998). Furthermore, a hairpin loop with a 9 bp stem \([AG = -10\text{–}90 \text{ kcal mol}^{-1} (45\text–}8 \text{ kJ mol}^{-1})]\), and a 4 bp loop is present 167 bp downstream of the GTG start codon. The loop is bordered by a Shine–Dalgarno-like sequence (AGGAGG) and comprises a GNRA tetraloop motif that can adopt a characteristic very stable fold (Jucker et al., 1996). These structures are likely to play a role in regulating expression of sblA. Translation of sblA probably occurs in the absence of a conventional Shine–Dalgarno sequence, as its transcriptional start site and the GTG translational start codon coincide.

sblA constitutes the fourth characterized locus involved in the regulation of aml expression. The three other loci are the glkA gene encoding the glucose kinase in S. coelicolor (Ikeda et al., 1984; Virolle & Gagnat, 1994), the LacI-like negative transcriptional regulator called Reg1 in S. lividans (Nguyen et al., 1997) and the Reg1 operator sites located in the aml promoter region (Virolle & Gagnat, 1994; Nguyen, 1999). In a strain of S. coelicolor mutated for the glkA gene, glucose repression of aml expression is abolished but the derepressed aml expression is further inducible by a low level of exogenous inducer (Virolle & Bibb, 1988). In S. lividans, the interruption of reg1 (Nguyen et al., 1997) or the deletion of operator-like sequences located in the aml promoter region and constituting the Reg1 binding site (Virolle & Gagnat, 1994; Nguyen, 1999) concomitantly abolishes both maltodextrin induction and glucose repression of aml expression. Similarly, in S. coelicolor, the interruption of glyR and malR encoding the negative transcriptional regulators of the glycerol operon glyX-ABC (Hindle & Smith, 1994) and the maltose transport operon malEFG (van Wezel et al., 1997), respectively, and the mutation of operator-like sequences located in the promoter region of chi (encoding chitinase) from Streptomyces pilatus (Delic et al., 1992; Ni & Westpheling, 1997) concomitantly abolish both substrate induction and glucose repression of these genes and

\[\text{Fig. 8. Effect of the disruption of sblA on the production of } \alpha\text{-amylase. (a) Maximal growth-phase-related } \alpha\text{-amylase activity detected in the supernatant of glucose- and glycerol-grown cultures of S. lividans TK24- (pTS6000) (□) and S. lividans TK24(pTS6000) sblA::Ωaac (■). (b) Maltotriose-induced } \alpha\text{-amylase production detected in the supernatant of glucose- and glycerol-grown cultures of S. lividans TK24(pTS6000) (□) and S. lividans TK24(pTS6000) sblA::Ωaac (■). A², } \alpha\text{-amylase activity at } t = 0; A⁰, \alpha\text{-amylase activity at } t = 1 \text{ h; } A¹, \alpha\text{-amylase activity at } t = 1 \text{ h after the addition of } 10^{-4} \text{ M maltotriose. The induction ratio (IR) was calculated as follows: } (A¹ − A²)/(A⁰ − A²). \alpha\text{-Amylase activity values are means of triplicate experiments and the so never exceeded 15% of the mean.} \]
negative transcriptional regulators are mediating the catabolite repression in operons. These observations suggest either that inducer exclusion is the main mechanism contributing to catabolite repression in *Streptomyces* or that the specific negative transcriptional regulators are mediating the process. The latter situation would be unusual since in *E. coli* or *Bacillus subtilis* catabolite repression is mainly mediated by the presence or absence of positive or negative pleiotropic transcriptional regulators, the cAMP–CRP (cAMP receptor protein) complex and CcpA, respectively (Saier et al., 1995). Nevertheless, the contribution to catabolite repression of specific regulators containing a phosphotransferase system regulation domain (PRD regulators) has been demonstrated in *B. subtilis* (Stulke et al., 1998).

The apparent relief of catabolite repression of *aml* expression observed in the *sblA* mutant strain is not easy to rationalize. It could simply be due to an absence of glucose transport/metabolism resulting from the early growth arrest characteristic of this mutant. Nevertheless, in the *sblA* mutant, Reg1, the negative transcriptional regulator of *aml* expression has obviously less affinity for its binding sites than in the wild-type strain. The affinity of transcriptional regulators for their target sites could be modulated by many mechanisms. A classical way is the binding of an effector molecule inducing a conformational change leading to the reduction or the enhancement of the affinity of the transcriptional regulators for their target sites (Matthews & Nichols, 1998). Alternatively, a post-translational modification (phosphorylation) of a regulator or its interaction with another protein could modulate its affinity for target sites. For instance, in *B. subtilis*, the phosphorylation state of PRD regulators governs their DNA-binding ability (Martin-Verstraete et al., 1998), and interaction of the pleiotropic catabolite repressor CcpA with a phosphorylated form of the phosphotransferase Hpr, Hpr Ser 46P, modulates its affinity for the catabolite-responsive elements present in the promoter regions of genes sensitive to glucose repression (Deutscher et al., 1995). The SblA protein bears similarities to various phosphatases of the IMP family. These enzymes are usually involved in the dephosphorylation (or the phosphorylation) of small phosphorylated molecules. Considering these structural similarities, as well as the enhancement of *aml* expression in the absence of exogenous inducer in the *sblA* mutant, we propose that SblA is usually involved in the degradation of an internal inducer of *aml* expression or of a precursor of such an inducer. For instance, a phosphorylated glucose derivative (e.g. glucose-1-P as in *E. coli*; Decker et al., 1993) might accumulate in the *sblA* mutant and be used as a precursor for the intracellular synthesis of an inducing maltodextrin. Alternatively, SblA might be involved in the production of a signalling molecule playing a role in catabolite repression in *Streptomyces*. In the glucose-grown cultures of the *sblA* mutant, an internal inducer of *aml* expression would be made (or would not be degraded) or the synthesis of a signalling molecule for catabolite repression would not occur, leading to the observed enhanced *aml* expression.

The identification of the SblA substrate should allow a better understanding of the biological role of this protein and of its connection with the phenomenon of catabolite repression in *Streptomyces*.

ACKNOWLEDGEMENTS

We thank Eriko Takano for providing RNA samples; Janet White and M. J. Bibb for their general help, comments and interest; and S. Aymerich, P. Boulou; M. Guérineau and J.-L. Pernodet for their interest and critical reading of the manuscript.

REFERENCES


Janssen, G. R. & Bibb, M. J. (1985). Derivatives of pUC18 that have BglII sites flanking a modified multiple cloning site and that retain the ability to identify recombinant clones by visual screening of *Escherichia coli* colonies. *Gene* 124, 133–134.
Annu. Mol Microbiol


Transcriptional activator LevR.

 PTS-catalysed phosphorylation on the Bacillus subtilis A3(2) chromosome.

and a detailed genetic and physical map for the 8 Mb Streptomyces chitinase gene in Streptomyces. Proc Natl Acad Sci USA

Mutational cloning in streptomycetes.

13116–13121.

Direct repeat sequences in the Streptomyces lividans AUD1 for selection of transposable DNA and characterization of a new IS derivative in Streptomyces lividans. J Bacteriol

1096–1104.

DNA sequencing with chain-terminating inhibitors. Proc Natl Acad Sci USA

Reg1 regulated by a pleiotropic regulatory gene. J Bacteriol

257–266.

The synthesis and product.

A simple and reliable turbidimetric and kinetic assay for alpha-amylase that is readily applied to culture supernatants and cell extracts. J Ind Microbiol

A mutation that enhances synthesis of sigma 32 and suppresses temperature-sensitive growth of the rpoH15 mutant of Escherichia coli. J Bacteriol

A mutation that

From the molecular analysis of the par cluster of Streptomyces alboniger. J Biol Chem

Cloning, characterization and

Cloning, characterization and functional properties and structure. Prog Nucleic Acid Res Mol Biol

and a detailed genetic and physical map for the 8 Mb Streptomyces coelicolor A3(2). J Bacteriol 175, 3422–3429.

A set of ordered cosmids and a detailed genetic and physical map for the 8 Mb Streptomyces coelicolor A3(2) chromosome. Mol Microbiol 21, 77–96.


Use of sodium trichloracetate and mung bean nuclease to increase sensitivity and precision during transcript mapping. Anal Biochem 158, 165–170.


Diverse proteins homologous to inositol monophosphatase. FEMS Lett 294, 16–18.

The regulatory protein Reg1 of Streptomyces lividans binds the promoter region of several genes repressed by glucose. FEMS Microbiol Lett 175, 51–58.


A selection media for transpositional mutagenesis. J Ind Microbiol


A set of ordered cosmids and a detailed genetic and physical map for the 8 Mb Streptomyces coelicolor A3(2) chromosome. Mol Microbiol 21, 77–96.


Received 5 February 1999; revised 19 May 1999; accepted 25 May 1999.
