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kasT Gene of *Streptomyces kasugaensis* M338-M1 Encodes a DNA-binding Protein which Binds to Intergenic Region of *kasU-kasJ* in the Kasugamycin Biosynthesis Gene Cluster

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We previously reported that a 4.2 kb *Sac*I-*Eco*RI DNA region from *Streptomyces kasugaensis* M338-M1, a kasugamycin (KSM) producer, included KSM transporter genes (*kasKLM*). As an extension of that study, a 3.7 kb *Pst*I-*Sac*I DNA region, located at 1.5~5.2 kb upstream of *kasK*, was cloned and sequenced, revealing three complete open reading frames, designated *kasT*, *kasU* and *kasJ*. The *kasJ* gene encodes a protein (KasJ) with a conserved dinucleotide (FAD)-binding motif. Homology search for KasJ showed its similarity to NADH: N-amidino-*scyllo*-inosamine oxidoreductase (StsB) which is involved in biosynthesis of the streptidine moiety of streptomycin (SM) in *S. griseus*. The *kasT* gene encodes a DNA-binding protein (KasT), including a helix-turn-helix motif near the center of the sequence. This protein is similar in structure to a pathway-specific activator protein (StrR) that plays a role in regulating the SM biosynthesis gene cluster of *S. griseus*. A fusion protein (Trx-KasT) clearly showed DNA binding activity with the intergenic region of *kasU-kasJ*, suggesting that KasT is a pathway-specific regulator of the KSM biosynthesis gene cluster.

The genus *Streptomyces* is a group of Gram-positive bacteria that produce a wide variety of secondary metabolites including antibiotics and other pharmacologically active agents. Mechanisms and regulation of biosynthesis of these bioactive compounds are poorly understood. Elucidation of biosynthesis pathways and regulatory mechanisms of production may help to increase antibiotic productivity and/or to design new antibiotics with hybrid structures with enhanced properties.

Kasugamycin (KSM) is an aminoglycoside antibiotic produced by *Streptomyces kasugaensis* M338-M1[1], effective against *Piricularia oryzae* and widely used in agriculture in Japan to prevent the rice blast. From *S. kasugaensis* MB273-C4, another KSM producing strain, a gene encoding the enzyme that acetylates the 2′-NH_2 of KSM and thereby inactivates the antibiotic was cloned and named *kac* by HIRASAWA *et al.* (JP. A-05-23187, 1993). Genes required for antibiotic biosynthesis are usually clustered in streptomycetes and linked to genes for self-protection against the endogenous antibiotic. Genes for regulation of antibiotic biosynthesis are also often found in the clusters. We described in the previous papers that some KSM biosynthetic genes[2] and KSM transporter genes[3] were found in the upstream region of KSM acetyltransferase gene (kac^{338})[4], a self-protection gene, from *S. kasugaensis* M338-M1.

In the present paper, we report the cloning, sequencing and characterization of a putative transcriptional regulator gene for the KSM biosynthetic pathway.

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Materials and Methods

Strains and Plasmids

Strains and plasmids used in this work are summarized in Table 1. *S. kasugaensis* M338-M1 has been maintained at the Institute of Microbial Chemistry. The following strains and plasmids were of commercial origins: *E. coli* TH2[5] (TaKaRa), *E. coli* DH5α[6] (TOYOBO), *E. coli* BL21(DE3) (STRATAGENE), pKF 3[5,7] (TaKaRa), pUC118[8] (TaKaRa) and pET-32a$_{(+)}$[9] (Novagen). Other plasmids were produced in the present study.

Growth Conditions

S. kasugaensis M338-M1 was grown in MR medium (KSM producing medium)[3] under shaking at 27°C for 72 hours. *E. coli* TH2 transformants were grown at 37°C in L-broth containing 12 μg/ml chloramphenicol and 50 μg/ml streptomycin. *E. coli* DH5α and BL21(DE3) transformants were grown at 37°C in Luria-Bertani (LB) medium containing 50 μg/ml ampicillin.

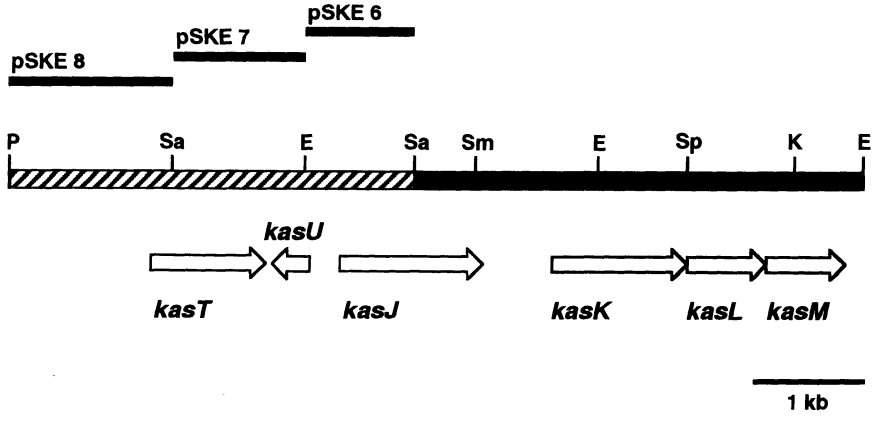
Cloning and Sequencing

Isolation of genomic DNA from *S. kasugaensis* M338-M1 was conducted as described previously[4].

The *E. coli* TH2/pKF 3 cloning system[5,7] was used to clone pSKE 6 (Fig. 1). The cloned DNA region (1.1 kb *Eco*RI-*Sac*I fragment) was digested with appropriate restriction endonucleases, and the fragments were subcloned into pUC118. Nucleotide sequence was determined for both strands using an ALF*red*™ DNA sequencer (Amersham Biosciences). Sequencing reactions were carried out with Cy5™ AutoCycle™ Sequencing Kit (Amersham Biosciences) according to the supplier's instructions.

To clone the DNA region of pSKE 7 (Fig. 1), the genomic DNA was digested with *Sac*I, and the restriction fragments were ligated themselves with T4 ligase. After self-ligation, an unknown DNA region (1.2 kb, *Sac*I-*Eco*RI) was amplified by PCR using oligonucleotides 5′-pKS26b (5′-CGGCTCACACAGGCCCGCACCGAAA-3′) and 3′-pKS26a (5′-GCACAGTTCAGCCTCATTTCCTTGT-3′). For cloning of pSKE 8, the genomic DNA was digested with *Pst*I. After self-ligation, an unknown DNA region (1.5 kb, *Pst*I-*Sac*I) was amplified with 5′-SKE72 (5′-CCAAGATCGCACATGCGGCAGGGGT-3′) and 3′-SKE73 (5′-TCCGCTCCGTCGAAGAACCGCACCT-3′). To avoid misreading of the nucleotide sequences of the amplified fragments for pSKE 7 and pSKE 8, the PCR products were used as templates for the dideoxy chain-termination method. As sequencing primers, we used M13-40 universal primer, M13-reverse primer and some synthesized oligonucleotide primers (labeled with Cy5, purchased from Amersham Biosciences). After direct sequencing, these PCR products were cloned into pUC118 to make pSKE 7 and pSKE 8 (Table 1).

Fig. 1. Restriction map of the cloned DNA region from *S. kasugaensis* M338-M1, including kasugamycin transporter genes (*kasKLM*).



On the restriction map, the striped region is dealt with the present paper. The solid region (right) has been reported[3]. The open arrows indicate the deduced ORFs and direction of transcription. The inserts of plasmids pSKE 6, pSKE 7 and pSKE 8 are indicated above the map. Abbreviations: E, *Eco*RI; K, *Kpn*I; P, *Pst*I; Sa, *Sac*I; Sm, *Sma*I; Sp, *Sph*I.

Table 1. Strains and plasmids.

Strains and plasmids	Genotype and genetic construct	Source or reference
Strains		
S. kasugaensis M338-M1	Kasugamycin producing strain	1)
E. coli DH 5α	φ80*lacZ*ΔM15 Δ(*lacZYA-argF*) U169 *deoR recA*1 *endA*1 *hidR*17(r_K^-, m_K^+) *phoA supE*44 λ⁻*thi*-1 *gyrA*96 *relA*1	TOYOBO
TH 2	*supE*44 *hsdS*20(r_B^-, m_B^+) *recA*13 *ara*-14 *proA*2 *lacY*1 *galK*2 *rpsL*20 *xyl*-5 *mtl*-1 *thi*-1 *trpR*624	TaKaRa
BL21(DE3)	F' *ompT* (r_B^- m_B^-)	Novagen
Plasmids		
pUC118	Cloning vector. Amp^r. 3.1 kb.	TaKaRa
pKF 3	Cloning vector. Sm^s, Cm^r. 2.2 kb.	TaKaRa
pET-32a(+)	Amp^r, expression vector derived from pBR322, containing *trxA [1-109]* and His-tag expressed from T7 promoter for construction of Trx hybrid proteins.	Novagen
pSKE 6	pKF 3 derivative containing 1.0 kb *Eco*RI-*Sac*I fragment. 3.2 kb	This work
pSKE 7	pUC118 derivative containing 1.2 kb *Sac*I-*Eco*RI fragment. 4.3 kb.	This work
pSKE 8	pUC118 derivative containing 1.5 kb *Pst*I-*Sac*I fragment. 4.7 kb.	This work
pET-KasT	pET-32a(+) derivative containing 1.0 kb *Nco*I-*Bam*HI fragment. Trx-KasT expression plasmid.	This work

Computer Analysis of DNA and Protein Sequences

DNA and protein sequences were analyzed with the DNASIS-Mac version 3.7 (Hitachi Software Engineering). FramePlot 2.3.1[10] was used to search for open reading frames (ORF). Amino acid sequences of potential gene products were compared with those in the databases (SWISS-PROT and PIR) by means of FASTA[11] and BLAST[12].

Nucleotide Sequence Accession Number

The nucleotide sequence data reported in this paper will appear in the DDBJ, EMBL and GenBank nucleotide sequence databases with the accession number AB076838.

Rapid Amplification of cDNA Ends (RACE)

The transcription start site of *kasJ* was determined by the 5′ RACE method with 5′-Full RACE Core Set (TaKaRa) according to the manufacturer's instructions[13]. Isolation of total RNA from *S. kasugaensis* M338-M1 was conducted as described previously[3]. RT reaction was performed in 15 μl containing 200 pmol of 5′-phosphorylated primer 3′-PKasJ (5′-CCAGCACGATGTACTCGCGGCCCAGTCGTT-3′), 5 U of AMV reverse transcriptase XL and 5 μg of the total RNA. The primer was annealed stepwise (80°C for 2 minutes and 45°C for 10 minutes) before the reverse transcriptase was added. The RT reaction mixture was incubated at 50°C for 1 hour. A negative control lacked reverse transcriptase. The template mRNA was hydrolyzed with RNase H (60 U) at 30°C for 1 hour, and the resulting cDNA was ligated with T4 RNA ligase (40 U) at 15°C for 18 hours. The first strand cDNA was circularized and/or connected into a concatemeric form. The first PCR mixture contained 20 pmol each of 5′-RACE26 (5′-GGCTCGAGTGGATACGGCGGTAATCGGGTC-3′) and 3′-RACE26 (5′-GGGCATGCGCACAGTTCAGCCTCAT-TTCCT-3′). The reaction was carried out with 20 cycles under the following conditions: 97°C for 30 seconds (denaturation), 66°C for 1 minute (annealing), and 72°C for 1 minute (extension). The resulting PCR product (1 μl) was used as a template for the second nested PCR amplification with primers 5′-RACE26b (5′-GGGCATGCCCGAACTG-GAACGACT-3′) and 3′-RACE26b (5′-CGCTCGAGTC-CGGCGTGCCGCTGT-3′) under the same conditions as described above. The 140 bp product was digested with *Sph*I and *Xho*I (recognition sites are underlined in the primers) and cloned into a plasmid vector pUC118. The

DNA sequence of the product was determined by the dideoxy chain-termination method.

Transcription start site of kasU was also determined using 5′-PKasU (5′-CGACTTCCGGACCGCGTCGCAC-AGT-3′) for the first strand synthesis. Pairs of primers [5′-RACE7a (5′-TTGGTTGAACACAGGTGGAG-3′)/3′-RACE7a (5′-GGAATTTCCTGGGTTGAACA-3′) and 5′-RACE7b (5′-GGGCATGCGGTGCGCACGTACGGGGA-C-3′)/3′-RACE7b (5′-GCGTCGACCCGCCCGTTGCAG-CCA-3′)] were used for the first and second PCR, respectively. The 5′-RACE for *kasU* mRNA was performed as described above for the 5′-RACE for *kasJ* mRNA.

Overexpression and Purification of Trx-KasT

The coding region of *kasT* was amplified by PCR using 5′-THIS6 (5′-GGCCATGGTTCATCATCATCATCATCA-CGTGGCTGAAACA-3′) and 3′-TBgl1 (5′-CCAGATC-TTCACGCACTTGCCCGTCCACGC-3′), designed to include *Nco*I and *Bgl*II recognition sites, respectively. The amplified fragment was digested with *Nco*I and *Bgl*II. The 1073 bp *Nco*I-*Bgl*II fragment was ligated into *Nco*I-*Bam*HI digested pET-32a$_{(+)}$. The construct (pET-KasT, Table 1) was transformed into *E. coli* BL21(DE3). In pET-KasT, *kasT* was fused in frame to the 3′ end of *trxA* (thioredoxin gene) under the control of the T7 promoter. In this host strain, the T7 polymerase gene was controlled by the *tac* promoter that could be induced by isopropyl-β-D-thiogalactopyranoside (IPTG). The fusion protein (Trx-KasT) contained two His(6x)-Tag (Fig. 4A). The transformants were grown at 37°C to 0.5 OD_{660}, then induced with 1 mM IPTG and cultured further at 30°C for 20 hours. The cells were collected by centrifugation and disrupted by sonication. Insoluble materials were separated by centrifugation for 30 minutes at 10,000 *g*. Trx-KasT in the supernatant was bound to Ni-nitrilotriacetic acid (Ni-NTA) resin and eluted with imidazole, as described by the supplier (Qiagen). The eluate (Trx-KasT) was inspected by sodium dodecyl sulfate-polyacrylamide gel electrophoresis (SDS-PAGE, Fig. 4B). The Trx-KasT was stored at −70°C in the presence of 10% glycerol.

Gel Retardation Assay

The intergenic region of *kasU-kasJ* was separated into two regions; 26A (nt 2713~2917, Fig. 2) and 26B (nt 2918~3060, Fig. 2), each amplified by PCR using pairs of primers 5′-GS26a (5′-GGGAATTCCGGGGTCGGCGGC-ACAC-3′) and 3′-GS26a (5′-CACACACCTGAGTCCGG-GCAAGG-3′) for 26A and 5′-pKS26a (5′-CTCGACACT-TCTCGACGCTCTCCCT-3′) and 3′-pKS26a (5′-GCACA-GTTCAGCCTCATTTCCTTGT-3′) for 26B. The upstream region of *kasT* (nt 705~1313) was amplified in three separate segments (8A, 8B and 8C, Figs. 2, 5). Pairs of PCR primers were 5′-GS8a (5′-GGCGATGCGGTCGTCGGA-AC-3′) and 3′-GS8a (5′-GTTTCGACTGGTCACGCGTT-3′) for 8A (nt 705~902, Fig. 2), 5′-GS8b (5′-GCCTAC-CGAACCGTGGGAGATG-3′) and 3′-GS8b (5′-AGATCG-GCCATTTTCCCCGAGG-3′) for 8B (nt 903~1131, Fig. 2), and 5′-GS8c (5′-CGTGCTATGGCCGAACTTTTGC-3′) and 3′-GS8c (5′-GAGCCTCTCGGTCGATGATGTT-3′) for 8C (nt 1132~1313, Fig. 2). These PCR fragments were ^{32}P labeled at the 5′ ends with [γ-^{32}P]ATP and T4 polynucleotide kinase. For the gel retardation assay, 0.3 to 0.5 ng of the ^{32}P-labeled DNA fragments (10,000 to 15,000 cpm) were incubated with 3 to 5 μg of Trx-KasT at 30°C for 1 hour in a buffer containing 10 mM Tris-HCl (pH 8.0), 50 mM KCl, 5 mM DTT, 10% (v/v) glycerol, 12.5 mM spermidine and 1 μg of poly(dI-dC)·poly(dI-dC) in a total volume of 20 μl. Protein-DNA complexes were separated from free DNA on 4% polyacrylamide gels by electrophoresis at 150 V for about 1 hour (Figs. 5, 6).

Results

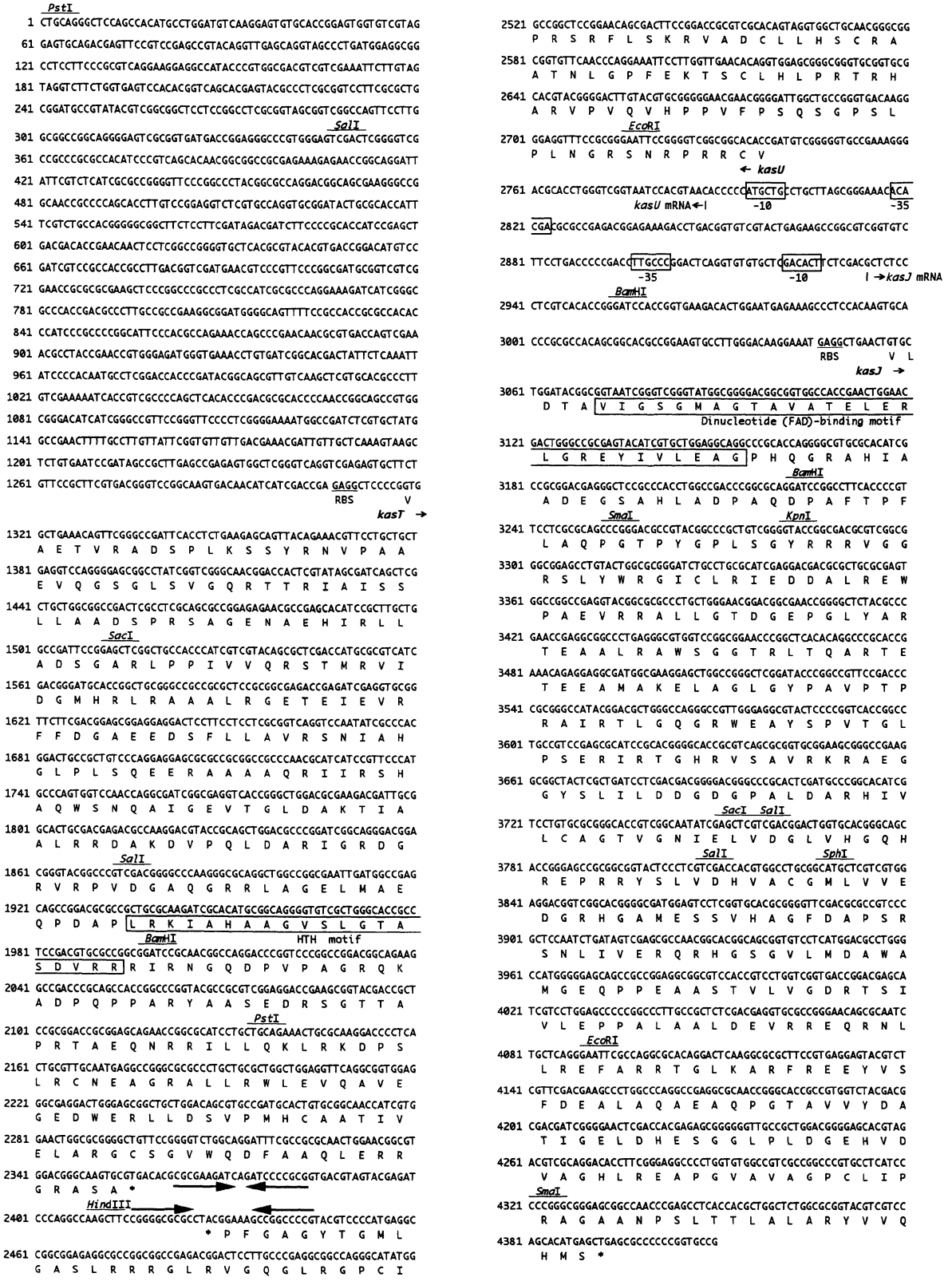
Cloning and DNA Sequence Analysis

The newly cloned 3.7 kb *Pst*I-*Sac*I region was located upstream of *kasKLM*, the KSM transporter genes. As shown in Fig. 1, the region was separated into three short fragments and cloned separately. The inserted fragment of pSKE 6 was shotgun-cloned as described previously[3]. These inserted fragments of pSKE 7 and pSKE 8 were cloned by a method using PCR technique (see Methods).

The 3755 bp *Pst*I-*Sac*I region from pSKE 6~8 was sequenced (Fig. 2). The GC content of the region was calculated to be 67.9% from the sequence. ORFs were searched for based on the codon usage and third codon position bias which are characteristic of streptomyces genes[14]. Within this region two complete ORFs, designated *kasT* (nt 1318~2358) and *kasU* (nt 2737~2426, complementary), and the 5′ region of already reported ORF J[3] were recognized. We designated ORF J as *kasJ*. No ORFs were found upstream (nt 1~1317) of *kasT*. There was only a relatively low GC content region (nt 870~1230, 57.6% GC) for streptomyces genomes.

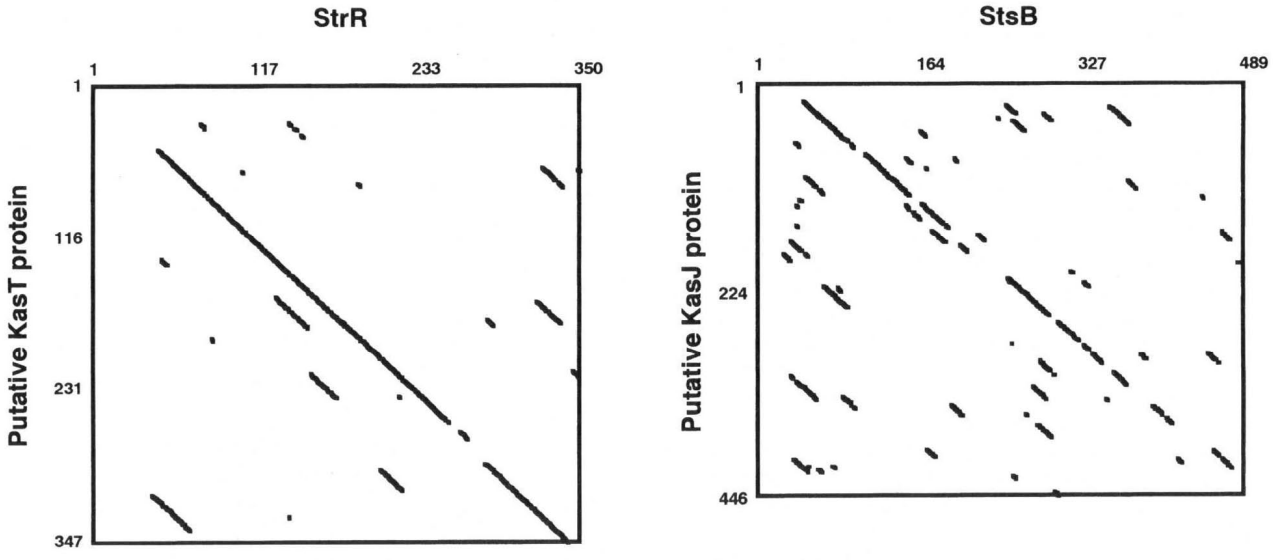
The putative initiation codon for *kasT* is nt 1318 GTG, preceded by a potential ribosome binding site (RBS) (nt 1307~1310, GAGG). The stop codon for *kasT* is nt 2356 TGA. The *kasU* gene runs in the opposite direction to *kasT* and *kasJ*. The putative start and stop codons for *kasU* are nt 2737 GTG and nt 2428 TAG (complementary, Fig. 2),

Fig. 2. Nucleotide sequence of the 4410 bp region including *kasT*, *kasU* and *kasJ* from *S. kasugaensis* M338-M1.



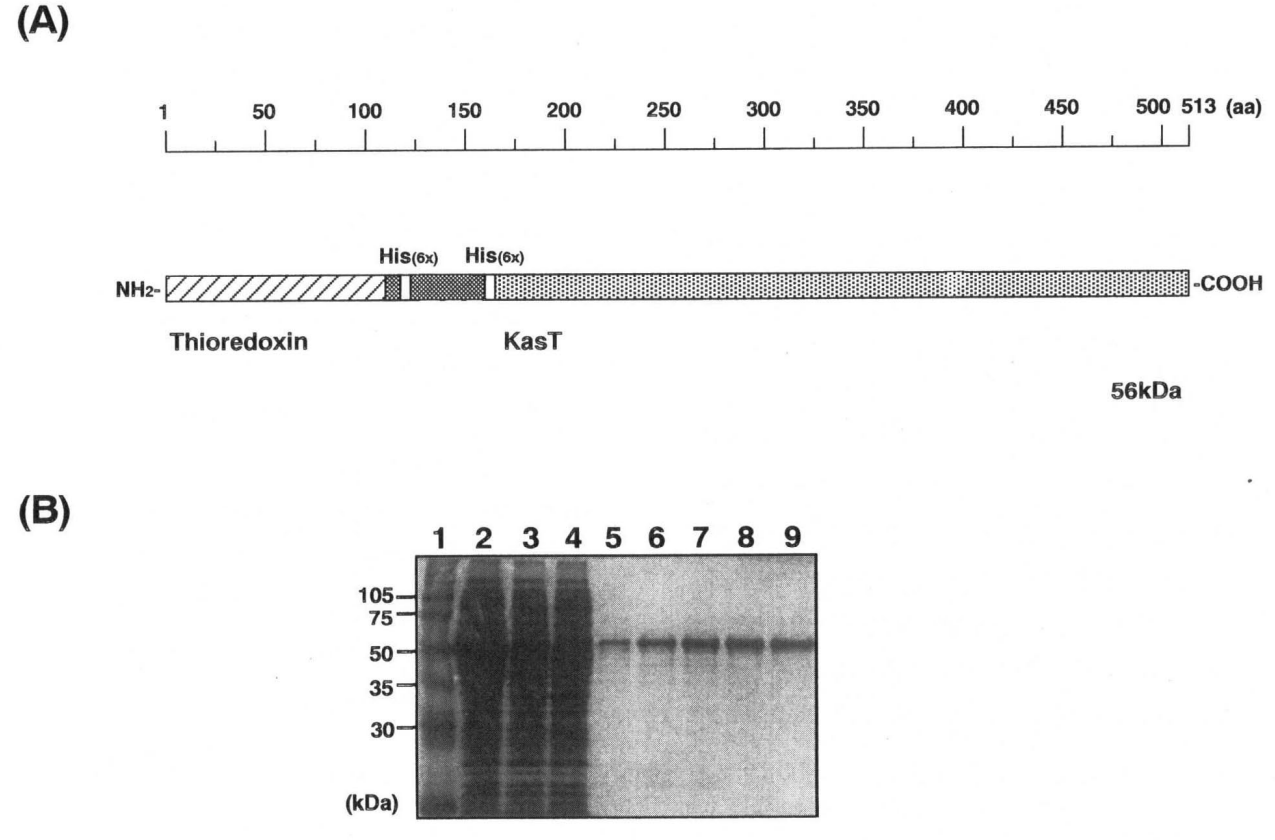
Deduced amino acid sequences of KasT, KasU and KasJ were shown in single letter code below the nucleotide sequence. Thick arrows indicate the putative transcriptional terminators for *kasT* and *kasU*. Boxed nucleotides indicate −35 and −10 hexamer of the potential promoters for *kasU* and *kasJ*. The helix-turn-helix motif (KasT) and the dinucleotide (FAD)-binding motif (KasJ) are boxed.

Fig. 3. Homology plot.



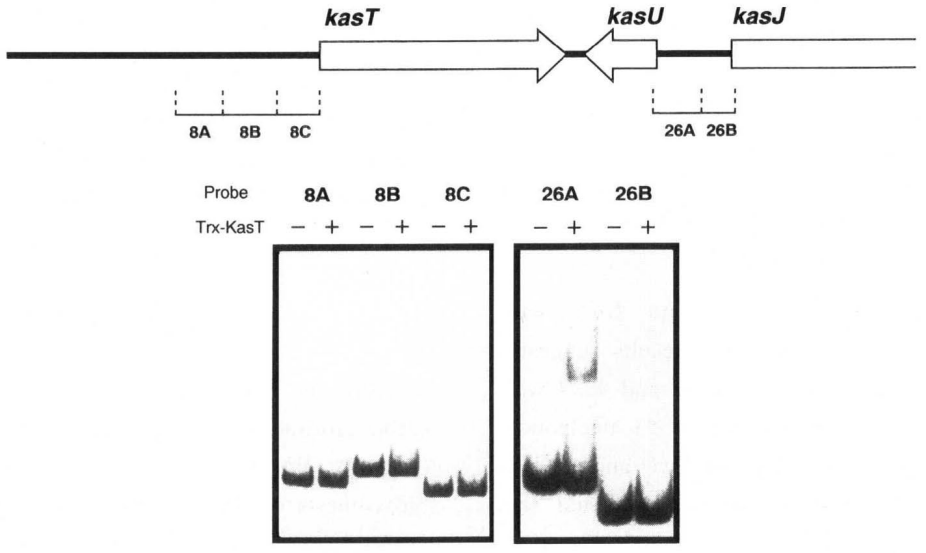
Deduced amino acid sequences of KasT and KasJ were compared with StrR[15] and StsB[19] from *S. griseus*, respectively. These data were compared using a window of 30 and a stringency of 8.

Fig. 4. Overexpression of Trx-KasT in *E. coli* BL21(DE3).



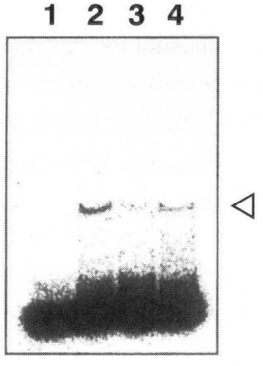
(A) The putative primary structure of Trx-KasT. (B) Purification of Trx-KasT with Ni-NTA. Lane 1, Size marker; Lane 2, Cell lysate; Lane 3, Flow-through; Lane 4~5, Wash (20 mM imidazole); Lane 6~9, Elution (250 mM imidazole).

Fig. 5. Gel retardation assays demonstrating the binding of Trx-KasT.



Thick line and open arrows indicate the cloned DNA and the putative structural genes, respectively. The location of the DNA regions used as probe is shown under the map.

Fig. 6. Gel retardation assays demonstrating the specific binding of Trx-KasT.



An open triangle indicates shifted band. A 259 bp *Sph*I-*Sal*I fragment from pKF 3 was used as noncompetitor. Lane 1, free probe (26A); Lane 2, Trx-KasT; Lane 3, Trx-KasT and competitor (200 ng); Lane 4, Trx-KasT and noncompetitor (400 ng).

respectively. There are two imperfect palindromic sequences (nt 2363~2383, nt 2416~2444) in the intergenic region of *kasT-kasU*. These sequences might be transcriptional terminators for each gene. The putative start codon for *kasJ* is nt 3057 GTG, preceded by a potential RBS (nt 3046~3049, GAGG). The stop codon for *kasJ* is nt 4392 TGA. The intergenic region of *kasU-kasJ* (nt 2738~3056) includes two possible promoters for each direction.

Characterization of Putative KasT, KasU and KasJ Proteins

The deduced product (KasT) of *kasT* was a protein containing 346 amino acid residues, with a molecular mass of 37,551 Da and a pI of 10.3. Homology search using the FASTA and BLAST programs suggested that KasT was a DNA-binding protein with a conserved helix-turn-helix (HTH) motif (Fig. 2). The deduced amino acid sequence of KasT showed 50% similarity with StrR[15], a pathway-specific activator of SM biosynthesis from *S. griseus* (Fig. 3). KasT was also similar to various other pathway-specific transcriptional regulators controlling the expression of biosynthetic gene clusters for antibiotics in *Streptomyces*, such as SpcR[16] (44%) from *S. flavopersicus*, NovG[17] (45%) from *S. spheroides* and ComG[18] (44%) from *S. lavendulae*.

The deduced KasU protein containing 103 amino acid residues showed no significant similarities with any proteins in the databases.

The *kasJ* gene encoded protein (KasJ) containing 445 amino acid residues, with a molecular mass of 47,662 Da and a pI of 5.68. The deduced amino acid sequence contained a dinucleotide (FAD)-binding motif (Fig. 2) and showed 36% similarity with NADH:N-amidino-*scyllo*-inosamine oxidoreductase (StsB)[19] for SM biosynthesis in *S. griseus* (Fig. 3).

Determination of Transcription Start Sites of *kasJ* and *kasU* by Rapid Amplification of cDNA Ends (RACE)

Transcription start sites of *kasJ* and *kasU* were determined by the RACE method. The results suggested that the transcription start sites of *kasU* and *kasJ* were located at G (nt 2788, complementary), 51 nucleotides upstream of the putative start codon of *kasU* and at G (nt 2934), 123 nucleotides upstream of the predicted start codon of *kasJ*, respectively (Fig. 2).

Most *Escherichia coli* promoters, recognized by RNA polymerase holoenzyme containing σ^{70}-factor ($E\sigma^{70}$), have two conserved hexamer sequences at -35 and -10. Some streptomycete promoters have similar structures, thus called streptomycete *E. coli*-like promoter (SEP)[20]. The consensus sequences of SEP are TTGAC[Pu] (-35 hexamer) and TAG[Pu][Pu]T (-10 hexamer)[21], 16 to 18 nucleotides apart.

As shown in Fig. 2, the -35 and -10 hexamer sequences of the putative *kasU* promoter (*kasU*-p) were TCGTGT (nt 2823~2818, complementary) and CAGCAT (nt 2800~2795, complementary), respectively, 17 nucleotides apart. The -35 and -10 hexamer sequences of putative *kasJ* promoter (*kasJ*-p) were TTGCCC (nt 2897~2902) and GACACT (nt 2921~2926), respectively, 18 nucleotides apart. These results suggested that *kasU*-p and *kasJ*-p belonged to SEP. The transcription start site of *kasT* remains to be determined.

Overexpression and Purification of Trx-KasT

To demonstrate the function of KasT, we overexpressed in *E. coli* BL21(DE3) a fusion protein in which Trx-KasT was preceded by a thioredoxin peptide and six histidine residues, and purified the product by affinity chromatography with a Ni-NTA column. Purity was confirmed by SDS-polyacrylamide gel electrophoresis (Fig. 4B). The molecular mass of 56 kDa agreed well with that (Mr=55,819) deduced from the nucleotide sequence.

Trx-KasT Binds Specifically to the Intergenic Region of *kasU-kasJ*

DNA binding ability of the purified fusion protein was demonstrated by gel retardation assay. As shown in Figs. 5 and 6, the protein bound to the intergenic region of *kasU-kasJ* (nt 2713~2917, Fig. 2) but not to the upstream region of *kasT* (nt 705~1313, Fig. 2).

It was confirmed that the thioredoxin peptide part alone did not bind to DNA (data not shown).

Discussion

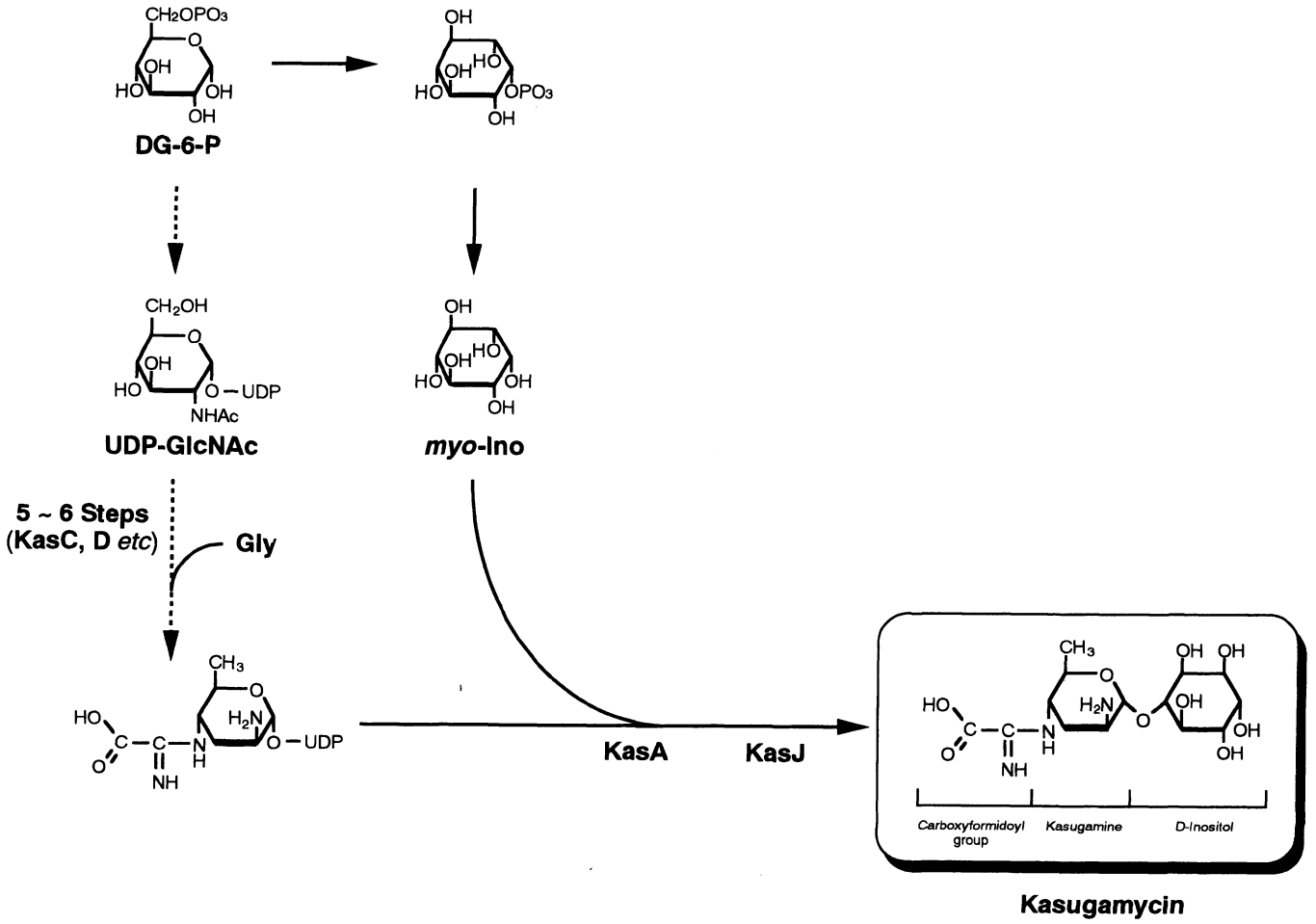
KSM, an aminoglycoside antibiotic, is composed of carboxyformidoyl, kasugamine and D-inositol moieties (Fig. 7). We have found three genes responsible for biosynthesis of the kasugamine moiety (*kasA*, *kasC*, and *kasD*) located upstream of *kac*[338]. In this region of the *S. kasugaensis* genome, we also found the KSM transporter genes (*kasKLM*) but did not find any biosynthetic genes for the carboxyformidoyl or the D-inositol moiety. In the present study, we report that KasJ, containing a dinucleotide- (FAD-) binding motif in the *N*-terminal region, is similar to StsB which is a putative oxidase involved in keto group formation during the streptidine biosynthesis in *S. griseus*. The substrate of StsB should be an inositol derivative (N-amidino-*scyllo*-inosamine). It was inferred, therefore, that KasJ might be responsible for biosynthesis of the D-inositol moiety (Fig. 7). FUKAGAWA *et al.*[22] reported that a precursor of the D-inositol moiety was not D-inositol, but *myo*-inositol. It remains to be established whether KasJ catalyzes the epimerization (from *myo*-inositol to D-inositol).

KasT showed high degrees of similarity with StrR, a pathway-specific activator protein of SM biosynthesis. The HTH motif of KasT shared 75% identity with that of StrR. As shown in Fig. 5, KasT did not bind to the upstream region of its own gene, *kasT*, but did bind to an intergenic region of *kasU-kasJ*. This result suggests that KasT might be a pathway-specific regulator of the KSM biosynthesis gene cluster, but not autoregulator.

The binding sites of StrR have a partial palindromic consensus sequence [GTTCGActG$(N)_{11}$CagTcGAAc][23] and are located upstream of the *str/sts* promoters in SM producer strains. Although we found a partial palindromic sequence GAAGCCGGCGTCGGTGTCTTC (nt 2863~2883, Fig. 2) in the intergenic region, the sequence had no similarity with that of StrR-binding site.

Use of a rare codon UUA is a characteristic of some

Fig. 7. A tentative pathway of kasugamycin biosynthesis.



Abbreviations: DG-6-P, D-glucose 6-phosphate; *myo*-Ino, *myo*-Inositol; Gly, Glycine; UDP-GlcNAc, UDP-N-acetylglucosamine.

actinomycete pathway-specific regulators[24,25] including *strR*. This codon is not used in *kasT*, however, indicating that *kasT* is not regulated by *bldA*[26].

In the biosynthesis of SM, expression of *str* is regulated by a complicated regulatory cascade involving pleiotropic and pathway-specific factors. The start point of the cascade is controlled by A-factor[27], an autoinducer produced by SM producing strains. Future studies of *kasT* will be necessary to show whether the transcription is regulated by A-factor or related γ-butyrolactone(s)[28].

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