A Bacillus subtilis spore coat polypeptide gene, \textit{cotS}

Akiko Abe,\(^1\) Hidekatsu Koide,\(^2\) Takeyuki Kohno\(^1\) and Kazuhito Watabe\(^1\)

Author for correspondence: Kazuhito Watabe. Tel/Fax: +81 720 66 3112.
e-mail: QWB03314@niftyserve.or.jp

A gene, \textit{cotS}, encoding a spore coat polypeptide of \textit{Bacillus subtilis}, was isolated from an EcoRI fragment (5–4 kb) of the chromosome by using synthetic oligonucleotide probes corresponding to the NH\(_2\)-terminal amino acid sequence of Cot40-2 previously purified from the spore coat of \textit{B. subtilis}. The nucleotide sequence (2603 bp) was determined and sequence analysis suggested the presence of two contiguous ORFs, ORF X and \textit{cotS}, followed by the 5'-region of an additional ORF, ORF Y, downstream of \textit{cotS}. The \textit{cotS} gene is 1053 nucleotides long and encodes a polypeptide of 351 amino acids with a predicted molecular mass of 41 083 Da. The predicted amino acid sequence was in complete agreement with the NH\(_2\)-terminal amino acid sequence of Cot40-2. The \textit{orfX} gene is 1131 nucleotides long and encodes a polypeptide of 377 amino acids with a predicted molecular mass of 42 911 Da. The gene product of \textit{cotS} was confirmed to be identical to Cot40-2 by SDS-PAGE and immunoblotting from \textit{Escherichia coli} transformed with a plasmid containing the \textit{cotS} region. Northern hybridization analysis indicated that a transcript of \textit{cotS} and \textit{orfX} appeared at about 5 h after the onset of sporulation. The transcriptional start point determined by primer extension analysis suggested that –10 and –35 regions are present upstream of \textit{orfX} and are very similar to the consensus sequence for the $\sigma^E$-dependent promoter. Terminator-like sequences were not found in the DNA fragment (2603 bp) sequenced in this paper, which suggested that the \textit{cotS} locus may be part of a multicistronic operon. The \textit{cotS} gene is located between \textit{dnaB} and \textit{degQ} at about 27.2° on the genetic map. Insertional mutagenesis of the \textit{cotS} gene by introducing an integrative plasmid resulted in no alteration of growth or sporulation, and had no effect on germination or resistance to chloroform.

**Keywords**: \textit{Bacillus subtilis}, spore coat gene, \textit{cotS}, insertional mutagenesis

---

**INTRODUCTION**

Endospore formation in the genus \textit{Bacillus} is a relatively simple model for cell differentiation that involves sequential changes in the cell physiological state and ultrastructure. The spore coat represents one of the most conspicuous morphological structures formed during sporulation. Spore coat polypeptides are synthesized only in the mother cell compartment beginning at 3–4 h of sporulation (t\(_{3-4}\)), and in a defined temporal order (Cutting \textit{et al.}, 1991; Jenkinson \textit{et al.}, 1981; Sandman \textit{et al.}, 1988; Zheng \textit{et al.}, 1988; Zheng \& Losick, 1990). Some of the coat polypeptides have been prepared from \textit{B. subtilis} spores by solubilization using alkaline and/or detergent treatments, and the genes encoding some of them, designated \textit{cotA–D} (Donovan \textit{et al.}, 1987), \textit{cotE} (Zheng \textit{et al.}, 1988), \textit{cotF} (Cutting \textit{et al.}, 1991), and \textit{cotT} (Aronson \textit{et al.}, 1989) have been cloned. Additional \textit{cot} genes, whose products are localized in the insoluble fraction of the \textit{B. subtilis} spore coat, have recently been cloned and designated \textit{cotV–Z} (Zhang \textit{et al.}, 1993). The \textit{cot} genes are controlled by a regulatory cascade (Zheng \& Losick, 1990), and their transcription is induced by the successive appearance of the regulatory proteins: $\sigma^E$, SpoIID, $\sigma^K$ and GerE. Most \textit{cot} genes are transcribed by RNA polymerase containing $\sigma^K$ (E$\sigma^K$); the \textit{cotE} gene alone has
dual promoters for σB and σN dependent RNA polymerase. The cots genes and their products are involved in normal morphogenesis of the spore coat and also in the germination process as components of receptors for germinants or of permeability barriers (Aronson & Fitz-James, 1976; Moir, 1981; Aronson et al., 1989; Bourne et al., 1991).

Our approach toward understanding the physiological role of spore coat proteins was to purify the uncharacterized coat components and to identify the genes that encode them. In a previous paper (Abe et al., 1993), we reported the purification of two coat polypeptides (termed Cot40-1 and Cot40-2) each having a molecular mass of about 40 kDa. Determination of the NH₂-terminal amino acid sequences showed that they were different from each other and not homologous to sequences of previously described coat polypeptides (Donovan et al., 1987; Zheng et al., 1988; Aronson et al., 1989; Cutting et al., 1991; Zhang et al., 1993). In this paper, we report the cloning and mapping of the cots gene encoding coat polypeptide Cot40-2. In addition, we examined the effects of insertional mutagenesis of cots gene on growth, sporulation, ability of the spores to respond to germinants, and spore resistance properties.

METHODS

Bacterial strains, phage, and plasmid. The cells of B. subtilis 60015 (trpC2 metC7) (derived from strain of 168 trpC2, originally provided by E. Freese, NIH, Bethesda, MD, USA) were grown in DS medium (Schaeffer et al., 1965). Escherichia coli XLI-Blue, helper phage VCS-M13 and phagemid vector pBluescriptIK(+) (Stratagene) were used for sequencing, and E. coli was grown in LB medium at 37 °C. When necessary, ampicillin or tetracycline were added to final concentration of 50 or 12.5 µg ml⁻¹, respectively.

Preparation and purification of spores. B. subtilis cells were grown in DS medium for 48 h at 37 °C, and spores were harvested by centrifugation and purified by washing and lysozyme treatment (100 µg ml⁻¹, at 20 °C for 20 min), as previously described (Watabe et al., 1981). On the treatment of cell suspension with lysozyme, no change was observed in the spores as monitored with a phase microscope.

Synthetic oligonucleotides. Oligonucleotides were synthesized in an Applied Biosystems DNA Synthesizer (model 380 A). As probes for Cot40-2, short and mixed oligonucleotides (17 bases long), corresponding to all possible codon combinations for residues 3 through 8 and 20 through 25, respectively, were designed on the basis of the NH₂-terminal amino acid sequence of Cot40-2. The synthetic oligonucleotides were as follows: 5'-C-A-A/G-A-A-A/G-G-A-A/G-C-A-T/C-G-A-A/G-G-A-3' for probe A, and 5'-T-T-T/C-C-A-T/C-A-T-T/C/A-G-A-T/C-C-A-T/C-G-T-3' for probe B.

Preparation of DNA. Chromosomal DNA was prepared from vegetative cells by the method of Sambrook & Miura (1963). Large- and small-scale plasmid preparations were performed as described by Sambrook et al. (1989).

Cloning and DNA sequencing of cots. Synthetic oligonucleotides were labelled at their 3' termini with digoxigenin-ddUTP and terminal transferase according to the manufacturer's instructions (Boehringer Mannheim).

For DNA cloning and sequencing, the 5.4 kb EcoRI fragment was isolated by 0.7% (w/v) agarose gel electrophoresis and cloned into pBlueScriptIK(+) phagemid. It was digested again with EcoRI and then partially digested with SspI, and the resulting 2.6 kb fragment was positive on hybridization with probes A and B. This fragment was further digested with appropriate restriction enzymes and subcloned into pBlueScriptIK(+) to construct a series of plasmids containing overlapping fragments ranging in size from about 0.1 to 1.8 kb. Where an appropriate restriction site was not available, deletion with exonucleases III and mung bean nuclease (Deletion Kit, Takara Shuzo) was used. The nucleotide sequence was determined for both strands by the dideoxy chain-termination method (Sanger et al., 1977), using Sequencing High (Chemiluminescent DNA Sequencing Kit, USB) (Tabor & Richardson, 1987) and M13 forward biotin-labelled primer.

Insertional mutagenesis. The cots gene was inactivated by introducing a 2.4 kb ampicillin-chloramphenicol resistance gene cassette (amp®, cm®) from plasmid pCX18 (2.4 kb) (Sato et al., 1994; Yamada, 1989) as shown in Fig. 2. The PsI−HindIII segment (302 bp), corresponding to a central region of cots1, was isolated and cloned in the PsiI−HindIII sites of plasmid pCX18 to yield plasmid pCX18S. Competent cells of B. subtilis 60015, prepared as previously described (Anagnostopoulos & Spizizen, 1961), were transformed with the plasmid, and the cots1 insertion mutant, BS-1, was obtained by integration of the plasmid into the chromosome by single reciprocal recombination (Campbell-like) between B. subtilis DNA sequences in pCX18S and the corresponding homologous sequences on the chromosome. The single recombination event was confirmed by restriction enzyme digestion of chromosomal DNA and Southern hybridization to appropriate probes (data not shown).

RNA preparation and Northern analysis. B. subtilis cells, grown on a DS plate at 37 °C for 12 h, were suspended in a small amount of DS medium, and added to 100 ml DS medium to an initial OD₆₀₀ ~ 0.1 and incubated at 37 °C with shaking. Samples (25 ml) were harvested at the end of the exponential phase (t₉) and during sporulation, and RNA was prepared as described by Igo & Losick (1986). The RNA (20 µg) was analysed by size fractionation through a 1.5% (w/v) agarose gel containing 2% M formaldehyde, transferred to a positively charged nylon membrane (Boehringer Mannheim), and then hybridized to the probe DNAs (Northern probes for orfX and cots1, Fig. 1), which were directly labelled with the horseradish peroxidase according to the procedure for direct nucleic acid labelling and detection systems provided by Amersham.

Mapping the 5' terminus of cots mRNA. Primer extension analysis was performed as previously described (Sambrook et al., 1989). The synthesized 18-mer oligonucleotide primers, Pr.1 (5'-GAATGGGACTGCCCTAAA-3'), Pr.2 (5'-CTCCT-
CGAACCGATGGGA-3') and Pr. 3 (5'-GCTCTTTTTTGGTACACTC-3'), were complementary to 72-89 bp upstream and 38-55 bp downstream of the putative translational start point of orfX, and to −2−16 bp downstream of the putative translational start point of cotS, respectively (Fig. 2). The primers labelled at their 5' terminus with biotin were purchased from Funakoshi. Total RNA (100 μg) extracted from sporulating cells at different stages was hybridized with 1 pmol primer at 30 °C overnight and used for the assay. Extension reactions were done with Rous-associated virus 2 reverse transcriptase (Takara Shuzo). The lengths of the primer-extended products were determined by comparison with sequencing ladders generated by using the same primer and the single-stranded DNA template containing orfX and cotS.

Mapping of cotS. The location of the cotS gene on the chromosome was determined as described by Iwaya & Tanaka (1991). B. subtilis 168 trpC2 chromosomal DNA, digested with NotI and SfiI, was loaded into the well of an agarose gel (10 x 10 cm) placed in a contour-clamped homologous electric field (CHEF) gel apparatus. Running conditions were as follows: 1% (w/v) agarose, TBE [45 mM Tris/borate (pH 8.0), 45 mM boric acid, 1 mM EDTA] solution (14 °C), 30 s pulse time, 3 V cm⁻¹, 30 h running time. After running the CHEF electrophoresis, the gel was stained with ethidium bromide (1 pg ml⁻¹) and photographed. DNA in the CHEF gels was transferred onto a nylon membrane (Nytran 13N, Schleicher & Schuell) by capillary blotting for 15−17 h (Sambrook et al., 1989). A non-radioactive labelled nucleotide, digoxigenin-11-dUTP, was used for preparing DNA probes. The random primer labelling technique, pre-hybridization and hybridization procedures and colour development were according to the protocol of Boehminger Mannheim.

Preparation of lysates from E. coli harbouring the cotS gene. The plasmid pBluescriptIISK(+) harbouring the cotS DNA was introduced into E. coli XL1-Blue by transformation. The cells were grown in LB medium containing 50 μg ampicillin ml⁻¹ and 1 mM IPTG to OD₆₀₀ ~ 1 to induce the expression of the cotS gene. The cells (1 ml) were pelleted and suspended into 20 μl of 62.5 mM Tris/HCl buffer (pH 6.8) containing 2% (w/v) SDS and 5% (v/v) 2-mercaptoethanol, and were treated in boiling water for 3 min. The cell lysate was obtained by centrifugation at 12000 r.p.m. for 10 min at room temperature.

SDS-PAGE and immunoblotting. The cell lysate was mixed with 0.1 vol. BBP/glycerol buffer [0.05% bromophenol blue, 70% (v/v) glycerol and 0.25 mM Tris/HCl buffer, pH 6.8], and then fractionated by SDS-12.5% (w/v) PAGE as described previously (Abe et al., 1993). Gels were stained in 0.25% (w/v) Coomassie Brilliant Blue (R250)/50% (v/v) methanol/10% (v/v) acetic acid for 20−40 min. For immunoblotting, proteins were transferred onto a polyvinylidifluoride membrane (Immobilon, 0.45 μm pore size, Millipore), and detected using rabbit IgG against the spore coat protein fraction as the first antibody, and goat (anti-rabbit IgG) IgG−horseradish peroxidase conjugate as the second antibody (BioRad) (Abe et al., 1993).

Germination. Purified spores were heat activated at 65 °C for 15 min and suspended in 0.05 M Tris/HCl, pH 7.5, to OD₆₀₀ ~ 0.8. Either (i) 10 mM L-alanine, (ii) 10 mM glucose plus 10 mM KCl, or (iii) 5.6 mM glucose, 5.6 mM fructose, 3.3 mM l-asparagine, and 10 mM KCl (GFAK) were then added. Germination was monitored by measurement of the decrease in OD₆₀₀ of the spore suspensions at 37 °C for up to 90 min.

Spore resistance assays. Cells were grown in DS medium at 37 °C for at least 12 h after exponential growth and spore resistance was assayed as follows: the cultures were heated at 80 °C for 30 min or were treated with 10% (v/v) chloroform at room temperature for 10 min, and viable cells were determined as previously described (Nicholson & Setlow, 1990).
RESULTS

Cloning and sequencing of the Cot40-2-encoding gene, cotS

The strategy for identifying and cloning the structural gene for this spore coat polypeptide was to use synthetic oligonucleotides as probes that were designed on the basis of the partial NH₂-terminal amino acid sequence. Two different probes (A and B) for Cot40-2 hybridized to a 5·4 kb EcoRI fragment and also to a 2·6 kb EcoRI–SacI fragment (data not shown), so the latter was cloned and sequenced (see Methods).

The restriction map of the 5·4 kb insert is shown in Fig. 1. The restriction sites were used to construct a series of plasmids containing various parts of the Cot40-2-encoding region. The 2·6 kb EcoRI–SacI fragment was positive on Southern blot analysis with probes A and B, plasmids containing various parts of the Cot40-2 gene were detected (data not shown), so the latter was cloned and sequenced (see Methods).

The predicted amino acid sequence from one of the ORFs was found to be in complete agreement with the results of the partial NH₂-terminal amino acid sequence of Cot40-2 for the first 30 residues (Abe et al., 1993). The ninth amino acid residue Glu (E) was erroneously recorded and should be replaced by Gln (Q). This ORF was designated cotS; the cotS sequence is 1053 nucleotides long, beginning with a GUG start codon at position 1388 and ending with a UGA stop codon at position 2441. Alternative start codons GUG, UUG and AUU are frequently used in prokaryote genes (Parker, 1989; Sorokin et al., 1993). The cotS gene encodes a polypeptide of 351 amino acids with predicted molecular mass of 41083 Da.

The other complete ORF, designated orfX, is 1131 nucleotides long, beginning with an AUG start codon at position 240 and ending with a UAG stop codon at position 1371. orfX potentially encodes a polypeptide of 377 amino acids with predicted molecular mass of 42911 Da. While the biological function of the product remains unclear, the predicted amino acid sequence of orfX is partially homologous (18·8%) to the product of the Salmonella typhimurium gene rfaK (Fig. 4), that is believed to encode N-acetylglucosamine transferase (Maclachlan et al., 1991). This enzyme is involved in lipopolysaccharide synthesis in S. typhimurium and is associated with the membrane.

A part of the 5' region of an additional ORF, termed orfY, was found just downstream of the cotS sequence and 53 amino acids were predicted (Fig. 3). orfY has a potential ribosome-binding site with optimal distances from the first codon as well as orfX and cotS. Sequences homologous to the predicted orfY gene product were not found in recent database searches. No terminator-like sequences such as rho-independent terminators or stem-loop structures were found in the 2·6 kb EcoRI–SacI fragment reported here, which suggests that the cotS locus may be part of a multicistronic operon. Determination of the whole sequence of the putative operon is in progress.

Northern analysis of cotS mRNA

To determine the size and approximate time of appearance of the RNA product, the in vivo transcript of cotS and orfX was detected by Northern blot analysis with total RNA of B. subtilis 60015 harvested at the onset (t₀) and at hourly intervals (t₁ to t₉) during sporulation. The 0·76 kb PstI–SacI and 0·47 kb AflI fragments (Fig. 1) were used as specific probes for cotS and orfX, respectively. The PstI–SacI probe detected the transcript of an approximately 2·9 kb fragment that appeared about 5 h after the onset of sporulation (Fig. 5a). The same result was obtained when the 0·47 kb AflI fragment was used as probe (data not shown). Positive bands were also found in the walls of the samples prepared from t₅ to t₉, suggesting that there may have been some denatured DNA in the samples. The nature of an additional RNA species that migrated faster than 2·9 kb in the t₅ sample is unknown. The synthesis of mRNA for cot genes and that of most coat polypeptides starts around t₅ to t₉ during sporulation (Setlow, 1993). According to these results, the synthesis of mRNA for coat polypeptides should be completed by t₉, so the positive fragment observed in the t₉ sample is quite questionable.

Analysis of the 5' terminus of cotS mRNA

To determine the transcriptional start point(s), we performed extension analysis with primers Pr.1, Pr.2 and Pr.3. Fig. 5(b) shows that primer Pr.2 generated an extension product from RNA isolated from cells at t₅ or t₆ but not from that of cells at t₄ or t₆. From the electrophoretic mobility of the extension product relative to that of a Pr.2-generated sequencing ladder (Fig. 5b), we infer that the 5' terminus of mRNA for orfX and cotS maps to the base pair 204 in the sequence of Fig. 3, i.e. 36 bp upstream of orfX. This inference was strongly supported from the primer extension analysis in which other primers, Pr.1 or Pr.3, complementing either the upstream part of orfX or the downstream part of the cotS, respectively, failed to detect any extension products (data not shown).

The sequence preceding the 5' terminus of orfX is aligned with several promoters recognized by σ⁰. The nucleotide sequence of the −35 (AC) and −10 (CgTAtcaTg) regions in the upstream sequence of orfX is similar to the consensus sequence for the −35 (AC) and −10 (CATAT--TA) sequences for σ⁰-controlled promoters (Fig. 6).

Analysis of an E. coli lysate

The above results indicated that a transcript containing both orfX and cotS is co-expressed during a late stage of sporulation. To identify the products of these genes, we prepared a 1·7 kb SacI fragment containing about the 3'-half of the orfX sequence, the full-length cotS region and the 5' region of orfY (Fig. 1). This DNA was inserted in-frame into the multicloning site of vector pBluescriptII(SK+). The expression of the inserted region is controlled by the lacZ promoter and is inducible.
Fig. 3. Nucleotide sequence of 2603 bp of the cloned EcoRI-SacI fragment and deduced amino acid sequence. A putative promoter region is indicated at -35 and -10. SD, ribosome-binding sites preceding each ORF; rr, a possible initiation site, determined by primer extension (shown in Fig. 5). Nucleotide sequences complementary to the synthetic oligonucleotides (Pr.1, Pr. 2, and Pr. 3) used in primer extension are underlined. Asterisks indicate stop codons.

by the addition of IPTG. Plasmids pSB or pSA, in which the 1.7 kb SacI fragment was inserted in forward or reverse direction, respectively, were transformed into E. coli, and the cell lysates were analysed by SDS-PAGE. When expression of the inserted region was induced by the addition of IPTG during exponential growth, no significant cell lysis was observed (data not shown), so overproduction of the Cots protein is not toxic for E. coli. As shown in Fig. 7, E. coli cells harbouring plasmid pSB strongly produced two additional polypeptides with molecular mass of about 40 and 25 kDa in the presence of IPTG (Fig. 7, lane 8), while cells harbouring pSA (reverse direction) did not make any additional gene products (Fig. 7, lane 7). To identify the newly produced polypeptides in an E. coli cell lysate, the products were analysed by immunoblotting. The 40 kDa polypeptide alone reacted with anti-spore-coat-protein antibodies (data not shown), and its size coincides with the cots gene.
components of the spore coat are located at widely scattered sites on the chromosome as are the interesting that the genes by Southern hybridization using NotI- or SfiI-digested st/bt\(\text{Ilis}\) fragments containing and 6). The physical map analysis using NotI and were obtained using the Sac1 fragment (1.8 kb) (lanes 5 was hybridized with NotI fragment 27N (60 kb) and the same results fragment MS (143 kb) (lane 2 and 3), and the same results (1991). As shown in Fig. 8(b), the EcoRI fragment (5.4 kb) (Itaya, 1993). Based on the physical map of the chromosome (full length 4165 kb) constructed by Tanaka (1991), the cotS gene is located at 3119–3179 kb, which maps between dnaB and degQ (Fig. 8c). The location of the cotS gene is again shown in Fig. 8(d) by comparison with the other cot genes previously reported. The position of the cotS gene is at about 270–275° on the genetic map of Henner & Hoch (1980), and its location is distinct from those of cotB (290°) or cotD (200°). The cotV, -W, -X, -Y and -Z genes are clustered and map at 107° between thiB and metA on the chromosome (Zheng et al., 1993). From our results and the previous reports, it is interesting that the genes so far identified as encoding components of the spore coat are located at widely scattered sites on the chromosome as are the tpo genes.

**Fig. 4.** Alignment of predicted amino acid sequences of orfX and S. typhimurium rfaK. Identical and similar amino acids are indicated by asterisks and dots, respectively.

**Map position of cotS**

The position of cotS on the chromosome was determined by Southern hybridization using NotI- or SfiI-digested B. subtilis 168 trpC2 genomic DNA fragments and the DNA fragments containing cotS as described by Itaya & Tanaka (1991). As shown in Fig. 8(b), the EcoRI fragment (5.4 kb) was hybridized with NotI fragment 27N (60 kb) and SfiI fragment MS (143 kb) (lane 2 and 3), and the same results were obtained using the SacI fragment (1.8 kb) (lanes 5 and 6). The physical map analysis using NotI and SfiI fragments confirmed that the genomic map of B. subtilis 168 trpC2 is identical to that of our strain (60015 trpC2 metC7) (Itaya, 1993). Based on the physical map of the B. subtilis chromosome (full length 4165 kb) constructed by Itaya & Tanaka (1991), the cotS gene is located at 3119–3179 kb, which maps between dnaB and degQ (Fig. 8c). The location of the cotS gene is again shown in Fig. 8(d) by comparison with the other cot genes previously reported. The position of the cotS gene is at about 270–275° on the genetic map of Henner & Hoch (1980), and its location is distinct from those of cotB (290°) or cotD (200°). The cotV, -W, -X, -Y and -Z genes are clustered and map at 107° between thiB and metA on the chromosome (Zheng et al., 1993). From our results and the previous reports, it is interesting that the genes so far identified as encoding components of the spore coat are located at widely scattered sites on the chromosome as are the tpo genes.

**Fig. 5.** Northern analysis of cotS mRNA (a) and determination of the transcriptional start site by primer extension analysis (b). (a) Each lane corresponds to RNA (20 µg) from sporulating cells at \(t_0\) to \(t_{10}\) respectively. Northern hybridization was performed with the labelled probe DNA (0.76 kb PstI–SacI, see Fig. 3) as described in Methods. The position and estimated size of the cotS mRNA is indicated by an arrowhead on the right. The positions of the 23S rRNA (2.9 kb) and 16S rRNA (1.6 kb) in the B. subtilis rrnB operon (Green et al., 1985) are indicated. (b) RNA was hybridized with biotin-5'-end-labelled primer Pr.2, which is complementary to 38–55 bp downstream of the putative translational start point of orfX (Fig. 3). Primer-extended products generated by primer Pr.2 were analysed as described in Methods. Each lane corresponds to RNA (100 pg) from sporulating cells at \(t_0\) to \(t_{10}\) respectively.

**Mutation in cotS**

We examined the effects of mutation in the cotS gene on growth, sporulation, germination, and spore resistance.


The mutant of strain BS-1, carrying a Campbell-like insertion in the central region of \( cotS \), was indistinguishable from the wild-type for growth (data not shown) and sporulation (Table 1). The spores of the mutant were as resistant to chloroform as the wild-type (Table 1), and also resistant to lysozyme treatment (250 \( \mu \)g ml\(^{-1} \), 37°C, 10 min) (data not shown). In addition, the response to various germinants was the same as that of the wild-type (Fig. 9), the mutant spores germinated immediately on incubation with L-alanine and more slowly with GFAK, but with glucose the mutant did not germinate as well as the wild-type.

**DISCUSSION**

The spore coat reveals a unique morphology in dormant spores of *Bacillus* and consists of polypeptides of different size, whose synthesis and assembly are precisely regulated by \( spo \) genes coordinately with other biological events taking place during sporulation. Coat polypeptide synthesis begins at \( t_3 \) and some of them are deposited on the surface of the forespore to form the coat layer, while others are synthesized as precursors and converted to mature forms during sporulation. One example is CotT: it is first synthesized as a 14 kDa precursor and processed to the 12.5 kDa form (Aronson et al., 1989). CotE is thought to be a morphogenic protein required for outer coat assembly. CotE mutant spores are lysozyme sensitive and germinate slowly as compared with wild-type spores (Zheng et al., 1988). In this work, we isolated and sequenced a new \( cot \) gene, termed \( cotS \), the contiguous ORF X and part of ORF Y. The product of \( cotS \) was confirmed as Cot40-2 by comparison of the amino acid sequence and antigenic activity against anti-spore-coat-protein antibodies. The predicted amino acid sequences of \( cotS \) and \( orfX \) are not homologous to those of the known \( cot \) genes and coat polypeptides previously reported (Donovan et al., 1987; Zheng et al., 1988; Aronson et al., 1989; Cutting et al., 1991; Zhang et al., 1993). There is no significant homology in the analysis of the hypophosphorylation profile of \( cotS \) and \( orfX \) (data not shown). The product of \( cotS \) was shown to be one of the coat components as mentioned above, but we have no evidence that the products of \( orfX \) and \( orfY \) are also coat components.

Analysis of Northern blots suggested that \( cotS \) and \( orfX \) are simultaneously transcribed into mRNA during the late stages of sporulation. The synthesis of mRNA coincides with the time of synthesis of spore coat proteins (Zheng & Losick, 1990) and morphogenesis of spore coat structure observed by electron microscopy (Setlow, 1993). Since the estimated size of mRNA from gel electrophoresis was greater than the sum of the nucleotides of \( cotS \) (1053 bp) and \( orfX \) (1131 bp), and no termination signal was found between \( cotS \) and \( orfY \), these results suggest that \( cotS \) and \( orfX \) may be transcribed simultaneously with \( orfY \). It has been reported that \( cot \) genes are controlled both temporally and compartmentally by RNA polymerase containing mother-cell-specific \( \sigma^K \) (Cutting et al., 1989; Sandman et al., 1988; Zheng & Losick, 1990). The time-course experiments of coat protein mRNA show that transcripts of \( cotE \), \( cotA \), \( cotB \) and \( cotC \) appear 4, 6, 7 and 7 h after the start of sporulation, respectively, and many \( cot \) genes, except \( cotE \), are members of the so-called \( \sigma^K \)-controlled genes (Sandman et al., 1988; Cutting et al., 1989; Zheng & Losick, 1990). From the
Table 1. Effect of null mutation in \( \text{cotS} \) on sporulation and spore resistance

<table>
<thead>
<tr>
<th>Strain</th>
<th>Sporulation</th>
<th>Chloroform resistance; ( % )</th>
</tr>
</thead>
<tbody>
<tr>
<td></td>
<td>Spores ml(^{-1})* Percentage†</td>
<td></td>
</tr>
<tr>
<td>60015</td>
<td>( 8 \times 10^7 )</td>
<td>45:2</td>
</tr>
<tr>
<td>BS-1</td>
<td>( 4 \times 10^8 )</td>
<td>72:5</td>
</tr>
</tbody>
</table>

* Spores per ml culture: number of c.f.u. after heat treatment (80 °C, 30 min).
† Percentage sporulation: (spores ml\(^{-1}\)/viable cells ml\(^{-1}\)) \times 100.
‡ Chloroform resistance: percentage ratio of c.f.u. after treatment to c.f.u. viable cells.

Results of Northern blot analysis and comparison of \( \sigma^K \)-dependent promoter sequences, the putative \( \text{cotS} \) operon seems to have a \( \sigma^K \)-controlled promoter. To address this question directly, we are now preparing \( \text{cotS} \)-lacZ fusions to test \( \sigma^K \)-dependence of the gene fusion expression. The \( \text{cotV}^- \text{Z} \) genes, encoding polypeptides present in the insoluble fraction of the spore coat of \( B. \) subtilis, were recently cloned. These genes are clustered on the chromosome and three possible \(-10\) sequences for \( \sigma^K \)-like promoters and potential stem–loop structures of transcriptional terminators were found in a 2.8 kb DNA region (Zhang et al., 1993). As shown in Fig. 3, a terminator-like sequence was not found in the 2.6 kb EcoRI–SacI frag-
ment. From the sequence data and the Northern blot analysis, the cotS locus may have a promoter that is recognized by σR, and may be part of a multicistronic operon consisting of orfX, cotS and orfY.

Since the physiological function of these gene products in Bacillus subtilis is unknown, we constructed an insertional mutant of the cotS gene using an integrative plasmid. The mutant cells grew and sporulated normally, which suggests that the gene is either a null mutant or apparently not essential for growth and spore formation. The spores produced by this null mutant responded to germinants and were as resistant to heat, chloroform and lysozyme as the wild-type spores. The CotE protein is of interest both because it is involved in lysozyme resistance and because it responds to L-alanine germination (Zheng et al., 1988). From these results, some biological functions of the cotS gene or its product are expected in morphogenesis of spores. While the present work did not provide information about any essential function of the gene in the development in Bacillus subtilis, progress is being made in the analysis of possible alterations in structure and location with ferritin-labelled antibody to pure Cot40-2.

ACKNOWLEDGEMENTS

We thank Mituhiro Itaya (Mitubishi Kasei Institute of Life Sciences) for extensive help in mapping the cotS and Sayoko Nakao for primer extension analysis and preparation of the insertional mutant. We are grateful to Tsutomu Sato and Yasuo Kobayashi for technical advice in the primer extension, helpful discussions and for plasmid pCX18. We also thank Lorella Spotila for reviewing the manuscript.

REFERENCES


Received 5 December 1994; revised 24 February 1995; accepted 14 March 1995.