Complete spore-cortex hydrolysis during germination of *Bacillus subtilis* 168 requires SleB and YpeB

Fiona M. Boland, Abdelmadjid Atrih, Haridasan Chirakkal, Simon J. Foster and Anne Moir

The role of the *sleB* gene of *Bacillus subtilis*, which encodes a putative spore-cortex-lytic enzyme, and the downstream *ypeB* gene were investigated. Both SleB and YpeB were required for normal germination to occur. The corresponding mutants formed phase-bright, heat-resistant spores with no apparent defects in dormancy. However, mutant spore suspensions lost optical density slower than the wild-type and spores were phase-grey even 12 h after the triggering of germination. Since the loss of heat resistance and release of dipicolinic acid was similar to the wild-type, these mutants were blocked in the later stages of germination. The mutants were nevertheless capable of outgrowth on rich agar to form colonies, indicating that other spore components can compensate for their function sufficiently to allow outgrowth. The expression and regulation of the operon was examined using a *lacZ* transcriptional fusion. Expression of the operon began 2 h after the onset of sporulation and was under the control of RNA polymerase containing the forespore-specific sigma factor, σG. The application of reverse phase HPLC revealed that the mutants do not have any structural defect in the dormant spore cortex and therefore these genes are not required for normal spore-cortex synthesis. The analysis of peptidoglycan dynamics during germination showed, however, that the cortex was only partially hydrolysed in both mutants. This analysis also revealed that the likely hydrolytic bond specificity of SleB is likely to be that of a lytic transglycosylase.

**Keywords:** *Bacillus subtilis*, endospores, germination, peptidoglycan, cortex hydrolysis

INTRODUCTION

The formation of resistant dormant endospores is a survival strategy used by members of the genera *Bacillus* and *Clostridium* during nutrient deprivation. The spore cortex maintains heat resistance and dormancy (Ellar, 1978). The cortex consists of a thick layer of peptidoglycan with a unique spore-specific structure (Atrih et al., 1996; Popham et al., 1996a). Hydrolysis of the cortex peptidoglycan is essential for later germination events and outgrowth (Atrih & Foster, 1999; Atrih et al., 1998; Popham et al., 1996b).

A number of spore-cortex-lytic enzymes have been isolated from spores of different organisms. Two lytic enzymes have been isolated from *Clostridium perfringens* S40 spores – a 31 kDa enzyme encoded by the gene *sleC* (Miyata et al., 1995) and a 38 kDa enzyme encoded by the gene *sleM* (Chen et al., 1997). The *Bacillus cereus* IFO 13597 gene *sleB* encodes a 24 kDa enzyme (Makino et al., 1994; Moriyama et al., 1996b), and its homologue has been identified and inactivated in *Bacillus subtilis*. The resulting mutant germinates slower than the wild-type (Moriyama et al., 1996a).

Foster & Johnstone (1987) isolated a germination-specific lytic enzyme (GSLE) that was capable of cortex hydrolysis from the spores of *Bacillus megaterium* KM. The enzyme was activated *in vivo* during germination and has a high specificity for intact spore cortex. Western blot analysis revealed cross-reactivity with proteins from spore fractions of other species and that the enzyme was

**Abbreviations:** GSLE, germination-specific lytic enzyme; MUG, methylumbelliferyl β-D-galactoside; RP-HPLC, reverse phase HPLC.
Table 1. Bacterial strains and plasmids

<table>
<thead>
<tr>
<th>Strain or plasmid</th>
<th>Genotype*</th>
<th>Source or reference†</th>
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</thead>
<tbody>
<tr>
<td>Strains</td>
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</tr>
<tr>
<td>168 HR</td>
<td>trpC2</td>
<td>Laboratory stock</td>
</tr>
<tr>
<td>FB101</td>
<td>trpC2 sleB–lacZ, Em⁺</td>
<td>(pFB101) → 168 HR</td>
</tr>
<tr>
<td>FB102</td>
<td>trpC2 ypeB–lacZ, Em⁺</td>
<td>(pFB102) → 168 HR</td>
</tr>
<tr>
<td>FB103</td>
<td>trpC2 spoIIGB::kan sleB–lacZ, Em⁺ Km⁺</td>
<td>(1295) → FB101</td>
</tr>
<tr>
<td>FB104</td>
<td>trpC2 spoIIABC::cat sleB–lacZ, Em⁺ Km⁺</td>
<td>(JE650) → FB101</td>
</tr>
<tr>
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<td>trpC2 spoIIIG::kan sleB–lacZ, Em⁺ Km⁺</td>
<td>(1296) → FB101</td>
</tr>
<tr>
<td>FB106</td>
<td>trpC2 spoIII::cat sleB–lacZ, Em⁺ Km⁺</td>
<td>(618) → FB101</td>
</tr>
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<td>FB107</td>
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<td>(pDG180) → FB101</td>
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<td>FB108</td>
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<td>(pRS11) → FB101</td>
</tr>
<tr>
<td>FB109</td>
<td>trpC2 Pspac-sigG sleB–lacZ, Em⁺ Km⁺</td>
<td>(pDG298) → FB101</td>
</tr>
<tr>
<td>FB110</td>
<td>trpC2 Pspac-sigK sleB–lacZ, Em⁺ Km⁺</td>
<td>(SH132) → FB101</td>
</tr>
<tr>
<td>HC145</td>
<td>trpC2 sleBΔ</td>
<td>(pGSB21) → 168 HR</td>
</tr>
<tr>
<td>SH132</td>
<td>sigKΔA19::pVO12 (Pspac-sigK), Cm⁺</td>
<td>Oke &amp; Losick (1993)</td>
</tr>
<tr>
<td>1295</td>
<td>trpC2 spoIIABC::kan, Km⁺</td>
<td>J. Errington, Oxford University, UK</td>
</tr>
<tr>
<td>650</td>
<td>trpC2 ilvB2 leuB16 spoIIABC::cat, Cm⁺</td>
<td>J. Errington, Oxford University, UK</td>
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<tr>
<td>618</td>
<td>trpC2 spoIII::cat, Cm⁺</td>
<td>Turner et al. (1986)</td>
</tr>
<tr>
<td>1296</td>
<td>trpC2 spoIIIG::kan, Km⁺</td>
<td>J. Errington, Oxford University, UK</td>
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<tr>
<td>Plasmids</td>
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<tr>
<td>pFB101</td>
<td>sleB–lacZ</td>
<td>This study</td>
</tr>
<tr>
<td>pFB102</td>
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<tr>
<td>pRS11</td>
<td>Pspac-sigF</td>
<td>R. Schmidt, Harvard University, USA</td>
</tr>
<tr>
<td>pDG298</td>
<td>Pspac-sigG</td>
<td>Sun et al. (1989)</td>
</tr>
</tbody>
</table>

* Cm⁺, chloramphenicol resistance; Km⁺, kanamycin resistance; Em⁺, erythromycin resistance.
† DNA transformation crosses are indicated; DNA source is in brackets and the arrow points to the recipient strain.
TG_{399}) where the internal sequence of the gene is italicized (numbering is with respect to the A of the translational start codon of the gene) and the HindIII site of the forward primer and the BamHI site of the reverse primer are underlined. The primers (5'-GCGGAGTCCTC_{315}TTCTATGCTAAATA- CGG_{174}) and (5'-CGGAGTTCA_{404}TATAGCTTTTATA- T_{393}) were used to amplify a 271 bp segment of the ypeB gene. pMUTin2 and the PCR fragments were digested with HindIII and BamHI and then ligated by the method of Sambrook et al. (1989).

(ii) Transformation of E. coli and B. subtilis. Transformation of E. coli was performed as described by Hanahan (1983). Transformation of B. subtilis 168 with pFB101 and pFB102 was performed by the competent cell method (Anagnostopoulos & Spizizen, 1961). Disruption of the yslB and ypeB genes by means of Campbell-type recombination was confirmed by Southern blot analysis, using the appropriate plasmid as probe. Hybridization, probe labelling and detection were done with the Boehringer Mannheim nonradioactive DNA labelling and detection kit.

Construction of yslB in-frame deletion mutant. To construct an in-frame deletion of yslB, a 5.6 kb DNA fragment spanning the yslB and ypeB coding sequence was synthesized by PCR using B. subtilis HR chromosomal DNA as template. Primers 5'-ATGCCTGTTGAGATGTTCTGACGATGCTT_1 and 5'-TTCGTTGAGATGTTCTGACGATGCTT_2 were used as forward and reverse primers, respectively (the chromosomal sequences are italicized and the SacI and SalI restriction sites added are underlined; the numbering is with respect to the A of the translational start codon of yslB). The PCR product was cloned in E. coli DH5α using plasmid pGEM3Z, after appropriate restriction digestion and ligation. A recombinant plasmid, pGSB1 containing the cloned DNA was isolated and this was used as template DNA for inverse-PCR using primers 5'-ATGCCTGTTGAGATGTTCTGACGATGCTT_1 and 5'-ATGATGTGATTACCCATACACGTTGAGATGTT_2 as forward and reverse primers, respectively (the chromosomal sequences are italicized and the restriction site for BamHI is underlined). The PCR product from this experiment resulted in a deletion of 399 bases in the coding region of the yslB gene. The PCR product was then restricted with BamHI and religated before transformation into E. coli DH5α. A plasmid, pGS2B1, carrying the yslB deletion was isolated and verified by restriction analysis. The yslB deletion was then transferred into B. subtilis HR by conjugation using pGS2B1 linearized with SacI and trp DNA. Congressant colonies (trp') were selected on SS minimal agar and then screened by PCR for the yslB deletion. One congressant, which showed the correct deletion, was verified by Southern blot and named HC145.

Spore preparation and germination. Sporulation was initiated in CCY medium and spores of B. subtilis were prepared as described by Stewart et al. (1981). Spores were stored at a concentration of 10 mg dry weight ml\(^{-1}\) in distilled water at \(-20^\circ\)C. Purified spores were heat-activated at 70 °C for 30 min and cooled in ice. Germination was initiated by the addition of l-alanine to a final concentration of 1 mM, or by the addition of aspartagine to 30 mM with glucose and fructose each to a concentration of 5·6 mM (AGF). Germinant was added to a 5 mg dry weight ml\(^{-1}\) spore suspension in 10 mM Tris/HCl pH 7 containing KCl (10 mg ml\(^{-1}\)). Spores were germinated at 37 °C and the extent of germination was monitored by recording the decrease in OD_{600} (Foster & Johnstone, 1987) over a 2 h period. Phase-darkening of spores was determined by phase-contrast microscopy.

(i) Determination of loss of heat resistance during germination. Germinating spore samples were diluted serially in 10 mM d-alanine and incubated at 70 °C for 30 min. After cooling in ice, viability was measured by plate counting on nutrient agar.

(ii) Measurement of loss of dipicolinic acid during germination. Samples of germination spore suspension (3 ml) were filtered through a 0·45 µm membrane and the dipicolinic acid content was measured as described by Scott & Ellar (1978).

RP-HPLC analysis of spore peptidoglycan. Cortex extraction from dormant and germinated spores, muropeptide separation by RP-HPLC, and amino acid and mass spectrometry analyses were performed as previously described (Atrih et al., 1996, 1998).

Analysis of gene expression

(i) Expression under the control of the Pspac promoter. Induced expression of sigma factor genes under the control of Pspac was carried out by adding IPTG (400 µM final concentration) to cells growing in LB at an OD_{600} of 0·25 (Sun et al., 1989).

(ii) Expression during sporulation. Synchronous sporulation was performed by the resuspension method of Sterlini & Mandelstam (1969). Samples were harvested every hour after the initiation of sporulation (t_0) for 8 h and sporulation morphology was monitored by microscopy.

(iii) Measurement of β-galactosidase activity. β-Galactosidase assays, using MUG (methylumbelliferyl β-d-galactoside) as the substrate, were performed as described by Youngman (1990), except that cells were permeabilized by incubation with lysozyme on ice for 20 min, MUG was used at a final concentration of 600 µg ml\(^{-1}\) in DMSO and the assay was incubated at 28 °C. Fluorescence was measured on a fluorometer (Hoefer). One unit of β-galactosidase activity was defined as the amount of enzyme which releases 1 pmol methylumbelliferone min\(^{-1}\) ml\(^{-1}\) (Zuberi et al., 1987), normalized to a culture OD_{600} of 1·0.

RESULTS

Characterization of the germination response of yslB and ypeB mutants

B. subtilis strains FB101 and FB102 contain an yslB–lacZ and a ypeB–lacZ transcriptional fusion, respectively, which resulted in insertional inactivation of the yslB and ypeB genes. An in-frame deletion in yslB was constructed to give strain HC145. In HC145, YpeB could still be produced in the absence of active SleB. All strains showed comparable sporulation efficiency to the parent. Spores prepared from these mutant strains were phase-bright and heat-resistant (70 °C, 30 min). During l-alanine-triggered germination, wild-type spores lost 55–60% of their initial optical density and became phase-dark, whereas mutant strains FB101 (yslB), FB102 (ypeB) and HC145 (sleBA) lost optical density at a slower rate, and became phase-grey (Fig. 1 and data not shown). Thus both SleB and YpeB are necessary for the germination process to occur normally. Similar results were obtained when germination was triggered in AGF (data not shown), suggesting that both yslB and ypeB are also required for the AGF germination pathway.
Peptidoglycan structural analysis of dormant spores

To determine whether the germination defect in the sleB and ypeB mutants is caused by a structural modification of spore peptidoglycan, the RP-HPLC profiles of Cellosyl-digested peptidoglycan from these mutants were compared to that of the wild-type. No peptidoglycan structural defect could be detected in strains FB101 (sleB), FB102 (ypeB) and HC145 (sleBA) compared to the wild-type (data not shown). The sleB and ypeB gene products are both likely therefore to be involved in the processes associated with cortex hydrolysis during germination.

(i) Peptidoglycan dynamics during germination. RP-HPLC profiles of germinated-spore-associated peptidoglycan in the wild-type and FB101 (sleB) are shown in Fig. 2(a) and 2(b), respectively. After 2 h germination, the ratio of dormant spore muropeptides and germination-associated muropeptides was altered between the wild-type (HR; Fig. 2a) and strain FB101 (sleB; Fig. 2b). In strain FB101 (sleB) there were less germination muropeptides (G1–G7) and correspondingly more dormant spore muropeptides (10, 11, 20, 21). Strains FB102 (ypeB) and HC145 (sleBA) showed identical profiles to strain FB101 (sleB) (data not shown). This result indicates a partial hydrolysis of the cortex in the sleB mutant. The amount of peptidoglycan released, calculated as the ratio of retained material to that of primordial cell wall (muropeptides 1 and 8) at time 0 and after 2 h germination, for strains FB101 (sleB), and FB102 (ypeB) was 44% and 38%, respectively. This amount is approximately 20% lower than that released from the wild-type, where 64% of peptidoglycan fragments were released in the germination exudate after 2 h.

FIG. 1. Spore germination of B. subtilis HR (wild-type, ○), FB101 (sleB, ●), FB102 (ypeB, □). Germination was monitored by measurement of OD600 at the times indicated after addition of 1 mM L-alanine and is expressed as the percentage loss of initial optical density.

FIG. 2. Analysis of muropeptides by RP-HPLC during germination of B. subtilis 168 HR spores. Muropeptide-containing samples were taken after 2 h germination and separated by RP-HPLC and the A102 of the eluates monitored. (a) B. subtilis HR germinated-spore-associated material; (b) FB101 (sleB) germinated-spore-associated material; (c) germination exudate from HR; and (d) germination exudate from FB101 (sleB).
Table 2. Calculated and observed m/z values for protonated sodiated and deprotonated molecular ions of new muropeptides from germination exudate of FB101 (sleB)

<table>
<thead>
<tr>
<th>Muropeptide*</th>
<th>Ion</th>
<th>m/z</th>
<th>Δm (Da)†</th>
<th>Identity</th>
</tr>
</thead>
<tbody>
<tr>
<td></td>
<td></td>
<td></td>
<td></td>
<td></td>
</tr>
<tr>
<td>G8A</td>
<td>[M + H]^+</td>
<td>785.9</td>
<td>989.0</td>
<td>-203.1</td>
</tr>
<tr>
<td></td>
<td>[M - H]^−</td>
<td>783.3</td>
<td>987.0</td>
<td>-203.7</td>
</tr>
<tr>
<td>G8B</td>
<td>[M + Na]^+</td>
<td>1600.0</td>
<td>1801.7</td>
<td>-201.7</td>
</tr>
<tr>
<td></td>
<td>[M - H]^−</td>
<td>1575.9</td>
<td>1777.7</td>
<td>-202.8</td>
</tr>
<tr>
<td>G8C</td>
<td>[M + Na]^+</td>
<td>1227.7</td>
<td>1429.4</td>
<td>-201.7</td>
</tr>
<tr>
<td></td>
<td>[M - H]^−</td>
<td>1203.2</td>
<td>1405.4</td>
<td>-202.2</td>
</tr>
</tbody>
</table>

* Muropeptides as numbered in Fig. 2(c) and 2(d).
† Difference between observed and calculated protonated, sodiated or deprotonated molecular mass values. Boldface characters denote deviations where the calculated values are the most likely combinations of the substituent components.

(ii) Germination exudate. The RP-HPLC profiles of germination exudate of the wild-type and the sleB mutant are shown in Fig. 2(c) and 2(d), respectively. The first impression from the RP-HPLC muropeptide profile of strain FB101 (sleB) is the relative abundance of muropeptides G8, G8A, G8B and G8C compared to the wild-type. Muropeptide G8 has been previously identified as a trisaccharide tetrapeptide (Atrih et al., 1998). The muropeptides G8A, G8B and G8C are present in the wild-type, but they are produced in substantial amounts in the sleB mutant only. Amino acid analysis and mass spectrometry revealed that muropeptides G8A, G8B and G8C are trisaccharide alanine, pentasaccharide tetrapeptide and pentasaccharide alanine, respectively (Table 2). These muropeptides are therefore the products of an N-acetylglucosaminidase already suggested to be involved in cortex hydrolysis during germination of B. subtilis endospores (Atrih et al., 1998).

The most striking difference in the peptidoglycan RP-HPLC profile of strain FB101 (sleB) compared to the wild-type is the apparent absence of muropeptides G9, G10, G12 and G13 (all are reduced by >90% compared to background levels). These muropeptides have previously been identified as anhydro-muropeptides generated by a lytic transglycosylase (Atrih et al., 1998). The RP-HPLC profile of peptidoglycan fragments from germination exudates of strains FB101 (sleB), FB102 (ypeB) and HC145 (sleBA) mutants are similar, suggesting the important role of the gene products in cortex hydrolysis during germination.

Expression of sleB during sporulation

Synchronous sporulation of the mutant strains was induced by the resuspension method and β-galactosidase activity from the sleB-lacZ and ypeB-lacZ transcriptional fusions was measured. In both cases, activity was first detected between t₀ and t₁ (2–3 h after the onset of sporulation, after asymmetric septation) and was maximal at around t₂, in two separate experiments, suggesting that the operon is regulated by a sporulation-specific sigma factor (Fig. 3). The time of induction of both sleB and ypeB correspond well with the published data for genes regulated by σE (Setlow, 1989). An apparent decrease in LacZ activity after t₁ of sporulation has been observed in experiments using fusions to forespore-specific genes such as gdh and gerA (Mason et al., 1988; Feavers et al., 1990) and is due to the progressive increase in resistance of the developing forespore to lysozyme used in the assay.

Chromosomal DNA carrying the sleB–lacZ fusion was transferred by transformation into strains carrying various spo mutations and β-galactosidase was measured during sporulation. The absence of expression of sleB–lacZ in strain FB105 carrying a mutation in the
sleB–lacZ expression which regulates mother-cell-specific gene expression (Fig. 3). Expression of sleB–lacZ in strains carrying various sporulation-specific sigma factors under Pspac promoter control during vegetative growth. Strain FB103 (Pspac-sigE, △), FB104 (Pspac-sigE, △), FB105 (Pspac-sigG, △) and FB106 (Pspac-sigK, △) were grown in L-broth and induced by the addition of IPTG to a final concentration of 1 mM. At various times, samples (1 ml) were harvested, treated with lysozyme and assayed for β-galactosidase activity.

**Fig. 4.** Expression of sleB–lacZ in strains carrying various sporulation-specific sigma factors under Pspac promoter control during vegetative growth. Strain FB103 (Pspac-sigE, △), FB104 (Pspac-sigE, △), FB105 (Pspac-sigG, △) and FB106 (Pspac-sigK, △) were grown in L-broth and induced by the addition of IPTG to a final concentration of 1 mM. At various times, samples (1 ml) were harvested, treated with lysozyme and assayed for β-galactosidase activity.

**DISCUSSION**

Recent analysis of *B. subtilis* and *B. megaterium* cortex hydrolysis during germination has revealed a complex common process involving at least three hydrolytic enzymes: an N-acetylglucosaminidase, a lytic transglycosylase and a possible amidase (Atrih & Foster, 1999; Atrih *et al.*, 1998, 1999). Another activity, suggested to be an epimerase, produces muropeptides with longer retention times than their counterparts in dormant spores. This activity has been extracted from germinated spores of *B. megaterium* along with an N-acetylglucosaminidase (Atrih *et al.*, 1999). In this study, we analysed the role of sleB and ypeB, which form a bicistronic operon (Moriyama *et al.*, 1999) involved in cortex hydrolysis. sleB has been previously insertionally inactivated in *B. subtilis* and was shown to be a crucial gene in germination (Moriyama *et al.*, 1996a). Peptidoglycan analysis of the spore-associated material of strain FB101 after 2 h germination revealed a partial hydrolysis of peptidoglycan. More interestingly, the analysis of the muropeptides in the germination exudate showed a major difference compared to that of the wild-type. The anhydromuropeptides generated by the lytic transglycosylase (Atrih *et al.*, 1998) were absent in the exudate, indicating that the gene may encode the lytic transglycosylase. Mutant spores release approximately 20% less peptidoglycan material than the wild-type and the spores remain phase-grey 12 h after addition of L-alanine. These observations indicate the crucial role of the enzyme and demonstrate that it is probably acting on spore-associated material as well as peptidoglycan fragments as previously suggested (Atrih *et al.*, 1998). Another interesting feature of the germination exudate of FB101 (sleB) is the increase of N-acetylgalactosaminidase products. The N-acetylgalactosaminidase was previously thought to have only a minor role in cortex hydrolysis during germination of *B. subtilis* (Atrih *et al.*, 1998). In *B. megaterium* KM, an extract from germinating spores contains primarily N-acetylgalactosaminidase activity and is able to cause germination-like changes in permeabilized spores of *B. subtilis* and *B. megaterium* (Atrih *et al.*, 1999). The increase in N-acetylgalactosaminidase activity may compensate for the absence of lytic transglycosylase, since both enzymes cleave glycan strands. Spore cortex is loosely cross-linked, links occurring at only 2.9% of muramic acid residues (Atrih *et al.*, 1996). This conserved spore peptidoglycan structural feature suggests that cleavage of relatively few bonds in the cortex may result in the mechanical constraint being removed (Atrih & Foster, 1999). The fact that N-acetylgalactosaminidase is only able to achieve partial hydrolysis of peptidoglycan suggests a co-operative action of the different GSLEs. It is possible that the glucosaminidase may have specific requirements and only cleaves at specific locations. The sleB gene was suggested to code an amidase by analogy to the gene in vegetative cells in response to σE induction may be artefactual, or may reflect further levels of regulation.
B. cereus (Moriyama et al., 1996a, 1999). However, our present result indicates that it is likely to be a lytic transglycosylase. Recent findings did not show an amidase activity in the form of amidase products during cortex hydrolysis of B. subtilis (Atrih et al., 1998).

The sleB gene is the first in the operon and its inactivation is likely to have an effect on the downstream gene, ypeB. Insertion inactivation of ypeB or in-frame deletion of sleB produced mutants with similar germination defects. This indicates that both genes are necessary for cortex hydrolysis during germination and therefore are essential for the activity of the lytic transglycosylase encoded by sleB. SleB has recently been shown to be located just inside the spore coat layer in the dormant spore and to exist in mature form but lacking a signal sequence (Moriyama et al., 1999). The enzyme is translocated across the forespore’s inner membrane by a secretion signal peptide and is deposited in cortex layer synthesized between the forespore inner and outer membrane (Moriyama et al., 1999).

The role of YpeB is still unclear. It appears to be required for either expression, localization, activation or function of SleB. The N-terminal region of YpeB could represent a hydrophobic anchor for the localization of the protein in the membrane or a signal peptide sequence involved in the translocation of the protein across the membrane. The ypeB gene has homologues in B. cereus and B. megaterium KM, all in the same operon organization, downstream of a sleB homologue. In B. cereus, the gene corresponding to ypeB encodes a protein that has 75% identity to YpeB from B. subtilis (Moriyama et al., 1996b) and the equivalent gene in B. megaterium KM encodes a protein having 65% identity (Pettigrew, 1996). These data suggest that ypeB may have the same role in B. cereus and B. megaterium as in B. subtilis.

There are two more homologues of SleB in B. subtilis, CwlJ and YkvT, which exhibit 28% and 30% identity, respectively, with the putative catalytic C-terminal domain of SleB. CwlJ, like SleB, is involved in the later stages of germination (Ishikawa et al., 1998), although its effects are less pronounced. The double mutant sleB cwlJ is blocked completely in later germination so that colony formation is not possible. Interestingly, the lack of cortex hydrolysis does not affect the loss of optical density or dipicolinic acid release, indicating that cortex hydrolysis and release of small solutes during germination are probably two separate events (Seigiuchi et al., 1995; Atrih et al., 1996, 1998; Popham et al., 1996b). However, unlike sleB, cwlJ and ykvT do not occur in an operon with a homologue of ypeB. The observation that the phenotype of the sleB or ypeB mutants are identical suggests that ypeB is not involved in the expression or the function of cwlJ. The genes sleB and cwlJ differ in their compartment-specific regulation during sporulation; cwlJ is transcribed by E$^R$ RNA polymerase in the mother cell (Ishikawa et al., 1998), and this work demonstrates that sleB expression is dependent on $\sigma^G$, a forespore-specific sigma factor. Expression of sleB has also recently been shown to be controlled by $\sigma^G$ using primer extension analysis (Moriyama et al., 1999).

The mechanism of SleB and CwlJ activation and their molecular interplay, as an integral part of the germination triggering response, is currently under investigation.

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