The *Bacillus subtilis* clpC operon encodes DNA repair and competence proteins

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ClpC of *Bacillus subtilis*, controlling competence gene expression and survival under stress conditions, is encoded by the fourth gene of a six-gene operon. The product of orf1 contains a potential helix-turn-helix motif, but shows no significant similarities with known protein sequences. The second and third genes encode proteins with similarities to zinc-finger proteins (orf2) and arginine kinases (orf3), respectively. The product of orf5 contains a zinc-finger motif and an ATP-binding domain, and is highly similar to the product of the *Escherichia coli* sms gene. A strain bearing a disruption of orf5 showed increased sensitivity to the alkylating agent methyl methanesulfonate. Furthermore, this mutant strain displayed decreased capacity for genetic recombination as measured by transformation experiments. The last open reading frame, orf6, encodes a protein with limited similarity in its C-terminal part to the *B. subtilis* comEA gene product and to the UvrC DNA repair excinuclease. Inactivation of orf5 resulted in strongly diminished transformation with all types of DNA. Mutations affecting either orf5 or orf6 resulted in strains with decreased resistance to UV-irradiation in the stationary phase, indicating that these proteins play a role in the development of a non-specific stationary-phase resistance to UV-irradiation. Moreover, these results suggest an involvement of both proteins in transformation and presumably in DNA repair.

**Keywords**: stress proteins, *Bacillus subtilis*, ClpC, DNA repair, competence

INTRODUCTION

For soil bacteria such as *Bacillus subtilis*, the ability to survive unfavourable environmental conditions is crucial. In order to respond to stressful situations or starvation, the cell has developed an adaptive network including stress responses and post-exponential-phase phenomena such as the development of genetic competence, motility, synthesis of degradative enzymes and finally sporulation. These processes are controlled by a complex and incompletely understood regulatory network accompanied by interactions and overlaps between the components (Msadek et al., 1995).

Genetic competence of *B. subtilis*, the ability to take up exogenous DNA molecules, is controlled by many regulatory genes, such as spo0A, comP, comA, degU, comS, mecA, clpC/mecB and comK. These genes are required for appropriate expression of the late competence genes, encoding DNA-binding and -uptake enzymes (Dubnau et al., 1994). Moreover, the SOS system is also part of the competence response, and is subject to a dual regulation: a damage-inducible pathway and a competence-dependent induction (Dubnau, 1991; Cheo et al., 1993).

Synthesis of bacterial stress proteins is induced by a wide variety of factors including heat shock, ethanol stress, pH and osmolarity changes, UV-irradiation, hydrogen peroxide, DNA-damaging agents and starvation (Bukau, 1993; Hecker et al., 1996). ClpC, a member of the stress-response-related Clp-ATPase family, is a pleiotropic regulator involved in stress tolerance and cell division (Krüger et al., 1994). The ClpC protein was also identified as MecB, controlling competence and synthesis of degradative enzymes (Msadek et al., 1994). Therefore, ClpC may provide links between the competence pathway and the stress response. Originally, the mecA and mecB mutations were isolated as allowing competence gene expression in complex media (Dubnau & Roggiani, 1990). Interaction of MecB with MecA

Abbreviation: MMS, methyl methanesulfonate.
negatively regulates the synthesis of ComK, a transcriptional activator required for the expression of late competence genes (Kong & Dubnau, 1994; Msadek et al., 1994). Expression of the clpC gene, encoding the general stress protein GSP12, was previously shown to be induced by various stress conditions (Krüger et al., 1994). The nucleotide sequence of a 180 kb region containing clpC was reported as part of the B. subtilis genome sequencing project, suggesting that clpC is the fourth gene of an operon containing six open reading frames (Ogasawara et al., 1994). We recently showed that the six genes are cotranscribed as an operon, preceded by two promoters. One resembles promoters that the six genes are cotranscribed as an operon,补偿ing for the a*-like promoter became inducible, completely the a*-like promoter became inducible, completely compensating for σB deficiency (Krüger et al., 1996). Even in the absence of σB this promoter switch ensures a similar rate of protein synthesis as in the wild-type. In addition, we found conditions which exclusively induce the vegetative σA promoter such as amino acid limitation or hydrogen peroxide (Krüger et al., 1996).

Two genes of the clpC operon, orf3 and orf5, were cloned previously and designated orfX and orfY (Msadek et al., 1994). Orf5 shares significant similarities with the Escherichia coli sms gene product (sensitivity to methyl methanesulfonate; Neuwald et al., 1992). Potential functions of the orf5 and orf6 gene products encoded by this operon were investigated in this study.

METHODS

Bacterial strains, plasmids and culture conditions. Bacterial strains are listed in Table 1. E. coli strains DH5α and RR1 were routinely grown in LB medium and used as hosts for DNA manipulation. B. subtilis was cultivated with vigorous aeration at 37°C in LB medium or a previously described synthetic medium (Stülke et al., 1993). Media were supplemented with the following antibiotics when necessary: ampicillin (100 µg ml⁻¹), chloramphenicol (5 µg ml⁻¹), spectinomycin (100 µg ml⁻¹) or erythromycin (1 µg ml⁻¹) plus lincomycin (25 µg ml⁻¹). The SPAC promoter (Pspac) (Yansura & Henner, 1984) was induced by treatment with 1 mM IPTG.

Sensitivity to methyl methanesulfonate (MMS) was tested according to Neuwald et al. (1992) by growing the cells in LB into the exponential growth phase and plating them in soft agar onto LB plates. A paper disc with 10 µl MMS was placed in the centre of the plate, giving a final concentration of 0.05% MMS. To investigate survival after UV-irradiation, appropriate dilutions of cells from the exponential phase, the transition phase or the stationary phase were plated onto LB agar and exposed to UV light for 10 s (8 W cm⁻², 312 nm, Vilbert Lourmat transilluminator) and incubated overnight at 37°C. The distance between the agar surface and the UV source was 1 cm.

General methods. Plasmid isolation, restriction enzyme analysis, transformation of E. coli, ligation of DNA fragments and filling in the recessed 3’ termini using the Klenow fragment of DNA polymerase I were performed according to standard protocols (Sambrook et al., 1989). Recombinant plasmids were sequenced by the dideoxy chain-termination method of Sanger et al. (1977). DNA fragments were amplified by PCR as described earlier (Krüger et al., 1994). Some oligonucleotides used for PCR included mismatches allowing creation of EcoRI and BamHI restriction sites. Chromosomal DNA from B. subtilis was isolated as described by Msadek et al. (1991). Transformation of B. subtilis with plasmid or chromosomal DNA was carried out using a two-step protocol (Hoch, 1991).

Construction of plasmids for generating orf5 and orf6 mutant strains. pMEC32 was constructed by deleting a 1826 bp HindIII fragment from pMCE28 (Msadek et al., 1994), removing the last 11 codons of orf3 and the first 497 codons of clpC. A 1238 bp Smal fragment carrying the spectinomycin resistance gene from Staphylococcus aureus (Murphy, 1985) was then cloned into the unique PsclI site within orf5 (codon 109) in plasmid pMEC32, to give pMEC39. Plasmid pMEC39 was linearized by EcoRI digestion and transformed into B. subtilis, selecting for spectinomycin resistance, indicating a double crossover event (strain BEK9). To exclude transformants carrying the mutation as a Campbell-type integration, spectinomycin-resistant transformants were tested for erythromycin sensitivity.

The orf5 disruption in strain BEK9 was verified by PCR using chromosomal DNA of the transformant as a template. Strain BEO1 was constructed by cloning the 531 bp Scal-BamHI orf5 fragment of pMEC28 into pDH88 (Henner, 1990) and transforming IS58 with the resulting plasmid pDSMS. In strain BEO1 orf5 is disrupted by a single crossover recombination event allowing reintroduction of transcription by Psac downstream of orf5.

pMEC60 was constructed by cloning a 200 bp BamHI PCR fragment internal to orf6 using oligonucleotides TM-116 (5’-GGAGGATCCGATGCCGGATGCCACAATTTC-3’) and TM-117 (5’-GGAGGATCCAGTGTTTGAATGGCTTGGTGTTTCCC-3’) into plasmid pHT181 (Lereclus & Arantes, 1993). When integrated by a Campbell-type event, this internal fragment gave rise to two truncated copies of orf6 (strain BEK60). All Campbell-type disruptions were verified by Southern-blot analysis using digoxigenin-labeled PCR fragments as probes according to the manufacturer’s recommendation (Boehringer Mannheim).

RESULTS

Predicted protein sequence analysis

The predicted amino acid sequences of the five other open reading frames cotranscribed with clpC (Fig. 1) were compared with the GenBank database using the BLAST (Altschul et al., 1990) network service at the National Center for Biotechnology Information, with the default parameter values provided. Only matches with a probability lower than e⁻⁷ were considered significant, except in cases noted below.

A chromosomal locus of the facultative pathogen Listeria monocytogenes was identified recently, displaying a genetic organization similar to that of the clpC locus in B. subtilis (Rouquette et al., 1996). Strong similarities were noted between Orf1, Orf2, Orf3, ClpC and Orf5 of B. subtilis and L. monocytogenes, with amino acid sequence identities of 64%, 29%, 30%, 73% and 70%, respectively (Rouquette et al., 1996).
Table 1. Strains and plasmids used in this study

<table>
<thead>
<tr>
<th>Strain/plasmid</th>
<th>Relevant genotype</th>
<th>Source/reference</th>
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<tbody>
<tr>
<td><strong>E. coli</strong></td>
<td></td>
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</tr>
<tr>
<td>RR1</td>
<td>F' mcrB mrr bsdS20 (r _m ) ara-14 proA2 lacY1 leu galK2 rpsL20 (Sm') xyl5 mtl-1 supE44</td>
<td>Bolivar et al. (1977)</td>
</tr>
<tr>
<td>DH5α</td>
<td>F' galU90 lacZ Y M15 Δ(lacZYA-argF)U169 deoR recA1 endA1 hsdR17 ( r _m ) supE44 thi-1 gyrA96</td>
<td>Hanahan (1985)</td>
</tr>
<tr>
<td><strong>B. subtilis</strong></td>
<td></td>
<td></td>
</tr>
<tr>
<td>IS58</td>
<td>trpC2 lys-3</td>
<td>Smith et al. (1980)</td>
</tr>
<tr>
<td>BE01</td>
<td>trpC2 lys-3 sms::pDH88</td>
<td>pDSMS → IS58</td>
</tr>
<tr>
<td>BEK9</td>
<td>trpC2 lys-3 sms::spc</td>
<td>pMEC39 → IS58</td>
</tr>
<tr>
<td>BEK56</td>
<td>trpC2 lys-3 amyE::(orf1-′lacZ aphA3)</td>
<td>Krüger et al. (1996)</td>
</tr>
<tr>
<td>BEK60</td>
<td>trpC2 lys-3 orf6::pHT181</td>
<td>pMEC60 → IS58</td>
</tr>
<tr>
<td><strong>Plasmids</strong></td>
<td></td>
<td></td>
</tr>
<tr>
<td>pAC7</td>
<td>Ap' Km' lacZ</td>
<td>Krüger et al. (1996)</td>
</tr>
<tr>
<td>pDH88</td>
<td>Ap' Cm' Pspac</td>
<td>Henner (1990)</td>
</tr>
<tr>
<td>pHT181</td>
<td>Ap' Em'</td>
<td>Lereclus &amp; Arantes (1993)</td>
</tr>
<tr>
<td>pHWH331</td>
<td>Neo' Cm'</td>
<td>Gartner et al. (1988)</td>
</tr>
<tr>
<td>pSPEC</td>
<td>Ap' Spc'</td>
<td>P. Trieu-Cuot, unpublished</td>
</tr>
<tr>
<td>pDSMS</td>
<td>pDH88 derivative with a 531 bp fragment of orf5</td>
<td>This work</td>
</tr>
<tr>
<td>pMEC28</td>
<td>Ap' Em' E. coli/B. subtilis shuttle vector containing part of orf3, clpC and part of orf5</td>
<td>This work</td>
</tr>
<tr>
<td>pMEC32</td>
<td>pMEC28 derivative constructed by deleting a 1826 bp HindIII fragment</td>
<td>This work</td>
</tr>
<tr>
<td>pMEC39</td>
<td>pMEC32 derivative carrying the spectinomycin resistance gene in the unique PstI site</td>
<td>This work</td>
</tr>
<tr>
<td>pMEC60</td>
<td>pHHT181 derivative containing a 200 bp BamHI PCR fragment internal to orf6</td>
<td>This work</td>
</tr>
</tbody>
</table>

However, an equivalent of orf6 of *B. subtilis* is not present in the reported *L. monocytogenes* nucleotide sequence (GenBank accession number U40604), where instead orf5 is followed by an open reading frame whose product shows similarities with that of a gene lying downstream from orf6 in *B. subtilis*. Except for ClpC, no functional role has been established for the products of orf1, 2, 3 and 5 in *L. monocytogenes* (Rouquette et al., 1996).

The product of orf1 (154 aa) of the *B. subtilis* clpC operon displays no significant similarities to proteins in the database. However, a predicted helix-turn-helix DNA-binding motif was detected in Orf1 using the weight matrix of Dodd & Egan (1990), beginning at amino acid 29 (RSEIDKFGVCPSQNYVIN, SD score 4.12, HTH1 probability > 90%). This suggests that Orf1 may have a regulatory role. Interestingly, this potential helix-turn-helix domain is highly conserved in the orf1 product of *L. monocytogenes*.

Similarities between Orf2 (185 aa) of *B. subtilis* and proteins in the database were noted with a large family of eukaryotic regulatory proteins, characterized by a zinc-finger nucleic-acid-binding domain (Klug & Rhodes, 1987; Vallee et al., 1991). Indeed, Orf2 contains two potential Cys3-Cys5 zinc-finger motifs, at positions C3_5-C3_2 and C3_8-C3_4 to C3_9-C102. orf3 encodes a putative protein (363 aa) with a domain that is highly conserved among ATP:guanidino phosphotransferases such as arginine kinases (e.g. *Homarus vulgaris*; Dumas & Camonis, 1993) or creatine kinases (e.g. *Schistosoma mansoni*; Stein et al., 1990). This domain extends from amino acids 119 to 251 of Orf3, presenting 35% sequence identity on average with members of this family of kinases.

As previously reported (Msadek et al., 1994; Ogasawara et al., 1994), the deduced amino acid sequence of orf5 (458 aa) shows 46% identity with that of the *E. coli* sms gene, whose absence confers sensitivity to MMS.
(Neuwald et al., 1992) (Fig. 2). The orf5 and sms gene products both contain conserved ATP-binding A and B motifs (Walker et al., 1982) as well as a potential zinc-finger nucleic-acid-binding domain (positions C10-C13 to C24-C27, Fig. 2). The sms gene appears to be highly conserved among prokaryotes and is also present in Salmonella typhimurium, Haemophilus influenzae and Synechocystis sp. Sms proteins also show similarities with RecA, in the vicinity of the ATP-binding site, and the carboxy-terminal region shows similarities with Lon proteases (Neuwald et al., 1992).

Although the potential orf6 gene product (360 aa, formerly orf360; Ogasawara et al., 1994) shows no strong sequence similarities with proteins in the database, we noted some slight similarities with several proteins that interact with nucleic acids, such as DNA ligase of Thermus thermophilus and ATP-dependent RNA helicase of Methanococcus jannaschii. Indeed, a short carboxy-terminal region of Orf6 (amino acids 300-358) shows approximately 30% sequence identity with a corresponding stretch in these proteins as well as the E. coli UvrC DNA repair excinuclease (Sancar et al., 1984) and ComEA of B. subtilis (Inamine & Dubnau, 1995).

Hydropathy profiles of the products of the six genes in the clpC operon, determined by the method of Kyte & Doolittle (1982), suggested that these proteins are all cytoplasmic since no significantly hydrophobic potential transmembrane regions were noted (cutoff value: 2.6).

### The sms phenotype of an orf5 mutant

As indicated above, the deduced product of the fifth open reading frame shows about 50% amino acid sequence identity with the E. coli sms gene product. The orf5 gene was disrupted, generating mutant BEK9.

To examine the possibility that orf5 is indeed an sms homologue in B. subtilis, sensitivity to the alkylating agent MMS was tested using a paper disc method as described by Neuwald et al. (1990). Several independent experiments were performed by plating exponentially growing cultures of the BEK9 (orf5) and BEK60 (orf6) mutants in parallel with the corresponding wild-type strain IS58 on agar plates with a paper disc containing MMS (see Methods). Diameters of clear inhibition zones were measured. For a given strain, the diameters varied by less than ±2 mm. Treatment with MMS (0.05%) resulted in average inhibition zones that were reproducibly larger in diameter for the mutant strain BEK9 (46 mm) than for the wild-type strain (40 mm), which is comparable to results obtained with the E. coli sms mutant. Strain BEK60 gave results nearly identical to the wild-type. These results suggest that a mutation in orf5 leads to increased sensitivity of the mutant cells to...
MMS, as described for E. coli. We therefore propose that orf5 be designated sns.

Survival of orf5 and orf6 mutants after UV-irradiation

Stationary-phase cells of E. coli are more resistant to UV-irradiation than exponentially growing cells, in a σ8-dependent manner (for a review see Hennge-Aronis, 1993). Functional similarities between the σ8 regulon in E. coli and the σB regulon in B. subtilis have been described for the katE gene (Engelmann et al., 1995; Engelmann & Hecker, 1996). Furthermore, the clpC operon is partly σB-dependent.

To investigate the UV survival response of mutants affected in the clpC operon, we first examined the survival of B. subtilis wild-type IS58 cells following exposure to UV-irradiation at different growth phases in glucose limitation medium (GLM) and under amino acid limitation (competence medium; CM). Samples were taken during exponential growth at an OD500 of 0.4, in the transition phase (OD500 0.8 for GLM; OD500 1.0 for CM) or 1 h after entry into stationary phase (OD500 1.0 for GLM; OD500 1.3 for CM). Only amino-acid-starved cells showed an approximately fivefold increased resistance to UV-irradiation; glucose-starved cells showed no increase in resistance (data not shown). Therefore, competence medium was used for further experiments.

Since Orf5 and Orf6 have similarities with DNA-repair enzymes, we investigated mutants in both genes for survival after UV-irradiation. To avoid polar effects of the insertional mutation within orf5 another mutant was constructed using plasmid pDSMS, allowing re-initiation of transcription by Pspac. This mutant, BE01, also shows the sns phenotype. In all experiments IPTG was added to the culture of strain BE01 to a final concentration of 1 mM. Several independent UV-irradiation experiments were performed, resulting in approximately 1% survival for the wild-type during the exponential growth phase. However, the number of viable wild-type cells increased to 7% and 5% during the transition and stationary phases, respectively. Setting survival of the wild-type to 100%, only 15–20% of the mutants BE01 and BEK60 cells survived this procedure in transition and stationary phase, whereas in the exponential growth phase the sensitivity of the mutants was less pronounced (Table 2). These results suggest the involvement of Orf5 as well as Orf6 in the development of a non-specific stationary-phase resistance to UV-irradiation of amino-acid-starved B. subtilis cells. Results obtained with the orf5 mutant BEK9 after UV-irradiation were similar to those with the BE01 mutant, indicating that polar effects do not play a role (data not shown).

Orf5 and Orf6 are involved in genetic competence

We had previously noted that a clpC deletion mutant showed a decrease in transformability compared to a mutant with a point mutation in clpC (T. Msadek, unpublished). Given the slight similarities of the carboxy-terminal domain of Orf6 with ComEA, which is essential for competence development in B. subtilis, we investigated the possible role of Orf6 in competence. Since the SOS response and the development of genetic competence overlap (Cheo et al., 1993), it was interesting to test whether competence is also influenced in an orf5 mutant. Transformation experiments were carried out by preparing competent cells of strains BE01, BEK60 and the corresponding wild-type strain IS58 in parallel. Cells were transformed with the replicative plasmid pWH331 (Gärtnert et al., 1988), with pAC7, a plasmid which cannot replicate in B. subtilis but integrates via a single crossover event in the amyE locus, or with chromosomal DNA of strain BEK56 requiring a double crossover event (Krüger et al., 1996), with selection for the corresponding antibiotic resistance. Transformation

**Table 2. Survival after UV-irradiation of B. subtilis wild-type strain in comparison to orf5 and orf6 mutants in different growth phases in competence medium**

<table>
<thead>
<tr>
<th>Growth phase</th>
<th>Wild-type IS58</th>
<th>orf5 mutant BE01†</th>
<th>orf6 mutant BEK60</th>
</tr>
</thead>
<tbody>
<tr>
<td>Exponential (OD500 0-4)</td>
<td>1.3 × 10⁴</td>
<td>0.9 × 10⁴ [69.2%]</td>
<td>1.1 × 10⁴ [84.6%]</td>
</tr>
<tr>
<td>Transition (OD500 1.0)</td>
<td>(±0.32 × 10⁴)</td>
<td>(±0.28 × 10⁴)</td>
<td>(±0.31 × 10⁴)</td>
</tr>
<tr>
<td>Stationary (OD500 1.3)</td>
<td>7.1 × 10²</td>
<td>1.04 × 10² [14.6%]</td>
<td>1.25 × 10² [17.6%]</td>
</tr>
<tr>
<td></td>
<td>(±1.0 × 10²)</td>
<td>(±0.5 × 10²)</td>
<td>(±0.6 × 10²)</td>
</tr>
</tbody>
</table>

*Survival after UV-irradiation is indicated as the ratio of colony-forming units with and without UV treatment. Means of five independent experiments are shown, with standard deviations indicated in parentheses. For the orf5 and orf6 mutants, percentage survival in comparison to the wild-type is shown in square brackets.

† Cells of strain BE01 were cultivated with the addition of 1 mM IPTG to induce Pspac.
Table 3. Transformability of orf5 and orf6 mutants in comparison to the wild-type

<table>
<thead>
<tr>
<th>DNA type</th>
<th>Frequency of transformation (%)*</th>
</tr>
</thead>
<tbody>
<tr>
<td></td>
<td>Wild-type IS58</td>
</tr>
<tr>
<td>Replicating plasmid (pWH331)</td>
<td>0.81</td>
</tr>
<tr>
<td>Non-replicating plasmid (pAC7)</td>
<td>0.12</td>
</tr>
<tr>
<td>single crossover</td>
<td></td>
</tr>
<tr>
<td>Chromosomal (BEK56)</td>
<td>0.18</td>
</tr>
</tbody>
</table>

*Frequency of transformation is indicated as (kanamycin-resistant transformants/viable cells) x 100. The means of four independent experiments are shown; standard deviations were less than 10% of the mean. The numbers in parentheses indicate x-fold decrease of transformation frequency of the mutant strains in comparison to the wild-type.

† Cells of strain BEO1 were cultivated with the addition of 1 mM IPTG to induce Pspac.

experiments are summarized in Table 3. Transformation with a replicating plasmid was not strongly influenced in the sms mutant BEO1 in comparison to the wild-type. However, transformation rates dropped significantly with chromosomal DNA, requiring recombination events. The orf6 disruption led to a strong decrease of competence in every case, indicating that orf6 might be a novel competence gene. We therefore suggest that orf6 be renamed comY.

DISCUSSION

To study the functions of the other five unknown gene products encoded by the clpC operon, database analysis was performed and phenotypes of selected mutants were investigated. The high probability of a helix-turn-helix motif within the amino acid sequence of Orf1 suggests a possible regulatory role for this protein. Preliminary results of our group indeed show that Orf1 may act as a repressor of the clpC operon expression under non-stressed conditions (E. Krüger & M. Hecker, unpublished).

For the fifth gene, orf5, whose product is similar to that of the E. coli sms gene (Neuwald et al., 1992), similar phenotypes were observed for the mutant, leading to mild sensitivity to the alkylating agent MMS during exponential growth phase. Hence, the gene product may participate in repair of DNA damage by alkylation or DNA repair in general. This assumption is underlined by the increased sensitivity of sms (orf5) mutants to UV-irradiation. The increased sensitivity was also observed for mutants in orf6, suggesting that Orf6, which shows some weak similarities to nucleases, is also involved in DNA repair. Recently, we found that a σB, and a presumably σA-dependent promoter direct stress-induced transcription of the clpC operon. Expression from the σA-like promoter alone could be induced in response to stress conditions that do not induce σB, such as hydrogen peroxide treatment or amino acid starvation (Krüger et al., 1996). Increased stationary-phase resistance to UV-irradiation was shown for amino-acid-starved but not for glucose-starved cells, indicating that this phenomenon is mediated by a σB-independent mechanism. Our results suggest that Sms (Orf5) as well as ComY (Orf6) are involved in this mechanism, emphasizing an important function for σA-dependent induction of the clpC operon. However, the function of both Sms (Orf5) and ComY (Orf6) might only be important for the development of a non-specific stationary-phase resistance to UV-irradiation in addition to the constitutive excision and recombination repair systems involving the recA and the uvrA loci (Friedman & Yashin, 1983).

Disruption of the sixth open reading frame, orf6, resulted in a significant decrease in competence for DNA transformation. Although there is no indication of the membrane association of Orf6, according to the hydrophathy calculation method of Kyte & Doolittle (1982), one cannot exclude a role for this protein in DNA uptake, as observed for mutants in the comEA locus (Albano et al., 1987; Hahn et al., 1993; Inamine & Dubnau, 1995). An sms (orf5) mutation led to decreased transformability with DNA requiring homologous recombination. In view of the results discussed above and the inducibility of the clpC operon by DNA-damage-inducing treatment with hydrogen peroxide (Krüger et al., 1996), an involvement of the sms and comY (orf5 and orf6) gene products in either DNA-damage repair or competence, or both, could explain the phenotypes of these mutants. The link between the two mechanisms is an apparent overlap in the regulatory mode of the competence-dependent induction of the SOS system and the regulation of the competence regulon itself (Cheo et al., 1993). However, previous data suggest that mutations in the regulatory genes of the competence pathway do not significantly affect vegetative-phase expression of a clpC–lacZ fusion (Msadek et al., 1994). Furthermore, the consensus sequence found upstream of clpC operon by DNA-damage-inducible genes (GAAC-N₄-GTTC; Cheo et al., 1993) is not present in the clpC operon. This suggests that DNA-damage induction of the clpC operon may involve a different mechanism from that of the din regulon. Protection of DNA or proteins against stress damage is essential for bacteria to keep existing cellular structures in a functional state. B. subtilis has developed efficient systems for detoxification and repair of DNA.
under stress conditions. Interestingly, these include $\sigma^B$-dependent and $\sigma^W$-independent general stress proteins. The H$_2$O$_2$-inducible genes katA and mrgA, the din genes, the alkyl hydroperoxide reductase operon ahpC/ahpF and the superoxide dismutase gene sod encode enzymes responsible for a specific oxidative stress resistance (Antelmann et al., 1996; Bol & Yasbin, 1994; Cheo et al., 1993; Chen et al., 1995). However, genes of the $\sigma^W$ regulon of B. subtilis seem to encode proteins that provide a non-specific protection of the cell against oxidative stress during starvation (Engelmann & Hecker, 1996). Our results suggest that Sms and ComY (Orf5 and Orf6) might belong to such non-specific systems. In this context, an overlap between the $\sigma^W$-dependent and $\sigma^B$-independent general stress responses, the SOS response and competence for DNA transformation seems plausible.

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Functional analysis of the B. subtilis clpC operon


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