## The Major Role of Spo0A in Genetic Competence Is To Downregulate *abrB*, an Essential Competence Gene

JEANETTE HAHN,<sup>1</sup> MANUELA ROGGIANI,<sup>2</sup> AND DAVID DUBNAU<sup>1\*</sup>

Public Health Research Institute, New York, New York 10016,<sup>1</sup> and Department of Microbiology, University of Minnesota Medical School, Minneapolis, Minnesota 55455<sup>2</sup>

Received 20 December 1994/Accepted 7 April 1995

We show that the major role for Spo0A in the development of genetic competence is to downregulate expression of *abrB*. AbrB is both a negative regulator and a positive regulator of competence. The negative effects are exerted at multiple points in competence regulation. A regulatory mechanism that is independent of *mecA* and *abrB* operates on *comK* expression.

Genetic competence in *Bacillus subtilis* develops in response to a complex regulatory network (6, 13, 18, 33) that culminates in synthesis of the transcription factor ComK (13, 32, 33). One gene that is involved in this network specifies the transcriptionally active protein AbrB (31), which acts positively for expression of ComK (2, 13, 33). In other forms of postexponential expression, such as sporulation, AbrB acts as a transcriptional repressor that must be downregulated during the transition from exponential phase to stationary phase (22, 26, 36). This downregulation requires activation of Spo0A by phosphorylation, resulting in repression of *abrB* transcription (4, 9, 30). Therefore, AbrB accumulates in *spo0A* mutants, and certain phenotypes that result from inactivation of *spo0A* can be suppressed by loss-of-function mutations in *abrB* (8, 22, 31, 36).

Null mutants of *spo0A* are poorly transformable (2, 28), and this effect is partially reversed by inactivation of *abrB* (2). This implies that AbrB plays both negative and positive roles in the development of competence and that its concentration must be closely adjusted for optimal expression of competence. Since a *spo0A abrB* double mutant exhibits the same reduced level of competence as an *abrB* mutant (2), we propose that the major role for Spo0A in competence is to limit the intracellular level of AbrB.

Perego et al. (25) have reported that the *spo0A9V* mutation disables Spo0A as a transcriptional activator without destroying its ability to downregulate *abrB*. If the major role of Spo0A in competence is to control *abrB*, *spo0A9V* should have no effect on transformability. In fact, a *spo0C* mutation, probably identical to *spo0A9V*, had a minimal effect on genetic competence (28). We have moved *spo0A9V* into BD630, yielding the Spo<sup>-</sup> strain BD1981. The level and time course of competence development in this strain were similar to those in the wild-type strain (data not shown), in support of the model that Spo0A acts in competence development as a negative regulator of *abrB*. This hypothesis was tested further in this study.

The strains used are listed in Table 1. The growth of competent cultures, transformation, preparation of selective media, and measurement of  $\beta$ -galactosidase specific activity were performed as previously described (1–3). Isopropyl- $\beta$ -D-thiogalactopyranoside (IPTG; at specified concentrations) or 5-bromo-4-chloro-3-indolyl- $\beta$ -D-galactopyranoside (X-Gal; 40  $\mu$ g/ml) was added as required.

Competence in a Pspac-abrB strain. To examine the roles of Spo0A and AbrB in competence, we placed *abrB* at the *amyE* locus under control of the IPTG-regulatable Pspac promoter (35) by using plasmid pDR66 (15). pDR66 contains the lacI gene, cat, pBR322 ori, and the Pspac promoter, followed by a multiple cloning site, as well as flanking segments of *amyE*. A 434-bp fragment that contained only the coding sequence of abrB was ligated between the XbaI and SphI sites of pDR66. The fragment was isolated from B. subtilis DNA by PCR, with primers 5'-GCTCTAGAGGATTTTGTCGAATAATG and 5'-ACATGCATGCAGTGTACGATGCTTACC, in which the underlined residues constitute XbaI and SphI sites, respectively. The ligation products were used to transform BD630 with selection for *cat*, and an AmyE<sup>-</sup> transformant was shown to contain abrB under Pspac control (see below). The cat marker of this construct was converted to spectinomycin resistance by transformation with DNA (21). Then the normal *abrB* gene in this strain was inactivated by introduction of  $\Delta abrB::kan$  or  $\Delta abrB::cat$  mutations.

When *Pspac-abrB* strains were streaked on sporulation agar, an oligosporogenic phenotype was apparent in the presence of IPTG (1 mM), but not in its absence (data not shown). Transcription of *spoVG* is repressed by AbrB (36). To test the *Pspac-abrB* construct, it was introduced into a *spoVG-lacZ* strain. As expected, growth of this strain in 1 mM IPTG resulted in nearly complete repression of  $\beta$ -galactosidase activity. In the absence of IPTG (data not shown), *spoVG-lacZ* expression increased sharply at the transition to stationary phase ( $T_0$ ).

BD2238 [*Pspac-abrB*(*spc*)  $\Delta abrB::cat$ ] was grown to competence in the presence of various concentrations of IPTG, and transformability was measured (Fig. 1). Growth was unaffected by IPTG. Full expression of competence was IPTG dependent in this strain, with a maximum at 0.025 mM IPTG, confirming that AbrB plays both positive and negative roles. The unnormalized transformation frequency in the presence of 0.025 mM IPTG was no different from that obtained with the wild-type (*abrB*<sup>+</sup>) strain. The culture was more transformable in the absence of IPTG than in the presence of 1 to 2 mM IPTG, principally because of the leakiness of the *Pspac* promoter. These results were confirmed with a *comG-lacZ* reporter by monitoring β-galactosidase activity (data not shown). Again, the optimum level of β-galactosidase expression was achieved at 0.025 mM IPTG.

**Bypass of** *spo0A* **in a** *Pspac-abrB* **background.** We tested the bypass of a *spo0A* null mutation by using the *Pspac-abrB* con-

<sup>\*</sup> Corresponding author. Mailing address: Public Health Research Institute, 455 First Ave., New York, NY 10016. Phone: (212) 578-0842. Fax: (212) 578-0804. Electronic mail address: dubnau@phri.nyu.edu.

TABLE	1.	Strains	used	in	this study	/
-------	----	---------	------	----	------------	---

Strain	Characters	Source or reference(s)	
IS8	trpC2 spo0A9V	25	
TT31	$\Delta abrB$ : kan	T. Tanaka	
BD630	hisA1 leuA8 metB5	This study	
BD1197	hisA1 leuA8 spo $0A\Delta 204$	2, 8	
BD1865	hisA1 leuA8 spo $0A\Delta 204 \Delta abrB::kan$	This study	
BD1866	hisA1 leuA8 metB5 $\Delta$ abrB::kan	This study	
BD1959	hisA1 leuA8 metB5 comG-lacZ(kan) <sup>a</sup>	This study	
BD1981	hisA1 leuA8 spo0A9V	25	
BD2180	hisA1 leuA8 metB5 comK-lacZ(spc) <sup>a</sup>	This study	
BD2188	hisA1 leuA8 metB5 $\Delta$ abrB::kan Pspac-abrB(cat) sinR::phl	10	
BD2189	hisA1 leuA8 metB5 Pspac-abrB(cat) $\Delta degSU::kan$	20	
BD2190	hisA1 leuA8 metB5 ΔabrB::kan Pspac-abrB(cat) srfA(Tn917)	16	
BD2192	hisA1 leuA8 metB5 Pspac-abrB(cat) spoVG-lacZ(kan)	37	
BD2238	hisA1 leuA8 metB5 $\Delta abrB$ ::cat Pspac-abrB(spc)	24	
BD2239	hisA1 metB5 \Delta brB::cat Pspac-abrB(spc) sp00A12	This study	
BD2245	hisA1 leuA8 metB5 $\Delta abrB$ :cat comK-lacZ(spc) <sup>a</sup>	This study	
BD2249	hisA1 leuA8 metB5 $\Delta$ abrB::cat Pspac-abrB(spc) $\Delta$ mecA::erm comG12-lacZ(kan) <sup>b</sup>	This study	
BD2261	hisA1 leuA8 metB5 $\Delta$ abrB::cat Pspac-abrB(spc) comG12-lacZ(kan) <sup>b</sup>	This study	
BD2312	hisA1 metB5 spo0A12 $\Delta$ abrB::cat Pspac-abrB(spc) comG12-lacZ(kan) <sup>b</sup>	This study	
BD2313	hisA1 metB5 spo0A12 $\Delta$ abrB::cat Pspac-abrB(spc) $\Delta$ mecA::erm comG12-lacZ(kan) <sup>b</sup>	This study	
BD2374	hisA1 leuA8 metB5 $\Delta$ abrB::cat comG12-lacZ(kan) <sup>b</sup>	This study	
BD2375	hisA1 leuA8 metB5 $\Delta$ mecA::erm comG12-lacZ(kan) <sup>b</sup>	This study	
BD2376	hisA1 leuA8 metB5 $\Delta$ abrB::cat $\Delta$ mecA::erm comG-lacZ(kan) <sup>a</sup>	This study	
BD2377	hisA1 leuA8 metB5 $\Delta$ mecA::erm comK-lacZ(spc) <sup>a</sup>	This study	
BD2378	hisA1 leuA8 metB5 $\Delta$ mecA::erm $\Delta$ abrB::cat comK-lacZ(spc) <sup>a</sup>	This study	

<sup>a</sup> These comG-lacZ (18) and comK-lacZ (13) constructs were translational (in-frame) fusions to lacZ which were integrated at the amyE locus. The original constructs carried cat cassettes, which were replaced by replacement recombination with kan or spc determinants.

<sup>b</sup> The comG12-lacZ construct (17) was a Tn917lacZ derivative which was integrated by Campbell-like recombination to place a transcriptional lacZ fusion upstream from an intact copy of comG.

struct. However, Spo0A represses transcription of *abrB* by binding to sites (Spo0A boxes) downstream from the *abrB* promoter (30). Since these sites are present in the *Pspac-abrB* construct, the presence or absence of Spo0A might still affect synthesis of AbrB. For unknown reasons, attempts to construct *Pspac-abrB* without the Spo0A boxes were unsuccessful. Nevertheless, complete bypass of *spo0A* by *Pspac-abrB* is shown by the fact that in the presence of 0.025 mM IPTG, the level of *comG-lacZ* expression with or without a *spo0A* null mutation



FIG. 1. Transformation of a  $Pspac-abrB(spc) \Delta abrB::cat$  strain (BD2238) grown in competence medium in the presence of the indicated concentrations of IPTG. Relative transformation frequencies are expressed as ratios to the frequencies obtained with cultures grown without IPTG.

was essentially that of the  $abrB^+$   $spo0A^+$  strain (Fig. 2A). However, in the spo0A mutant strain, the basal level of comG-lacZ expression was elevated compared with the basal level in the  $spo0A^+$  strain. This difference reflects the role of the Spo0A boxes and the leakiness of *Pspac*. It is clear that the positive requirement for AbrB in competence can be fulfilled by a low (basal) level of this protein. When 2 mM IPTG was used (Fig. 2B), comG-lacZ expression decreased dramatically, showing that repression by excess AbrB required a relatively large amount of AbrB.

Is the only role of Sp00A in competence to control *abrB*? Although our data strongly support this conclusion, Sp00A may be involved in regulatory mechanisms which operate under other conditions or in other genetic backgrounds. Overexpression of AbrB acts at several points in the regulatory cascade. It inhibits downstream from *mecA* (27), probably by directly binding to the *comK* promoter and thus inhibiting transcription of the latter gene (17). Overexpression of AbrB (in a *sp00A* mutant) partially inhibits induction of *srfA* at  $T_{-1}$ (12, 16) and can repress transcription of *sp00H*, an essential competence gene (34, 36, 37).

The use of both positive and negative controls is typical of global regulation (29). Redundancy may ensure that only appropriate responses are triggered and may permit integration of multiple signals. The positive and negative roles of AbrB and its regulation by Spo0A may permit cells to respond to environmental conditions that are appropriate for several postexponential responses (e.g., sporulation and competence), as well as to conditions that demand a choice among these various responses. A graded series of responses may be elicited as the concentration of AbrB in a cell decreases in response to the flow of phosphate to Spo0A. When the level of AbrB is elevated (as it is in exponential growth), both competence and



FIG. 2. Bypass of *spo0A* $\Delta 204$  by growth of *Pspac-abrB* strains in the presence of 0.025 (A) and 2 (B) mM IPTG, as shown by expression of  $\beta$ -galactosidase from a *comG-lacZ* fusion. Dashed lines, results obtained in the absence of IPTG; solid lines, results obtained in its presence. The strains used were *Pspac-abrB(spc)*  $\Delta abrB::cat$  *comG-lacZ(kan)* (BD2261) ( $\bigcirc$ ) and *Pspac-abrB(spc)*  $\Delta abrB::cat$  *comG-lacZ(kan)* spo0A $\Delta 204$  (BD2312) ( $\bullet$ ). Data for the *Pspac-abrB(spc)*  $\Delta abrB::cat$  *comG-lacZ(kan)* strain in panel B are buried beneath the solid dots.

sporulation are suppressed. As AbrB decreases to an intermediate level, competence is enabled but sporulation remains inhibited. As the concentration of AbrB drops even further, sporulation begins. Thus, a common set of signal transduction molecules can determine even mutually exclusive responses.

**Pspac-abrB** does not bypass srfA, degU, or sinR. degU, sinR, and a small open reading frame embedded in the srfA operon (5, 14) are required for expression of ComK. It is conceivable that one or more of these genes function on an unknown pathway prior to the action of AbrB. Therefore, we tested the ability of the *Pspac-abrB* construct to suppress null mutations in degU, sinR, and srfA. The transformabilities of appropriate mutant strains (Table 1) were monitored during growth in the presence and absence of IPTG. IPTG did not induce any increase in the level of transformation above background in any of these strains (data not shown), indicating no bypass of these inactivating mutations by AbrB synthesis.

Bypass of Spo0A deficiency and AbrB deficiency in a *PspacabrB*  $\Delta$ *mecA*::*erm* background. Loss-of-function mutations in *mecA* exhibit two distinct phenotypes (7, 19, 23, 27). They express competence regardless of the growth medium, and they bypass the effects of null mutations in many regulatory genes, including *abrB*, on competence. Therefore, the positive effect of AbrB is exerted prior to the action of MecA. In

contrast, since competence loss as a result of spo0A deficiency is not suppressed by mecA mutations, the negative effect of AbrB is exerted after or independently of MecA action. If mecA and spo0A null mutations were present in a Pspac-abrB background, we would expect mecA to bypass the positive effect of AbrB and the Pspac-abrB construct to permit control of abrB, suppressing the effect of Spo0A deficiency on competence. Indeed, in a Pspac-abrB  $\Delta mecA$ ::erm spo $0A^+$  background, comG-lacZ expression was similar to that of the  $abrB^+$ strain in the absence and presence of 0.025 mM IPTG (Fig. 3A). When spo0A was also inactivated, comG-lacZ expression was not markedly affected, since the Pspac-abrB construct controlled accumulation of the AbrB product. In both  $spo0A^+$  and spo0A backgrounds, the addition of 2 mM IPTG resulted in marked inhibition of comG-lacZ expression (Fig. 3B), demonstrating that the ability of AbrB to inhibit expression was unaltered.

**Redundancy in** *comK* regulation. MecA- and AbrB-dependent pathways converge to control the synthesis of ComK (13, 33). In the absence of MecA and with only a low basal level of AbrB, the expression of *comG-lacZ* still showed growth stage regulation (Fig. 3) (27). Thus, a third mechanism is capable of regulating *comG* expression.

To determine whether this mechanism affects comK, the ex-



FIG. 3. Expression of comG-lacZ in  $\Delta mecA::erm$  Pspac-abrB strains in the presence of 0.025 (A) and 2 (B) mM IPTG. Dashed lines, results obtained in the absence of IPTG; solid lines, results obtained in its presence. The strains used were Pspac-abrB(spc)  $\Delta abrB::cat \Delta mecA::erm comG-lacZ(kan)$  (BD2249) ( $\bigcirc$ ) and Pspac-abrB(spc)  $\Delta abrB::cat \Delta mecA::erm sp00A\Delta 204 comG-lacZ(kan)$  (BD2313) (O).



FIG. 4. Expression of comG-lacZ (A) and comK-lacZ (B) in  $\Delta mecA$ ::erm  $\Delta abrB$ ::cat strains. The strains used were comG-lacZ(kan) (BD1959) or comK-lacZ(spc) (BD2180) ( $\bullet$ ), comG-lacZ(kan)  $\Delta abrB$ ::cat (BD2374) or comK-lacZ(spc)  $\Delta abrB$ ::cat (BD2245) ( $\odot$ ), comG-lacZ(kan)  $\Delta mecA$ ::erm (BD2376) or comK-lacZ(spc)  $\Delta mecA$ ::erm (BD2377) ( $\triangle$ ), and comG-lacZ(kan)  $\Delta abrB$ ::cat  $\Delta mecA$ ::erm (BD2376) or comK-lacZ(spc)  $\Delta abrB$ ::cat  $\Delta mecA$ ::erm (BD2377) ( $\triangle$ ), and comG-lacZ(kan)  $\Delta abrB$ ::cat  $\Delta mecA$ ::erm (BD2376) or comK-lacZ(spc)  $\Delta abrB$ ::cat  $\Delta mecA$ ::erm (BD2377) ( $\triangle$ ), and comG-lacZ(kan)  $\Delta abrB$ ::cat  $\Delta mecA$ ::erm (BD2376) or comK-lacZ(spc)  $\Delta abrB$ ::cat  $\Delta mecA$ ::erm (BD2377) ( $\triangle$ ).

pression of *comG-lacZ* and *comK-lacZ* in  $\Delta abrB::cat \Delta mecA:: spc$  strains was analyzed (Fig. 4). Although higher levels of both fusions were expressed in the *mecA* background, the synthesis of  $\beta$ -galactosidase was still growth stage regulated. Therefore, the additional regulatory mechanism does not require MecA or AbrB and affects the level of *comK* expression. The gene(s) mediating this mechanism is unknown.

Why is ComK synthesis controlled by redundant mechanisms? When ComK is overexpressed, nucleoid separation is impaired (11) and colony-forming ability decreases. Therefore, redundant control mechanisms may prevent inappropriate, catastrophic expression of *comK*.

We thank Arturo Londoño, Yvette Weinrauch, I. Smith, and J. Dubnau for useful discussions. We also thank D. Henner, T. Tanaka, and the Bacillus Genetic Stock Center for providing strains.

This work was supported by Public Health Service grant AI10311.

## REFERENCES

- Albano, M., R. Breitling, and D. A. Dubnau. 1989. Nucleotide sequence and genetic organization of the *Bacillus subtilis comG* operon. J. Bacteriol. 171: 5386–5404.
- Albano, M., J. Hahn, and D. Dubnau. 1987. Expression of competence genes in *Bacillus subtilis*. J. Bacteriol. 169:3110–3117.
- Anagnostopoulos, C., and J. Spizizen. 1961. Requirements for transformation in *Bacillus subtilis*. J. Bacteriol. 81:741–746.
- Burbulys, D., K. A. Trach, and J. A. Hoch. 1991. Initiation of sporulation in B. subtilis is controlled by a multicomponent phosphorelay. Cell 64:545– 552.
- D'Souza, C., M. M. Nakano, and P. Zuber. 1994. Identification of comS, a gene of the srfA operon that regulates the establishment of genetic competence in *Bacillus subtilis*. Proc. Natl. Acad. Sci. USA 91:9397–9401.
- Dubnau, D. 1993. Genetic exchange and homologous recombination, p. 555–584. *In* A. L. Sonenshein, J. A. Hoch, and R. Losick (ed.), *Bacillus subtilis* and other gram-positive bacteria: biochemistry, physiology, and molecular genetics. American Society for Microbiology, Washington, D.C.
- Dubnau, D., and M. Roggiani. 1990. Growth medium-independent genetic competence mutants of *Bacillus subtilis*. J. Bacteriol. 172:4048–4055.
- Ferrari, F. A., K. Trach, D. LeCoq, J. Spence, E. Ferrari, and J. A. Hoch. 1985. Characterization of the *spo0A* locus and its deduced product. Proc. Natl. Acad. Sci. USA 82:2647–2651.
- Fürbass, R., M. Gocht, P. Zuber, and M. A. Marahiel. 1991. Interaction of AbrB, a transcriptional regulator from *Bacillus subtilis* with the promoters of the transition state-activated genes *tycA* and *spoVG*. Mol. Gen. Genet. 225: 347–354.
- Gaur, N. K., J. Oppenheim, and I. Smith. 1991. The *Bacillus subtilis sin* gene, a regulator of alternate developmental processes, codes for a DNA-binding protein. J. Bacteriol. 173:678–686.
- Hahn, J., J. Bylund, M. Haines, M. Higgins, and D. Dubnau. Inactivation of mecA prevents recovery from the competent state and interferes with cell division and the partitioning of nucleoids in *Bacillus subtilis*. Submitted for publication.
- 12. Hahn, J., and D. Dubnau. 1991. Growth stage signal transduction and the

requirements for *srfA* induction in development of competence. J. Bacteriol. **173:**7275–7282.

- Hahn, J., L. Kong, and D. Dubnau. 1994. The regulation of competence transcription factor synthesis constitutes a critical control point in the regulation of competence in *Bacillus subtilis*. J. Bacteriol. 176:5753–5761.
- Hamoen, L. W., H. Eshuis, J. Jongbloed, G. Venema, and D. van Sinderen. 1995. A small gene, designated *comS*, located within the coding region of the fourth amino acid-activation domain of *srfA*, is required for competence development in *Bacillus subtilis*. Mol. Microbiol. 15:55–63.
- Ireton, K., D. Z. Rudner, K. Jaacks-Siranosian, and A. D. Grossman. 1993. Integration of multiple developmental signals in *Bacillus subtilis* through the Spo0A transcription factor. Genes Dev. 7:283–294.
- Jaacks, K. J., J. Healy, R. Losick, and A. D. Grossman. 1989. Identification and characterization of genes controlled by the sporulation-regulatory gene spo0H in Bacillus subtilis. J. Bacteriol. 171:4121–4129.
- 17. Kausche, D., L. Hamoen, G. Venema, and M. Marahiel. 1994. Personal communication.
- Kong, L., and D. Dubnau. 1994. Regulation of competence-specific gene expression by Mec-mediated protein-protein interaction in *Bacillus subtilis*. Proc. Natl. Acad. Sci. USA 91:5793–5797.
- Kong, L., K. J. Siranosian, A. D. Grossman, and D. Dubnau. 1993. Sequence and properties of *mecA*, a negative regulator of genetic competence in *Bacillus subtilis*. Mol. Microbiol. 9:365–373.
- Kunst, F., M. Debarbouille, T. Msadek, M. Young, C. Mauel, D. Karamata, A. Klier, G. Rapoport, and R. Dedonder. 1988. Deduced polypeptides encoded by the *Bacillus subtilis sacU* locus share homology with two-component sensor-regulator systems. J. Bacteriol. 170:5093–5101.
- LeDeaux, J. R., and A. D. Grossman. 1995. Isolation and characterization of kinC, a gene that encodes a sensor kinase homologous to the sporulation sensor kinases KinA and KinB in *Bacillus subtilis*. J. Bacteriol. 177:166– 175.
- Marahiel, M. A., P. Zuber, G. Czekay, and R. Losick. 1987. Identification of the promoter for a peptide antibiotic biosynthesis gene from *Bacillus brevis* and its regulation in *Bacillus subtilis*. J. Bacteriol. 169:2215–2222.
- Msadek, T., F. Kunst, and G. Rapoport. 1994. MecB of *Bacillus subtilis* is a pleiotropic regulator of the ClpC ATPase family, controlling competence gene expression and survival at high temperature. Proc. Natl. Acad. Sci. USA 91:5788–5792.
- Perego, M., G. B. Spiegelman, and J. A. Hoch. 1988. Structure of the gene for the transition state regulator *abrB*: regulator synthesis is controlled by the *spo0A* sporulation gene in *Bacillus subtilis*. Mol. Microbiol. 2:689–699.
- Perego, M., J.-J. Wong, G. B. Spiegelman, and J. A. Hoch. 1991. Mutational dissociation of the positive and negative regulatory properties of the Spo0A sporulation transcription factor of *Bacillus subtilis*. Gene 100:207–212.
- Robertson, J. B., M. Gocht, M. A. Marahiel, and P. Zuber. 1989. AbrB, a regulator of gene expression in *Bacillus subtilis*, interacts with the transcription initiation regions of a sporulation gene and an antibiotic synthesis gene. Proc. Natl. Acad. Sci. USA 86:8457–8461.
- Roggiani, M., J. Hahn, and D. Dubnau. 1990. Suppression of early competence mutations in *Bacillus subtilis* by *mec* mutations. J. Bacteriol. 172:4056– 4063.
- Sadaie, Y., and T. Kada. 1983. Formation of competent *Bacillus subtilis* cells. J. Bacteriol. 153:813–821.
- Smith, I. 1991. Choice and commitment in sporulation initiation: the role of positive and negative control elements. Semin. Dev. Biol. 2:13–20.
- Strauch, M., V. Webb, G. Spiegelman, and J. A. Hoch. 1990. The Spo0A protein of *Bacillus subtilis* is a repressor of the *abrB* gene. Proc.

Natl. Acad. Sci. USA 87:1801-1805.

- Strauch, M. A., G. B. Spiegelman, M. Perego, W. C. Johnson, D. Burbulys, and J. A. Hoch. 1989. The transition state transcription regulator *abrB* of *Bacillus subtilis* is a DNA binding protein. EMBO J. 8:1615–1621.
- 32. van Sinderen, D., A. Luttinger, L. Kong, D. Dubnau, G. Venema, and L. Hamoen. 1994. *comK* encodes the competence transcription factor (CTF), the key regulatory protein for competence development in *Bacillus subtilis*. Mol. Microbiol. 15:455–462.
- van Sinderen, D., and G. Venema. 1994. *comK* acts as an autoregulatory control switch in the signal transduction route to competence in *Bacillus subtilis*. J. Bacteriol. 176:5762–5770.
- 34. Weir, J., M. Predich, E. Dubnau, G. Nair, and I. Smith. 1991. Regulation of

spo0H, a gene coding for the Bacillus subtilis  $\sigma^{H}$  factor. J. Bacteriol. 173: 521–529.

- 35. Yansura, D. G., and D. J. Henner. 1984. Use of the *Escherichia coli* lac repressor and operator to control gene expression in *Bacillus subtilis*. Proc. Natl. Acad. Sci. USA 81:439–443.
- Zuber, P., and R. Losick. 1987. Role of AbrB in Spo0A- and Spo0B-dependent utilization of a sporulation promoter in *Bacillus subtilis*. J. Bacteriol. 169:2223–2230.
- 37. Zuber, P., M. Marahiel, and J. Robertson. 1988. Influence of *abrB* on the transcription of the sporulation-associated genes *spoVG* and *spo0H* in *Bacillus subtilis*, p. 123–127. *In* A. T. Ganesan and J. A. Hoch (ed.), Genetics and biotechnology of bacilli. Academic Press, New York.