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A Negative Feedback Loop That Limits the Ectopic Activation of a Cell Type–Specific Sporulation Sigma Factor of Bacillus subtilis

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Abstract
Two highly similar RNA polymerase sigma subunits, σE and σG, govern the early and late phases of forespore-specific gene expression during spore differentiation in Bacillus subtilis. σE drives synthesis of σG but the latter only becomes active once engulfment of the forespore by the mother cell is completed, its levels rising quickly due to a positive feedback loop. The mechanisms that prevent premature or ectopic activation of σG while discriminating between σE and σG in the forespore are not fully comprehended. Here, we report that the substitution of an asparagine by a glutamic acid at position 45 of σG (N45E) strongly reduced binding by a previously characterized anti-sigma factor, CsfB (also known as Gin), in vitro, and increased the activity of σG in vivo. The N45E mutation caused the appearance of a sub-population of pre-divisional cells and the FCT. This work was supported by grants Praxis XXI/PCNA/C/BIO/13201/98 and PRAXIS/BIO/35109/99 from the FCT (http://alfa.fct.mctes.pt) to AOH and by C. activity. N45 is invariant in the homologous position of csfB B. subtilis. These authors contributed equally to this work.

Introduction
When cells of Bacillus subtilis enter stationary phase and face severe nutrient depletion, they may embark into a developmental pathway that results in the production of a dormant, highly resistant endospore [1]. Sporulation involves the asymmetric division of the rod-shape cell into a smaller forespore, the future spore, and a larger mother cell. Soon after asymmetric cell division, the mother cell engulfs the forespore, eventually releasing it as a free protoplast within its cytoplasm. Following engulfment completion, the forespore becomes ensased in a series of protective layers after which it is released into the environment through lysis of the mother cell [1]. Underlying the differentiation process are mother cell- and forespore-specific programs of gene expression administered by a cascade of cell type-specific RNA polymerase sigma factors. σE and σG govern the initial stages in development in the forespore and in the mother cell, respectively. At late stages of development, σF replaces σE (Figure 1A), whereas σH replaces σF. The sporulation-specific sigma factors are produced prior to their period of activity, and maintained inactive until the successful conclusion of key morphological events during development. Both σF and σH are synthesized in the predivisional cell. Proper septation is a prerequisite for the activation of σF in the forespore and soon after a signaling pathway is initiated by σF leads to the activation of σH in the mother cell. Likewise, synthesis of σG and σH is initially driven by σE and σF, respectively. However, σH-dependent gene expression is required for the activation of σG following engulfment completion and when active, σG initiates a signaling pathway that causes the activation of σH [1–3]. The double responsiveness of the cell-type specific σ factors to proper morphogenesis and to intercompartmental signaling pathways effectively links the forespore and mother cell programs of gene expression and keeps gene expression in close register with the course of morphogenesis. Importantly, proper timing of sigma factor activation is essential for the fidelity of the developmental process [reviewed by [1–3]].
Author Summary

Positive auto-regulation of a transcriptional activator during cell differentiation or development often allows the rapid and robust deployment of cell- and stage-specific genes and the routing of the differentiating cell down a specific path. Positive auto-regulation however, raises the potential for inappropriate activity of the transcription factor. Here we unravel the role of a previously characterized anti-sigma factor, CsfB, in a negative feedback loop that prevents ectopic expression of the spore-formation-specific sigma factor $\sigma^G$ of Bacillus subtilis. $\sigma^G$ is activated in the forespore, one of the two chambers of the developing cell, at an intermediate stage in spore development. Once active, a positive feedback loop allows the rapid accumulation of $\sigma^G$. Synthesis of both $\sigma^G$ and CsfB is under the control of the early forespore regulator $\sigma^F$, and CsfB may help prevent the premature activity of $\sigma^G$ in the forespore. However, CsfB is also produced under $\sigma^G$ control in non-sporulating cells, setting a negative feedback loop that we show limits its ectopic activity. We further show that an asparagine residue conserved among $\sigma^G$ orthologues is critical for binding and inhibition by CsfB, whereas the exclusion of asparagine from the homologous position in $\sigma^F$ confers immunity to CsfB.

This study addresses the mechanisms involved in the regulation of the activity of $\sigma^G$. Productive transcription of the $\sigma^G$ gene (coding for $\sigma^G$) is controlled by $\sigma^F$ [4,5]. However, $\sigma^G$ is not transcribed as soon as $\sigma^G$ becomes active. The delay appears to result from an as yet poorly understood dependency of $\sigma^G$ transcription upon the activity of $\sigma^G$ in the mother cell [6,7]. $\sigma^G$ can be detected in the forespore towards the end of the engulfment sequence, but its window of activity begins only after engulfment completion. Activity of $\sigma^G$ requires the assembly of a novel type of secretion system formed by eight mother cell proteins (AA through AH) coded for by the $\sigma^G$-controlled spoIII operon, and by the forespore-specific, $\sigma^G$-controlled protein SpoIIQ [8–14], with the assistance of the membrane protein translocase SpoIII [8,15–18]. The SpoIII-A-SpoIJ complex spans the intermembrane space that separates the forespore and the mother cell establishing a direct connection between the cytoplasm of the two cells [8,10,14,19]. Recent work has lead to the concept that the channel acts as a feeding tube, maintaining the potential for macromolecular synthesis when the forespore becomes isolated from the external medium [9]. This model brings the important implication that the activation of $\sigma^G$ in engulfed forespores does not necessarily involve counteracting a specific inhibitor or inhibitors of $\sigma^G$. However, once active, $\sigma^G$ recognizes its own promoter, creating a positive feedback loop that causes its levels to increase rapidly [4,5]. This autoregulatory effect implies the tight promoter, creating a positive feedback loop that causes its levels to increase rapidly [4,5]. This autoregulatory effect implies the tight promoter of the activity of $\sigma^G$ in the forespore [8,21,24]. A third negative regulator of $\sigma^G$ is CsfB (also known as Gin), a novel type of Zn$^{2+}$-anti-sigma factor [20,27,28]. CsfB combines two properties expected for a factor capable of inhibiting $\sigma^G$ prior to engulfment completion: specificity for $\sigma^G$ (unlike SpoIIAB, CsfB does not binds to $\sigma^E$) and its early presence in the forespore compartment [20,28,29]. However, although one group initially proposed that CsfB had a key role in the negative regulation of $\sigma^G$ in the pre-engulfed forespore [20], other groups did not observe massive premature activation of $\sigma^G$ in the forespore upon deletion of the $cysB$ gene [8,27].

While the auto regulatory nature of $\sigma^G$ seems to justify the existence of multiple negative regulators, none of the known regulators per se, seems to have a decisive role in preventing activation of the $\sigma^G$ positive feedback loop. Because $\sigma^G$ and $\sigma^F$ are very similar proteins, we reasoned that the residues in which the two proteins differ could hold the key to their differential regulation. We changed all the residues within conserved regions 1.2 through the beginning of region 2.3 of $\sigma^G$ in which it differs from $\sigma^F$ to the residue found in this latter protein. We report the identification of a mutation (N45E) that reduces binding of CsfB to $\sigma^G$ in vivo and in vitro. The mutation also results in the appearance of a population of stationary phase cells in which $\sigma^G$ becomes active. We show that $\sigma^G$ drives expression of $cysB$ in these cells, setting-up a negative feedback loop that limits its activation across the population.

We further show the importance of N45 in $\sigma^G$ and its equivalent in $\sigma^G$ (E39), in the different responsiveness of the two forespore-specific sigma factors to CsfB. While unable to bind to wild type $\sigma^G$, CsfB interacts with a form of $\sigma^G$ in which E39 is replaced by an N residue, found in the corresponding position of $\sigma^G$ (N45). Importantly, we show that the E39N substitution can strongly inhibit the forespore-specific activity of $\sigma^G$ and the efficiency of sporulation. Thus, a single amino acid residue allows CsfB to discriminate between the two highly similar forespore-specific sigma factors. This property is likely to be widespread, because N45 is invariant in Bacillus orthologues of $\sigma^G$, while with a single exception N is excluded from the equivalent position in the $\sigma^F$ proteins of the same species.

Results

A mutation in conserved region 2.2 that increases the activity of $\sigma^G$

Since $\sigma^G$ is active in the forespore in a temporal window when $\sigma^G$ is kept inactive (Figure 1A), we reasoned that we would be able to find one or more substitutions that would render $\sigma^G$ prematurely active. We initiated this study by changing most of the residues within regions 1.2 and 2.1 through the beginning of region 2.3 of $\sigma^G$ that differed from $\sigma^F$ to the amino acid found at the equivalent position in this latter protein (Figure 1B). The mutations were generated in vitro and transferred by congesion to the $\sigma^G$ locus (see the Materials and Methods section). We then screened for mutants exhibiting elevated levels of $\sigma^G$-directed gene expression under non-sporulation conditions (during growth in LB) as these conditions previously led to the identification of two negative regulators of $\sigma^G$ [21,22]. This is possible because active $\sigma^G$ utilizes its own promoter, leading to the establishment of a positive auto regulatory loop that reinforces its activity [5]. We
found a single substitution at codon 45 of the \( \sigma^G \) gene, an asparagine to a glutamic acid (henceforth N45E) that increased the activity of \( \sigma^G \) in vivo, as monitored using a fusion of the \( \sigma^G \)-responsive \( sspE \) promoter to \( lacZ \) [5]. The \( sspE \) gene codes for an abundant small acid-soluble protein required for the efficient return of spores to vegetative growth, and that is normally expressed in the forespore when \( \sigma^G \) becomes active [30–32]. The N45E mutation stimulated \( P_{sspE-lacZ} \)-\( lacZ \) transcription in colonies of cells growing on solid medium as well as in cells growing in liquid medium, where \( \beta \)-galactosidase activity was 2 fold higher in N45E mutant cells than in wild type cells (Figure 2A and 2B). On liquid medium, the activity of \( \sigma^{45E} \) was higher when the cells entered stationary phase (Figure 2B). The augmented expression of \( P_{sspE-lacZ} \) could be due to increased activity of \( \sigma^{45} \) or alternatively to the titration by \( \sigma^{45E} \) of a negative regulator of \( \sigma^F \), which at least under some conditions is also able to direct transcription from the \( sspE \) promoter [5]. To test the model that \( \sigma^{45E} \) could titrate an inhibitor of \( \sigma^F \), we first examined the effect of two additional point mutations, F91A and Y94A, in region 2.3 of \( \sigma^G \) (see Figure S1A). These residues are presumed to play a role in promoter melting.

Figure 1. Segregation of \( \sigma^F \) and \( \sigma^G \) activities and mutagenesis of \( \sigma^G \). Panel A shows the main stages in sporulation and the temporal windows of activity of \( \sigma^F \) and \( \sigma^G \) in the forespore. Shown is (1) a pre-divisional cell, (2) a cell that has completed asymmetric division forming a forespore (FS) and a mother cell compartment (MC), (3, 4) a cell during and (5) after engulfment completion, (6) the following assembly of the spore protective layers and (7) release of the mature spore upon mother cell lysis. The mother cell membranes are colored in green. \( \sigma^F \) is activated in the forespore after polar division, and transcribes the \( \sigma^G \) gene, but \( \sigma^G \) only becomes active following engulfment completion. Red and black denote inactive and active \( \sigma^G \), respectively. Panel B shows an alignment between the N-terminal regions of \( \sigma^F \) and \( \sigma^G \) from \( B. subtilis \). Residues that were subject to mutagenesis are indicated by yellow circles or, for N45, by a red arrow. The blue lines above the sequence delimit conserved regions 1.2 through 2.3. Residues previously implicated in binding of SpoIIAB to \( \sigma^G \) are marked with a blue circle. Panel C shows the alignment of region 2.1 of \( B. subtilis \) \( \sigma^G \) (highlighting residue N45 with a red arrow) with the same region of \( \sigma^G \) from other, selected, \( Bacillus \) species. The alignments (B and C) were prepared using ClustalW (http://www.ch.embnet.org/software/ClustalW.html). Black and grey backgrounds highlight identical or conserved residues, respectively.

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Figure 2. Identification of mutants with increased activity of $\sigma^G$. Panel A illustrates a colony screening for enhanced $\beta$-galactosidase production from the $\sigma^G$-controlled $P_\text{sspE}$-lacZ reporter fusion on LB plates containing X-Gal. Panel B shows the quantitative analysis of enzyme activity for the same strains shown in A, on liquid LB cultures at mid-log and at the onset of stationary phase. The following strains are shown (Table S1 shows the complete genotype of all strains): wild type background (pink in panel B), $\text{sigGN45E}$ (brown in panel B), $\text{sigGN45A}$ (light blue in panel B), $\text{sigGV44I}$ (purple in panel B), $\Delta\text{csfB}$ (green in panel B), and $\Delta\text{csfB sigGN45E}$ (blue in panel B). Controls for background levels are the wild type MB24 bearing no reporter fusion ("*" symbol in panel A, yellow bars in panel B), and a strain carrying the $P_\text{sspE}$-lacZ fusion in conjunction with a $\text{sigG}$ deletion mutation (dark blue in panel B). In panels C, D, E, and F the activity of wild type $\sigma^G$ or its mutant forms $\sigma^G_{\text{GN45A}}$, $\sigma^G_{\text{GN45E}}$, or $\sigma^G_{\text{GV44I}}$ was examined during sporulation in DSM medium in a wild type background or in strains carrying mutations in genes known to control the initiation of sporulation or to influence the activity of wild type $\sigma^G$. All strains used in this analysis carry the $\sigma^G$-controlled $P_\text{sspE}$-lacZ fusion. Panel C, shows the activity profile for wild type $\sigma^G$, and for $\sigma^G_{\text{GN45A}}$, $\sigma^G_{\text{GN45E}}$, or $\sigma^G_{\text{GV44I}}$ in an otherwise wild type background. Residual expression of $P_\text{sspE}$-lacZ in a $\Delta\text{sigG}$ mutant is included for reference. Panel D compares the activity of wild type $\sigma^G$ in a $\Delta\text{csfB}$ mutant to the activity of $\sigma^G_{\text{GN45E}}$ in a wild type background or in a $\Delta\text{csfB}$ mutant. Expression of $P_\text{sspE}$-lacZ in a $\Delta\text{sigG} \Delta\text{csfB}$ mutant is also represented. Panel E compares the activity of wild type $\sigma^G$ in a $\Delta\text{spolIIIU}$ mutant and a $\Delta\text{spolIIIU} \Delta\text{csfB}$ double mutant to that of $\sigma^G_{\text{GN45E}}$ in a $\Delta\text{spolIIIU}$ mutant. Panel F shows the activity $\sigma^G_{\text{GN45E}}$ in a wild type background, or in the absence of $\text{sigF}$ or $\text{spo0A}$ (AH6626, open triangles). The activity of wild type $\sigma^G$ in a wild type background is shown for reference. The various strains were grown in sporulation medium (DSM) and sampled at hourly intervals after T0 (denoting the end of the logarithmic phase of growth). $\beta$-galactosidase activity is shown in Miller Units. In all cases, the various forms of $\sigma^G$ are produced from the wt or $\text{sigG}$ mutant alleles present at the $\text{sigG}$ locus. Panels C-F show the results of representative experiments, which in all cases were conducted independently at least three times.

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(reviewed by [33]), and alanine substitutions at these positions, while allowing the accumulation of $\sigma^G$, inactivate the sigma factor (Text S1 and Figure S1). Importantly, the N45E-stimulated expression of $P_{\text{sgp}}$-lacZ was abolished in a N45E/F91A/Y94A triple mutant (data not shown). This finding established that the N45E-stimulated transcription of $P_{\text{sgp}}$-lacZ was dependent on $\sigma^G$ itself. None of the other $\sigma^G$ mutations screened increased expression of $P_{\text{sgp}}$-lacZ as illustrated by the $\text{sigG}^{44I}$ mutant, bearing a valine to isoleucine substitution at codon 44 (V44I) (Figure 2A and 2B).

We hypothesized that the N45 residue was a contact site for a putative inhibitor of $\sigma^G$, which was eliminated by the N45E substitution. As a test of this idea we replaced the asparagine residue by an alanine (henceforth N45A), a substitution expected to remove any positive contribution of the wild type amino acid side chain to a presumed interaction while maintaining protein structure [34]. Unexpectedly, the N45A substitution did not increase $\sigma^G$-directed transcription on colonies of cells growing on LB medium nor on liquid medium cultures (Figure 2A and 2B). This observation suggests that the side chain of N45 may not be essential for a direct interaction of $\sigma^G$ with an inhibitory factor. One alternative possibility is that N45E interferes with the binding of a putative inhibitor to $\sigma^G$.

Activity of $\sigma^{NG45E}$ during sporulation

We next studied the effect of the N45E substitution on the activity of $\sigma^G$ during sporulation in liquid Difco sporulation medium (DSM). In this system, sporulation is induced by exhaustion of key nutrients, and its onset defined as the point at which a culture enters stationary phase. None of the $\sigma^G$ mutants that we screened in LB medium caused a Spo - phenotype (data not shown), but we looked at $P_{\text{sgp}}$-lacZ transcription during sporulation as the mutations could alter the normal activity profile of $\sigma^G$. In wild type cells, expression of $P_{\text{sgp}}$-lacZ was sharply induced 4 hours after the onset of stationary phase and reached maximum levels around hour 6 (Figure 2C). In keeping with the link between the activity of $\sigma^G$ and engulfment completion, induction of $P_{\text{sgp}}$-lacZ expression at hour 4 coincided with forespore engulfment in most cells of the population, as judged by FM4-64 staining (not shown). In N45E cells $P_{\text{sgp}}$-lacZ expression followed a bimodal pattern, with an early period that peaked 2 hours after the onset of stationary phase and a second, starting at hour 4, superimposable to the window of $\sigma^G$ activity seen for wild type cells (Figure 2C). The activity profile of $\sigma^G$ and $\sigma^{NG45E}$ paralleled the accumulation of the proteins, as assessed by immunoblotting with an anti-$\sigma^G$ antibody [17]. Both $\sigma^G$ and $\sigma^{NG45E}$ accumulated to maximum levels at hour 4 of sporulation in consonance with the main period of $P_{\text{sgp}}$-lacZ expression, following engulfment completion (Figure S2C). However, $\sigma^{NG45E}$ began to accumulate earlier than the wild type protein, soon after the onset of stationary phase in DSM, which correlates with the first period of $P_{\text{sgp}}$-lacZ expression in the N45E mutant (Figure S2C).

Only the second period of $P_{\text{sgp}}$-lacZ expression was seen for the V44I and the N45A mutants (Figure 2C), consistent with the observation that these mutations did not enhance expression of the reporter fusion in our initial screen (see above). Also consistent with the conclusion of our initial screen that the increased expression of the $P_{\text{sgp}}$-lacZ reporter was not indirectly caused by titration of a negative regulator of $\sigma^G$ (see above), the N45E mutation did not increase expression of a lacZ fusion to the promoter for a gene, spoIHO, controlled by $\sigma^F$ (spoIHO-lacZ [13]) (Text S1 and Figure S2A). In addition, the first period of $\sigma^G$ activity was still observed independently of sigF, coding for $\sigma^F$, which normally drives transcription of sigG in the forespore (Figure 2F; see also below). While the spoF promoter can also be utilized by $\sigma^F$ [8,27], it is clear that the first period of $\sigma^{NG45E}$ activity is $\sigma^G$-independent. This first period also occurred in cells with deletion mutations of the spoIHO (Figure 2E) and spoIHI loci (not shown), which are required for $\sigma^F$ activity following engulfment completion. In fact, the first peak of $\sigma^{NG45E}$ activity was seen even in cells of a spoIHI deletion mutant ([35,36], and references therein), which codes for the master regulatory protein governing entry into sporulation and without which the asymmetric division that produces the forespore compartment does not take place [37] (Figure 2F).

Altogether, these results show that the effect of the N45E substitution on $P_{\text{sgp}}$-lacZ transcription during stationary phase in sporulation medium was dependent on and mediated by $\sigma^G$. The results also show that the second peak of $\sigma^{NG45E}$ activity remained dependent on the normal control mechanisms that govern $\sigma^G$ production and activation during sporulation.

c$\text{sorf}^{NG45E}$ is activated in a population of stationary phase cells

The results described in the preceding section could be explained if the N45E mutant segregated two distinct cellular populations, one with a normal pattern of $\sigma^G$ activity, the other activating $\sigma^G$ independently of sporulation. To test this possibility, the activity of $\sigma^{NG45E}$ was localized during stationary phase in DSM, using a $P_{\text{sgp}}$-cFP transcriptional fusion [10]. Note that under our experimental conditions, asymmetric division was completed in most of the cell population between hours 2 and 3 after entry into stationary phase (as assayed by staining with the membrane dye FM4-64), and engulfment was completed around hour 4 (above). In agreement with previous results, expression of $P_{\text{sgp}}$-cFP in wild type cells was only detected in the forespore at hour 4 after the onset of stationary phase, and only in cells in which the forespore had been engulfed by the mother cell (Figure 3 and Table 1). Note that no fluorescence was detected in cells of a sigG deletion mutant (Figure 3), confirming that the detected expression of the fluorescent reporter relied on $\sigma^G$. In the N45E mutant, however, around 1% of the cells scored between hour 0 and 2 after the onset of stationary phase showed strong whole-cell fluorescence (Figure 3 and Table 1). These cells had no morphological signs of sporulation, i.e., they did not show asymmetric septa or engulfing membranes as assessed by FM4-64 staining. Consistent with the absence of asymmetric septation, we found that these cells did not show $P_{\text{sgp}}$-cFP expression (not shown) and time-lapse microscopy experiments revealed that they eventually lysed (Figure S3). A second, larger population of N45E cells consisted of organisms that resembled the wild type in that they began to display forespore-specific cFP fluorescence at hour 3 (Figure 3; Table 1). These cells did not show premature, whole-cell expression of $P_{\text{sgp}}$-cFP. The results show that the first period of $\sigma^G$ activity in the N45E mutant can be accounted for by a subpopulation of cells that enter stationary phase and that do not enter in sporulation.

csfB and the sig$\text{NG45E}$ allele are epistatic

We then focused our attention in the mechanism of activation of $\sigma^{NG45E}$ in post-exponential phase cells. We considered the possibility that the N45E substitution made $\sigma^G$ less responsive to the SpoIIAB anti-$\sigma^G$ factor, which binds to and contributes to the negative regulation of $\sigma^G$ in non-sporulating cells [8,12,24]. However, we found the activity of $\sigma^{NG45E}$ to remain sensitive to SpoIIAB in vivo (Text S1 and Figure S2B). While the possibility that the N45E substitution made $\sigma^G$ refractory to SpoIIAB seemed discarded, the profile of $\sigma^{NG45E}$ activity, in particular the first period of activity detected in stationary phase DSM cultures,
was reminiscent of the effect reported for a mutation in cfsB, which codes for the CsfB anti-σ^6 factor [8,20,27]. For this reason, we examined the contribution of a cfsB deletion mutation to the effect of the sigGN45E allele on σ^6-directed gene expression. On LB medium supplemented with X-Gal, the double mutant exhibited levels of β-galactosidase activity similar to the single sigGN45E or cfsB mutants (Figure 2A and 2B). In DSM the double mutant showed the bi-modal temporal pattern of P^sspE-lacZ expression seen for the cfsB or sigGN45E single mutants, but with β-galactosidase levels during the first period of expression higher than those of the sigGN45E mutant (Figure 2D). There was no detectable effect of the mutations alone or in combination, on the second period of P^sspE-lacZ activity (Figure 2D). When examined by fluorescence microscopy, the sigGN45E/cfsB double mutant resembled the single mutants: about 1% of the cells displayed early whole-cell fluorescence (between hours 0 and 2 of sporulation) whereas most of the population showed CFP fluorescence in the forespore membranes following engulfment completion, and thus serves as a reporter of the engulfment status of the forespore. Fluorescence from P^sspE-cfp was false colored in green. Scale bars, 1 mm. The cartoons represent the classes of cells showing CFP accumulation at the indicated times and the numbers, the percentage of cells with CFP fluorescence in the indicated compartment.

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The N45E substitution reduces binding of CsfB to σ^G
The idea that both cfsB and the sigGN45E allele act on the same pathway suggested to us that the N45E substitution could interfere with binding of CsfB to the mutant form of σ^G. In earlier work, CsFB and σ^G were found to directly interact in a yeast two-hybrid assay, and the first 71 residues of σ^G to be required for the CsfB-dependent inhibition of σ^G in vivo [20]. We used a similar approach to investigate whether σ^G^N/GN45E was less efficiently bound by CsFB. σ^G^- σ^G/N/GN45A, σ^G/N/GN45B or CsfB were translationally fused to the C-terminus of the Gal4 DNA binding (BD) and activation domains (AD), and the various fusion proteins expressed in different combinations in yeast cells and checked for their ability to interact in vivo, as assessed by the expression of a lacZ gene preceded by a Gal4-responsive element. As shown in Figure 4A and 4B, CsFB interacts efficiently with σ^G and only slightly less well with σ^G/N/GN45A. In contrast, CsFB interacts only weakly with σ^G/N/GN45B.

We then used affinity chromatography to further investigate the interaction between CsFB and the different forms of σ^G. Whole cell extracts were prepared from cultures of a B. subtilis strain producing a functional CsFB-GFP fusion, 2 hours after the onset of sporulation, when σ^G is active and CsFB is known to accumulate [29]. The extracts were incubated with GST-σ^G WT, GST-σ^G/N/GN45A, GST-σ^G/N/GN45B or GST alone bound to glutathione agarose beads. Bound proteins were eluted and identified by immunoblot with an anti-GFP antibody (see Materials and Methods). These experiments showed that CsFB was pulled down efficiently by immobilized GST- σ^G WT but not by GST itself (Figure 4C). GST-σ^G/N/GN45A pulled down CsFB-GFP less efficiently that the wild type (the efficiency was 0.7× of the wild type) but importantly, for σ^G/N/GN45B the efficiency of the pull down was about 0.4× of the wild type (Figure 4C; note that the numbers in the panel represent

Figure 3. Localization of σ^G activity. The activity of σ^G was monitored by fluorescence microscopy 2 (T2) and 4 (T4) hours after the onset of stationary phase in sporulation medium (DSM), for the following panel of strains (A and B), all of which carrying a fusion of the σ^G-controlled P^sspE promoter to cfp at the non-essential ycfT locus: the wild-type, a ΔsigG mutant, the sigGN45E mutant, and the ΔcsfB mutant. These findings suggest that the ΔcsfB double mutant did not differ significantly from either single mutants: about 1% of the cells displayed early whole-cell fluorescence (between hours 0 and 2 of sporulation) whereas most

A

| sspE-cfp | CFP | membranes | merge |
|---------|-----|-----------|-------|
| ΔsigG   | T2  | 0         | 0     |
|         | T4  | 0         | 0     |

B

| sspE-cfp | CFP | membranes | merge |
|---------|-----|-----------|-------|
| sigGN45E | T2  | 0         | 0     |
|          | T4  | 0         | 0     |

| ΔcsfB   | T2  | 0         | 0     |
|         | T4  | 0         | 0     |
which contains high levels of Zn$^{2+}$.

Retained of CsfB by above; Figure S2A). To discard the possibility that the reduced competing protein present in the B. subtilis purified using a CsfB-Strep E. coli purified from a minimal medium only in the presence of Zn$^{2+}$.

We incubated purified CsfB with GST or the N45E substitutions do not significantly affect binding of SpoIIAB with similar efficiency (Figure 4C), suggesting that the N45A or N45E was still susceptible to SpoIIAB (see above). Therefore, and although the expression of csfB in the forespore is not thought to be controlled by σ$^{G}$ [30], it seemed plausible that transcription of csfB in pre-divulsional cells could be at least in part, controlled by σ$^{G}$. As a first test to this idea, we investigated whether expression of csfB and the activity of σ$^{G}$ co-localized. We first replaced the wild type cfb allele by a cfb-Strep fusion. This cfb-Strep fusion was subsequently transferred to strains carrying either the wild type or the N45E alleles of sigG and in addition, the σ$^{G}$ reporter P$_{fcb}$-yfp [10]. In the wt strain grown in DSM, organisms began to display forespore-specific yfp fluorescence between hour 1 and 2 after the onset of stationary phase (Table 2), consistent with the timing of septation and the activation of σ$^{G}$. No fluorescent organisms were observed before hour 1, or in cells of a ΔsigG mutant, as expected for a σ$^{G}$-controlled gene (Table 2; data not shown). Conversely, cfp fluorescence was only observed in the forespore 2 hours after the onset of sporulation, as expected for a σ$^{F}$-controlled gene and demonstrating the functionality of the cfb-Strep fusion. In the N45E mutant, between 1% to 4% of the bacteria displayed both whole-cell YFP and CFP fluorescence during the first hours of stationary phase in DSM (Table 2). Around hour 2, the first cells showing forespore-specific yfp expression of cfb-Strep were detected followed, around hour 3, by cells with engulfed forespores showing P$_{fcb}$-yfp expression. From this analysis, it is clear that the whole-cell expression of cfb-Strep early in stationary phase is confined to cells that also show activity of σ$^{G}$, suggesting that cfb-Strep was transcribed under the direction of σ$^{G}$. As a further test to the possibility that σ$^{G}$ controlled transcription of cfb, we made use of the sigG inactive allele described above in which the N45E mutation was combined with the F91A and Y94A “promoter-melting” mutations (Figure S1). In cells of the triple sigG mutant, no whole-cell YFP or CFP fluorescence was detected. In addition, and as expected, cells of the triple mutant did not display forespore-specific CFP fluorescence (which is σ$^{G}$-dependent) but showed forespore-specific YFP fluorescence (which is σ$^{G}$-dependent) (Table 2). These results strongly suggest that the expression of cfb in pre-divisonal cells is σ$^{G}$-dependent, a conclusion reinforced by the observation that deletion of sigF in a N45E background abolished both the forespore-specific YFP and CFP fluorescence (σ$^{G}$- and σ$^{G}$- dependent) while maintaining the early whole-cell expression of yfp and cfp (Table 2). Lastly, as a more direct test for the ability of σ$^{G}$ to control the expression of cfb, we monitored the expression of a P$_{fof}$-lac fusion upon artificial induction of σ$^{G}$ production from P$_{ydi}$ in vegetatively growing cells. The results in Figure 3A show that addition of xylose resulted in the induction of cfb-lac fusion.

### Table 1. Localization of CFP expressed from the σ$^{G}$-controlled P$_{spc}$ promoter.

| Genotype      | % of cells displaying CFP fluorescence in: |
|---------------|--------------------------------------------|
|               | PS$^a$  | MC$^b$  | WC$^c$  | Total cells |
| sigG$^{WT}$   | 0       | 0       | 0       | 1407       |
| 1             | 0       | 0       | 0.06    | 1591       |
| 2             | 0.19    | 0       | 0       | 1574       |
| 3             | 1.5     | 0       | 0       | 1070       |
| 4             | 19.5    | 0       | 0.075   | 1333       |
| 5             | 40.9    | 0       | 0       | 1287       |
| sigG$^{N45E}$ | 0       | 0       | 1.3     | 1282       |
| 1             | 0       | 0       | 0.68    | 1468       |
| 2             | 0       | 0       | 0.93    | 1070       |
| 3             | 2.1     | 0       | 1.1     | 1011       |
| 4             | 22      | 0.09    | 0.65    | 1070       |
| 5             | 50.3    | 0       | 0.5     | 1187       |
| cfb           | 0       | 0       | 0.61    | 1301       |
| 1             | 0       | 1       | 1.64    | 1465       |
| 2             | 0       | 0       | 2       | 678        |
| 3             | 0.68    | 0       | 1.02    | 1175       |
| 4             | 18.6    | 0.2     | 0.78    | 1020       |
| 5             | 47.2    | 0.19    | 0.56    | 1061       |
| cfb$^{G}$     | 0       | 0       | 1       | 1429       |
| 1             | 0       | 0       | 2.1     | 1153       |
| 2             | 0       | 0       | 1.5     | 1293       |
| 3             | 0.22    | 0       | 1.355   | 1207       |
| 4             | 12.7    | 0       | 1       | 2072       |
| 5             | 46.9    | 0.29    | 0.7     | 1032       |

$^a$- hours after the onset of sporulation (T0); $^b$PS – prespor; $^c$MC – mother cell; $^d$WC – whole cell expression prior to asymmetric division. No whole cell expression was detected in cells that had undergone asymmetric division.

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Avoiding the Ectopic Activity of a Sigma Factor

(csfB was first identified as a gene under the control of σ$^{F}$, and hence transcribed in the forespore soon after asymmetric septation [29]. Yet, in our hands, the main effect of a cfb deletion on the activity of σ$^{G}$ activity was manifested in predivisional cells, i.e., before the activation of σ$^{G}$ (Figure 3). Previously, Chary et al., (2007) have speculated that there is a basal level of σ$^{G}$-directed transcription during vegetative growth. However, our results suggest that the increased activity of σ$^{G}$ [30], which as we show is at least partially resistant to CsfB, was dependent solely on σ$^{G}$ (see above). Therefore, and although the expression of cfb in the forespore is not thought to be controlled by σ$^{G}$, we investigated whether expression of cfb and the activity of σ$^{G}$ co-localized. We first replaced the wild type cfb allele by a cfb-Strep fusion. This cfb-Strep fusion was subsequently transferred to strains carrying either the wild type or the N45E alleles of sigG and in addition, the σ$^{G}$ reporter P$_{fcb}$-yfp [10]. In the wt strain grown in DSM, organisms began to display forespore-specific yfp fluorescence between hour 1 and 2 after the onset of stationary phase (Table 2), consistent with the timing of septation and the activation of σ$^{G}$. No fluorescent organisms were observed before hour 1, or in cells of a ΔsigG mutant, as expected for a σ$^{G}$-controlled gene (Table 2; data not shown). Conversely, cfp fluorescence was only observed in the forespore 2 hours after the onset of sporulation, as expected for a σ$^{G}$-controlled gene and demonstrating the functionality of the cfb-Strep fusion. In the N45E mutant, between 1% to 4% of the bacteria displayed both whole-cell YFP and CFP fluorescence during the first hours of stationary phase in DSM (Table 2). Around hour 2, the first cells showing forespore-specific yfp expression of cfb-Strep were detected followed, around hour 3, by cells with engulfed forespores showing P$_{fcb}$-yfp expression. From this analysis, it is clear that the whole-cell expression of cfb-Strep early in stationary phase is confined to cells that also show activity of σ$^{G}$, suggesting that cfb-Strep was transcribed under the direction of σ$^{G}$. As a further test to the possibility that σ$^{G}$ controlled transcription of cfb, we made use of the sigG inactive allele described above in which the N45E mutation was combined with the F91A and Y94A “promoter-melting” mutations (Figure S1). In cells of the triple sigG mutant, no whole-cell YFP or CFP fluorescence was detected. In addition, and as expected, cells of the triple mutant did not display forespore-specific CFP fluorescence (which is σ$^{G}$-dependent) but showed forespore-specific YFP fluorescence (which is σ$^{G}$-dependent) (Table 2). These results strongly suggest that the expression of cfb in pre-divisonal cells is σ$^{G}$-dependent, a conclusion reinforced by the observation that deletion of sigF in a N45E background abolished both the forespore-specific YFP and CFP fluorescence (σ$^{G}$- and σ$^{G}$- dependent) while maintaining the early whole-cell expression of yfp and cfp (Table 2). Lastly, as a more direct test for the ability of σ$^{G}$ to control the expression of cfb, we monitored the expression of a P$_{fof}$-lac fusion upon artificial induction of σ$^{G}$ production from P$_{ydi}$ in vegetatively growing cells. The results in Figure 3A show that addition of xylose resulted in the induction of cfb-lac fusion.
expression, even in the presence of a sigF deletion mutation, consistent with the view that σG can also drive expression of csfB, and with the similarity of the −10 and −35 promoter elements recognized by σG and σF [39–41].

Taken as a whole, the results suggest that the capacity of σG to drive production of CsfB in pre-divisional cells may be part of a mechanism to limit the ectopic activation of σG should any condition promote its activation.

Genetic lesions that relax the regulation of σG also result in CsfB production

If production of CsfB is part of a regulatory circuit that self-restrains the activity of σG, then mutations in other factors known to negatively regulate σG should also induce expression of csfB, and the extent of the effect across the population should reflect the contribution of the affected regulator to the regulation of σG. Two such factors are known, the LonA protease and the SpoIIAB anti-sigma factor, which act independently to negatively regulate the activity of σG, mainly under non-sporulation conditions [21,22].

To determine the relative impact of mutations known to affect the regulation of σG on its activity across the population, and whether those mutations also increased the expression of csfB, we used fluorescence microscopy to simultaneously quantify the expression of PsspE-cfp and csfB-yfp at the onset of stationary phase in LB, in a panel of strains carrying PxylA fusions to wild type sigG, sigGN45E, sigGE156K (coding for a form of σG refractory to SpoIIAB; [24]),
The results in Figure 5C (top graph) show a clear correlation between the YFP and CFP signals for all strains tested. Cells that produce CFP also produce YFP, and an increase in the expression of one reporter is accompanied by an increase in the expression of the other (Figure 5C, top), highlighting the link between the activity of $s^G$ and the production of its negative regulator, CsfB. The middle and lower graphs of Figure 5C are cumulative frequency distributions of the CFP and YFP signals for the various strains. For the $s^G_{N45E}$, $lonA$, and $s^G_{N45E/E156K}$ strains, about 50% and 40% of the population shows CFP and YFP signals, respectively, above 2 arbitrary units. In contrast, only 10% of the $s^G_{N45E/E156K}$ populations show CFP or YFP signal intensities above this value (Figure 5C). Induction of $s^G_{N45E/E156K}$ increased the number of cells with high CFP fluorescence (above 8 arbitrary units) to 20% of the population, as compared to 10% for the $s^G_{N45E/E156K}$ and the single $s^G_{N45E/E156K}$ mutants, possibly reflecting reduced YFP stability. While CsfB, mainly, and LonA emerge as the principal regulators of $s^G$ activity during entry into the stationary phase of growth, SpoIIAB per se seems to have only a minor role (Figure 5C). Importantly, we were unable to combine the $s^G_{N45E/E156K}$ allele with a $lonA$ deletion, highlighting the convergent action of CsfB, SpoIIAB and LonA in the negative regulation of $s^G$, and suggesting that these are likely to be the main, if not the only, negative regulators of $s^G$ at play. The results also unravel a negative $s^G$ autoregulatory loop (Figure 5D), in which by commanding the expression of $csfB$, the fraction of cells with ectopic activity of $s^G$ is curtailed.

Since production of $s^G$ in the strains above was driven from the $P_xylA$ promoter, we expected the various forms of $s^G$ to accumulate to similar levels, independently of the number of cells showing $s^G$ activity. This was verified by immunoblotting analysis with an anti-$s^G$ antibody, for the $s^G_{N45E}$, $s^G_{E156K}$, $s^G_{N45E/E156K}$ and wild type $s^G$ in the $lonA$ background (Figure 5E).

CsfB discriminates between $s^F$ and $s^G$ via one single amino acid

Because changing N45 of $s^G$ for the residue found at the equivalent position in $s^F$, E39, makes $s^G$ less efficiently bound by CsfB, and since CsfB does not bind to $s^F$ [20], we reasoned that perhaps this position was essential for the discrimination by CsfB between the two forespore-specific sigma factors in vivo. This inference was strengthened by the observation that N45 is invariant in $s^G$ orthologues, whereas E39 is highly conserved among $s^G$ orthologues (Figure 1C).

Therefore, we decided to investigate whether E39 was important for the resistance of $s^F$ to CsfB, and for the regulation

| Genotype       | Time (h) | PS (%) | WC (%) | Total cells |
|----------------|----------|--------|--------|-------------|
| $s^G^{wt}$     | 0        | 0/0    | 0/0    | 1356        |
|                | 1        | 0.9/0  | 0/0    | 778         |
|                | 2        | 2.1/0.2| 0/0    | 1717        |
|                | 3        | 27.3/4.3| 0/0   | 1469        |
| $s^G_{N45E}$   | 0        | 0/0    | 3.7/2.8| 646         |
|                | 1        | 0/0    | 1.5/1.0| 397         |
|                | 2        | 2.8/0.3| 0.8/0.5| 769         |
|                | 3        | 30.1/1.3| 0.9/0.3| 626         |
| $s^G_{N45E/E156K}$ | 0       | 0/0    | 25.0/0 | 629         |
|                | 3        | 0/0    | 2.5/1.6| 947         |
| $s^F/s^G_{N45E}$ | 0      | 0/0    | 1.2/1.0| 1317        |
|                | 2        | 0/0    | 0.5/0.2| 864         |
|                | 3        | 0/0    | 0.2/0  | 925         |

*ah* - hours after the onset of sporulation (T0);  
*PS* – prespore;  
*WC* – whole cell expression prior to asymmetric division. No whole cell expression was detected in cells that had undergone asymmetric division.

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of its activity in vivo. We conducted GAL4-based yeast two-hybrid experiments to test the interaction between wild type σ^F and a mutant form of the protein with the E residue at position 39 replaced by an N (E39N; Figure 1B). In agreement with the results of an earlier study [20], CsfB did not interact with σ^F in our assay (Figure 6A and 6B). In contrast, CsfB interacted efficiently with σ^F39N (Figure 6A and 6B). Thus, the E39N substitution is sufficient to allow binding of CsfB to σ^F.

We next wanted to test whether the presence of an N at position 39 of σ^F, expected to make it susceptible to CsfB, would affect spore development. We found the E39N substitution to cause a 5-fold decrease in the efficiency of sporulation (data not shown). Chary et al.
found that when csfB is expressed from the IPTG-inducible P_{hyd}/P_csfB promoter prior to the activation of σ^G, spore formation was severely reduced [27]. However, in this strain the activity of σ^G was not impaired and spore formation was blocked in the developmental pathway just after engulfment completion [27]. We used a similar assay to test for the effect of the E39N mutation on the activity of σ^G. We transferred the IPTG-inducible P_{hyd}/P_csfB fusion to strains mutant for sigF and with a second copy of the entire sigF operon (with either the wild type sigF or sigFE39N) integrated at the amyE locus under the control of its native promoter. In the strain carrying the wild type allele of sigF grown in the presence of IPTG to induce csfB expression prior to the activation of σ^G, spore formation showed the reported 10^3-fold reduction relative to cultures without IPTG (Figure 6C) confirming the results of Chary et al. [2007]. Strikingly, induction of csfB expression in the strain carrying the sigFE39N allele of sigF reduced spore formation 10^5-fold compared to the uninduced cultures (Figure 6C). To investigate whether the more drastic sporulation defect observed in the strain carrying the E39N allele was due to impaired σ^F activity, we used a fusion of the σ^F-dependent yutC promoter to gfp [42]. GFP fluorescence was monitored by microscopy during sporulation in the strains with IPTG inducible expression of csfB and bearing either the wild type or sigFE39N alleles. We found that the induction of csfB reduced the activity of σ^F to 10% of the levels observed when CsF was produced prior to asymmetric division in the presence of wild type σ^F (Figure 6D). Thus, CsfB can interfere strongly with the activity of σ^F in vivo.

Discussion

CsfB and the feedback inhibition of σ^G

The production of transcription factors often leads to the activation of gene expression during cell differentiation and development. In some instances, positive auto-regulation of the transcription factor drives gene expression in the differentiating cell down a specific developmental path. However, the power of these positive feedback loops raises the potential for inappropriate expression of the transcription factor in the wrong cell or at the wrong time. Therefore, the expression of autoregulatory transcriptional activators must be tightly controlled. We show here that CsF has a function in preventing the activation of the forespore-specific, auto-regulatory σ^G factor, in stationary phase cells, in either a medium that does not support sporulation or in a sporulation medium, prior to the asymmetric division that initiates the program of compartment-specific gene expression that leads to differentiation of the spore.

This role of CsF was uncovered because the N45E substitution in σ^G, which reduces binding by CsF, also results in activation of the sigma factor in a fraction of stationary phase cells. We show that CsF is also produced, under σ^G control, in the same stationary phase cells where σ^G^{N45E} becomes active. Hence, a negative feedback loop is established which, with the help of SpoIIAB and LonA, dominates the positive feedback loop involving σ^G, and keeps its activity low. The role of LonA and SpoIIAB in the negative regulation of σ^G in stationary phase cells was shown before [9,12,17,21,22], but our analysis suggests that CsF and LonA are the main regulators of σ^G. Nevertheless, the role of SpoIIAB is evidenced when the N45E and E156K substitutions are combined, and by our inability to construct a strain additionally carrying a lonA deletion. The lethality of this triple mutant further suggests that CsF, SpoIIAB and LonA may be the only negative regulators of σ^G at play in stationary phase cells.

Although mutations that interfere with the function of CsF, SpoIIAB or LonA may cause strong expression of σ^G-dependent genes in pre-divisional cells, this only occurs in a fraction of the population (Figure 5). We do not presently know whether the cells which show σ^G activity are somehow different from the rest of the population at some fundamental level, or whether σ^G activity arises because of random fluctuations in the levels of σ^G itself, and its negative regulators. In any case, high-level expression of even wild type σ^G in stationary phase cells causes cell lysis, emphasizing the importance of limiting the potential for σ^G activation (Figure S6). Lysis may be a consequence of high levels of σ^G activity [20], an indirect effect of the release of σ^G through titration of SpoIIAB by σ^G [20] or both, as induction of σ^G production in LB leads to lysis even in the absence of σ^G (data not show).

CsfB and the activation of σ^G

CsF was initially proposed to be a key factor in keeping σ^G inactive in the forespore prior to engulfment completion [20]. However, a more consensual view of the role of CsF is that the anti sigma-factor acts as a timing device, to help prevent σ^G activity prior to engulfment completion [8,9,27,38]. The results of our investigation are in line with this view, as in our hands deletion of csfB or the N45E substitution in σ^G (which we show prevents binding of CsF to σ^G) did not bypass the genetic and morphological controls that link the activity of σ^G to engulfment completion. We postulate that during sporulation the negative feedback loops contributes to counter the positive feedback loop involving σ^G until CsF is inactivated, or its synthesis is reduced by an unknown second regulator, or σ^G accumulation overwhelms that of CsF. It is not known if CsF is inactivated in the forespore following engulfment completion, but the anti-sigma factor seems to rapidly disappear from the forespore once σ^G becomes active (our unpublished results). It is also likely that an additional factor prevents expression of csfB in the engulfed forespore. For example, σ^G drives production of SpoVT a forespore-specific transcription factor, which represses at least 27 σ^G-dependent transcriptional units [41,43]. SpoVT has a C-terminal GAF (cGMP-specific and cGMP-stimulated phosphodiesterases, Anabaena adenylate cyclases, and Escherichia coli PIIA-like domain, which is essential to modulate the DNA-binding activity of the N-terminal domain, and may respond to nucleotides or other small molecules [44]. The accumulation of nucleotides in the engulfed forespore in turn, may be essential for the activity of σ^G and may depend on the action of the SpoHIA-Q channel [9].

Binding of CsF to σ^G

Two observations are consistent with the interpretation that the N45E substitution interferes with binding of CsF to σ^G. First, wild type σ^G could pull down CsF from extracts of B. subtilis in sporulation medium, but σ^G^{N45E} did so less efficiently, a difference that was amplified when purified CsF was used (Figure 4; see also below). Second, CsF interacted with wild type σ^G but not with σ^G^{N45E} in a yeast two-hybrid system (Figure 4). CsF was purified from E. coli cells as a C-terminal fusion to the Strep II tag because in vivo a CsF-GFP fusion was fully functional (this work). The CsF-Strep II protein had Zn^{2+} bound with a stoichiometry of 1:1. The Zn^{2+} was released by oxidation of the protein with H_2O_2, suggesting the involvement of the conserved Cys residues in CsF in its coordination (see Figure S4). Recently, a MalE-CsF fusion protein was purified from sporulating cells of B. subtilis with Zn^{2+} bound with a stoichiometry of 0.5 mol/mol [28]. Together with genetic data, this suggested that CsF could act as a dimer (or higher order multimer) and possibly alternate between an active and an inactive state [28]. Importantly, the activity of σ^G was efficiently inhibited in E. coli cells, when co-produced with CsF [28], and the CsF-Strep II protein purified from E. coli cells clearly discriminated σ^G and σ^G^{N45E} in our pull-down assays (Figure 4E).
The N45 residue in σ^G may contribute to the interaction with CsfB. If so, however, this contact does not seem to be essential because the N45A substitution did not result in increased activity of σ^G in vivo, and caused only a small reduction in the ability of CsfB to interact with σ^G (Figure 4). Additional mutagenesis studies may illuminate if and how the N45 residue contributes to the interaction with CsfB, and how the N45E substitution interferes with the interaction. CsfB is likely to contact σ^G at other positions, and these other contact sites are likely to be present in σ^F as well. First, because no other single mutation was found within the first 150 residues of σ^G that would affect its activity in vivo and second, because while incapable of binding to wild type σ^F ([20]; this work), CsfB bound efficiently to σ^FE39N (see also below). The location of the N45 residue within region 2.2 of σ^G and its role in permitting binding by CsfB, is also consistent with previous work in which a σ^F/σ^G chimeric protein allowed the target for CsfB to be mapped within the first 77 residues of σ^G [20]. The N45 residue is invariant among σ^G orthologues of *Bacillus* species and related organisms but less conserved among the σ^G proteins of the Clostridia (Figure 1C). These observations highlight the importance of N45 (and homologous residues) in a sub-group of sporeformers including *B. subtilis* and related organisms, in which σ^G is regulated by the anti-sigma factor CsfB.

The N45E substitution may also affect a contact with the β-subunit of core RNA polymerase

The observation that the N45E substitution reduces binding of CsfB to σ^G provides a plausible explanation for the increased

Figure 6. Interactions of CsfB with σ^F and σ^FE39N. Panels A and B show the results of a colony lift (A) or a quantitative assay on liquid medium (B) for the detection of lacZ transcription in yeast strains expressing fusions of CsfB to the activation domain (AD; two colonies are shown) and fusions of σ^F or σ^FE39N to the binding domain (BD) of GAL4. Negative controls (“-”) included BD and AD expressed from empty vectors. β-galactosidase activity was detected as described in the legend for Figure 4. The results in B are the average of three independent experiments. Panel C shows the efficiency of sporulation of strains bearing a wild type copy of the σ^F operon, or a copy with the σ^FE39N allele, at amyE. In addition, the strains carry the cfr gene inserted at the thrC locus under the control of the IPTG inducible P_{spac} promoter (Table S1). The two strains (P_{spac-csfB} spolAABC wt and P_{spac-csfB} spolAABCE39N; NB: the third cistron of the spolA operon, also called sigF, codes for σ^F) were grown in DSM in the presence (+) or in the absence (−) of IPTG and the titer of heat resistant spores measured 18 hours after the onset of stationary phase (gray bars, viable cells; white bars, heat resistant cells). Panel D, shows the quantitative analysis of GFP expression in strains similar to those described for panel C, except that they additionally carry a fusion of the σ^F-controlled yuiC promoter to gfp. The two strains (P_{spac-csfB} sigFwtP_{puc-gfp}; gray bars; P_{spac-csfB} sigFE39N P_{puc-gfp}, white bars) were grown in sporulation medium (DSM) in the presence of IPTG and samples taken at the indicated times (hours) after the onset of stationary phase for scoring the number of cells showing GFP expression by fluorescence microscopy.

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activity of $\sigma^G$E in vivo. However, we cannot at present discard the possibility that the N45E alteration, which affects a residue positioned within conserved region 2.2, also increases binding of $\sigma^G$ to core RNA polymerase. The position homologous to N45 is often occupied by an acidic residue in proteins of the $\sigma^G$ family of sigma factors (the $\sigma^G$ orthologues of Bacillus species and related organisms being a conspicuous exception), and in the crystal structure of the $\sigma^G$-containing RNA polymerase holozyme from Thermus aquaticus [45], E189 (homologous to N45 in the $\sigma^G$ protein of B. subtilis) is involved, with other neighboring residues, in a direct contact with residue K159 in the $\beta$ subunit (Text S1 and Figure S6). An asparagine residue, as is found in $\sigma^G$, could also contribute to the interaction with $\beta$ at this site. However, an acidic residue would most likely make a stronger, electrostatic, contribution to the interaction. This in turn suggests that the N45E substitution could also enhance the activity of $\sigma^G$ by favoring interaction with the $\beta$ subunit of core RNA polymerase. If so, then the regulation of $\sigma^G$ activity in vivo could involve competition between CsfB and $\beta$ for binding to $\sigma^G$. In any event, the possible contact involving N45 and $\beta$ is in line with the view that one mechanism by which anti-sigma factors function is by occluding sigma-core binding interfaces [46,47]. Two of the mutations known to impair binding of SpoIIAB to $\sigma^G$ map within region 2.2, and mark residues that are conserved in $\sigma^G$ [24,48]; see also Figure 1B). This suggests that SpoIIAB and CsfB may use partially overlapping interfaces in binding to $\sigma^G$ and may explain the competition between the two anti-sigma factors for binding to $\sigma^G$ under certain conditions [20,28,48]. However, $\sigma^{GN45E}$ was still bound by SpoIIAB and was still susceptible to SpoIIAB in vivo. Therefore binding of SpoIIAB to $\sigma^G$ does not seem to require the N45 residue.

Discrimination between $\sigma^G$ and $\sigma^G$

The strict conservancy of N45 among $\sigma^G$ proteins of other Bacillus species and related organisms, together with its nearly absolute exclusion from orthologues of $\sigma^G$, suggests an important, conserved role for this residue. CsfB does not seem to negatively modulate the activity of $\sigma^G$, consistent with its inability to bind to this $\sigma$ factor [20,27,28,38]; this work). Because the E39N substitution is sufficient to allow binding of CsfB to $\sigma^G$, the E39/N45 position in the $\sigma^G$/$\sigma^G$ families of proteins seems critical for the discrimination by the CsfB anti-sigma factor. Perhaps strengthening this idea, the only exception to the rule that an N is excluded from the critical position in $\sigma^G$ is B. clausii (Figure 1C), but in this organism no csfB orthologue could be identified (not shown).

Recently, a protein related to CsfB, and termed Fin, was shown to inhibit the activity of $\sigma^G$ and to play an important role in promoting the switch from $\sigma^G$ to $\sigma^G$ in the forespore [38]. It is possible that the N45/E39 residues are functionally equivalent to N45 in $\sigma^G$, if so, and because an acidic residue (E) is found at the position equivalent to N45 in $\sigma^G$, it follows that in the context of the $\sigma^G$ protein binding by CsfB is likely to involve other residues.

Materials and Methods

Strains and general methods

The B. subtilis strains used in this work are congenic derivatives of the Spo+ strain MB24 (tpcG2 metC3), and are listed in Table S1. The plasmids used in strain construction are described in the sections below and in Text S1. LB medium was used for growth or maintenance of E. coli and B. subtilis, and sporulation was induced by growth and exhaustion in Difco sporulation medium (DSM) [24]. The Quick Change site-directed mutagenesis system (Stratagene) was used for the generation of all site-specific mutations, which were always confirmed by sequencing.

Mutagenesis of the sigG gene

We used pMS45, containing the sigG gene [24] and sigG-specific primers (all primers are listed in Table S2) to convert the residues highlighted in Figure 1B (orange and red circles) into the aminoacid found in $\sigma^F$. The various mutations were then transferred to the sigG locus by asporulation as has been observed that certain mutations cause a greater increase in the activity of $\sigma^G$ when sigG is located at an heterologous locus such as amyE [27]; our unpublished observations). For conformation, pMS45 and its derivatives carrying the different sigG mutations, together with chromosomal DNA from AH6566 (ΔsigG ΔynrC: P<j>α-gal [ΔespE: P<j>α-gal-lac]] were used to co-transform strain AH2452 (ΔsigG ΔespE: P<j>α-gal-lac]] with selection to CmR. Spo+ congeners appeared at a frequency of about 3%. One congrant for each sigG allele for which the presence of the desired mutation was confirmed by PCR and sequencing was kept for further study. Mutants that showed increased β-galactosidase production from the P<α-gal-lac]] reporter fusion were identified on LB plates containing 5-bromo-4-chloro-3-indolyl-b-D-galactopyranoside (X-Gal).

Promoter and reporter gene fusions

The construction of fusions of the xylose-inducible xylA promoter to different sigG alleles, and of csfB- zeo, -yfp and lacZ fusions is described in detail in Text S1, accompanying this article.

Construction of the sigF E39N mutant

First, the entire spoIIB operon was PCR amplified with primers sigF219D and sigF2032R (Table S2 lists all primers used in this study), the 1813 bp product digested with EcoRI and SalI and inserted between the same sites of pAS2-1 (Clontech) yielding plasmids pMS387 and pMS388. The various mutations were then transferred to the sigF locus by asporulation as has been observed that certain mutations cause a greater increase in the activity of $\sigma^G$ when sigF is located at an heterologous locus such as amyE [27]; our unpublished observations). For conformation, pMS45 and its derivatives carrying the different sigF mutations, together with chromosomal DNA from AH6566 (ΔsigF ΔynrC: P<j>α-gal [ΔespE: P<j>α-gal-lac]] were used to co-transform strain AH2452 (ΔsigF ΔespE: P<j>α-gal-lac]] with selection to CmR. Spo+ congeners appeared at a frequency of about 3%. One congrant for each sigF allele for which the presence of the desired mutation was confirmed by PCR and sequencing was kept for further study. Mutants that showed increased β-galactosidase production from the P<α-gal-lac]] reporter fusion were identified on LB plates containing 5-bromo-4-chloro-3-indolyl-b-D-galactopyranoside (X-Gal).

Yeast two-hybrid analysis

The coding regions of sigG, sigF and csfB were PCR amplified with primers sigF219D and sigF2032R (Table S2 lists all primers used in this study), the 1813 bp product digested with BamHI and HindIII and inserted between the same sites of pDG364 [50]. This created pMS393. Next, primers sigFE39ND and sigFE39NR were used to substitute the glutamate codon at position 39 of the sigF gene in pMS393 by an asparagine codon, which resulted in pMS394.

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between the same sites of pACT2 (Clontech) yielding plasmid pMS356. Mating of S. cerevisiae strains and detection of β-galactosidase activity were performed as described before [31].

Overproduction and purification of SpoIAB

The spoIAB coding region was PCR amplified with primers spoIAB1890D and spoIAB6980R. The PCR product was digested with BamHI and XhoI and inserted between the same sites of pET30a (+) (Novagen) creating pMS111, in which the sequence for the His6 tag was introduced between the first and second codons of spoIAB. pMS111 was introduced into competent cells of BL21 (DE3) pLysS (Novagen). Growth, induction, and lysis preparation was essentially as described [52]. The His6-SpoIAB fusion protein was partially purified on His-Trap chelating columns as described by the manufacturer (Amersham Pharmacia Biotech) and used to raise a polyclonal anti-SpoIAB antibody in rabbits (Eurogentec, Belgium).

Overproduction and purification of CsfB

First, primers cslB191D and cslBstrepR, which include the sequence coding for the Stop 2 tag (IBA GmbH) were used to PCR amplify the coding region of cslB. The resulting PCR product was digested with NolI and BamHI and cloned between the same sites of pET16b (Novagen) to create pMS350, which was then transformed into E. coli strain BL21 (DE3). The E. coli expression strain was grown to mid-log phase in LB (0.6 optical density at 600 nm), induced with 1 mM isopropyl-D-thiogalactopyranoside (IPTG), and grown for 3 h before harvesting the cells. The cell pellets were resuspended in 3 ml portions of buffer A (100 mM NaCl, 10 mM Tris pH 8.0, 10% glycerol) per 50 ml of induced culture and lysed in a French pressure cell (18,000 lb/in²). The lysate was centrifuged to remove cell debris. CsfB-Stop 2 tag was purified on Strep-Tactin Sepharose columns following the manufacturer instructions (IBA GmbH). The metal content of the purified protein was analyzed by atomic absorption.

GST pull-down experiments

Primers sigG2016D and sigG2964R were used to PCR amplify the coding regions of sigG, sigGN45A and sigGN45E from pMS45, pJS4, and pJS2 (see above). The PCR products were digested with BglII and XhoI and cloned between the same sites of pGEX4T-3 (GE Healthcare) to create pMS357, pMS356, and pMS357, respectively, which bear in-frame N-terminal GST fusions to the different forms of σG. Derivatives of BL21(DE3) bearing each of these plasmids or pGex4T-3 (GST-alone) were transformed into E. coli, strain BL21 (DE3). The expression was monitored during sporulation in the following strains: 

- ΔyycR
- Δcfp
- ΔsspE
- ΔG

Overproduction of CsfB

For the CsfB interaction assay, 100 nM of purified CsfB-Strep II tag was incubated for 30 min at room temperature with the glutathione Sepharose beads complexed with the GST fusion proteins or with glutathione Sepharose beads alone. The mixtures were washed three times with buffer B (above) and resuspended in a final volume of 30 μl. The samples were subjected to SDS-PAGE and immunoblotting. An anti-Strep 2 tag polyclonal antibody was used at a 1:1000 dilution (IBA GmbH). For graphical representation of the data, the immunoblots were scanned and analyzed using the ImageJ software (http://rsbweb.nih.gov/ij).

Accumulation of σG

Immunoblot analysis was used to monitor the accumulation of σG during growth or sporulation as previously described [17]. An anti-σA antibody was used as described before [36].

β-Galactosidase assays

β-Galactosidase activity was assayed with the substrate o-nitro-β-D-galactopyranoside (ONPG), with enzyme activity expressed in Miller units [52].

Fluorescence microscopy

Samples (0.6 ml) of LB or DSM cultures were collected, resuspended in 0.2 ml of phosphate-buffered saline (PBS) and the membrane dye FM4-64 (Molecular Probes) added to a final concentration of 10 μg ml⁻¹. Microscopy was carried out as described previously [53]. Quantitative analysis of fluorescence intensity was done using the MetaMorph software package (MDS Analytical Technologies). Data was analyzed and plotted using the "R" statistical computing and graphics software package (www.r-project.org).

Supporting Information

**Figure S1** Panel A shows the sequence alignment of the subregion from σG of B. subtilis with the same region of σG from B. subtilis and σA from E. coli. The amino acids (F91 and Y94) of σG changed to alanine are highlighted. Panel B shows the expression of a σG-dependent P_σg^-lac_2 fusion during stationary phase in DSM in the following strains: wild type background (AH6567, ΔyycR-P_σg^-cfp ΔσgE-P_σg^-lac_2, closed circles), the σG^_P_yycR^_A_1^A_A mutant (AH6539, sigGF91A/Y94A ΔyycR-P_σg^-cfp ΔσgE-P_σg^-lac_2 open circles). Samples were collected every hour during stationary phase in DSM and assayed for β-galactosidase activity (shown in Miller Units). Panel C shows the immunoblot analysis of σG accumulation during sporulation in a wild-type background (AH6567, ΔyycR-P_σg^-cfp ΔσgE-P_σg^-lac_2, panel E), and in the σG^_P_yycR^_A_1^A_A mutant (AH6539, sigGF91A/Y94A ΔyycR-P_σg^-cfp ΔσgE-P_σg^-lac_2, panel F). Samples from sporulating cultures were collected at the onset of stationary phase in DSM and at hourly intervals thereafter, as indicated by the numbers above the lanes. Lanes labelled “ΔSp” in all panels contain an extract prepared from a ΔsigG deletion mutant at hour 4, as a control for the specificity of the antibody. σA levels were monitored as a control for loading. The position of σG^ and σA is indicated by arrowheads.

**EPS**

**Figure S2** Panel A, expression of a σG^^-dependent P_σg^-GFP_2 fusion was monitored during sporulation in the following strains:
wild type background AH3447 (ΔspoIIA;P_spoIIC-lacZ, closed squares), and σ^{GN45E} mutant AH6610 (sigGN45E ΔspoIIA;P_spoIIC-lacZ, open squares). Samples from stationary phase cells in DSM were collected every hour and assayed for β-galactosidase activity (shown in Miller Units). Panel B; SpoIAB inhibits the activity of σ^{G} or σ^{GN45E} in vivo. B. subtilis strains carrying a P_spoIIA-lacZ fusion as a reporter of σ^{G} activity, a P_spoIIC-lacZ fusion to allow the inducible production of SpoIAB, and xylose-inducible fusions to sigG (AH2492; P_xylA-sigG), sigGE156K (AH2493; P_xylA-sigGE156K) or sigGN45E (AH6556, P_xylA-sigGN45E) were grown in LB in the presence (1 mM) or in the absence of IPTG. Samples were taken at indicated times during growth and assayed for β-galactosidase production. The graph shows the percentage of the activities of σ^{G} (black bars), σ^{GE156K} (white bars) or σ^{GN45E} (gray bars) found in the absence and in the presence of IPTG. Panel C documents the accumulation of σ^{G} and σ^{GN45E} during stationary phase in DSM using an anti-σ^{G} antibody. The accumulation of σ^{G} and σ^{GN45E} was examined in a wild-type background and in a ΔcfsB mutant. Samples were collected at the onset of stationary phase in DSM and at hourly intervals thereafter, as indicated by the numbers above the lanes. The lanes labeled “ΔG” in all panels contain an extract from a sigG deletion prepared at hour 4, as a control for the specificity of the antibody. σ^{A} levels were monitored as a loading control. The position of σ^{A} and σ^{G} is indicated by arrowheads. (EPS)

**Figure S3** Time-lapse microscopy of P_spoIIC-cfp. Sporulating cells were incubated on agarose pads at 30 °C. Images sequences were initiated 2 hours after the onset of sporulation in DSM and the first image was set to t = 0 min. Minutes after t = 0 is indicated in the lower right corner of each CFP image. The upper panels show phase contrast; the lower panels show whole cell CFP. The arrow indicates a cell with whole cell CFP accumulation. (EPS)

**Figure S4** Panel A: The B. subtilis CsfB protein shows structural similarity to several proteins containing zinc finger domains. Several of these proteins belong to the family of nuclear hormone receptor transcriptional regulators, with one of the most significant hits to the human vitamin D3 receptor protein (pdb code: 1kk2). The critical Cys are shown in blue (numbering is from the beginning of the sequences shown); other identical (yellow) or conserved residues (green) are also highlighted. Panel B; an E. coli strain expressing a C-terminal fusion of the Step II tag to CsfB under the control of the T7lac promoter was grown in minimal medium in the presence of iron (lanes 1–3) or zinc (lanes 4–6) and induced with 1 mM IPTG for 2 hours. Lanes are as follows: 1 and 4, total extract; 2 and 5, insoluble fraction; 3 and 6, soluble fraction. Panel C depicts the induction of CsfB-Step II tag by an auto-induction regime, and its purification. A strain with an “empty” vector is used as a control for the auto-induction (lanes 1, 3, and 5). Lanes are as follows: 1 and 2, total extract; 3 and 4, insoluble fraction; 5 and 6, soluble fraction; 7, protein (CsfB-Step II tag) purified after a streptavidin affinity column. Panel D depicts the time-course of oxidant-induced (1 mM H2O2) zinc release by purified CsfB, as monitored after reaction with 4-(2-pyridylazo) resorcinol (PAR), by measuring the OD at 500 nm. No zinc is released when the protein is kept reduced in the presence of DTT. (EPS)

**Figure S5** Panel A: growth curves for strain AH6689 in LB containing the indicated xylose concentrations. Panel B; expression of P_xylA-sigG and cspF-sigG was monitored in the same cells, by fluorescence microscopy, at the onset of stationary phase in LB. The strain used (AH6689) additionally carries a deletion of the sigG gene, and a second copy of the wild type sigG gene under the control of the xylose inducible P_xylA promoter inserted at the amyE locus. Cells were grown in the presence of different concentrations of xylose, as indicated (NB: images obtained in the presence of 0.001% xylose are not represented for simplicity). Scale bar; 2 μm. Panel C; quantitative analysis of CFP and YFP expression for the AH6689 strain (as in panel B), at the xylose concentrations indicated in panel A. The top graph shows the correlation between the YFP (cspF-sigG) and CFP (P_xylA-sigG) signals for the various concentrations of xylose. The middle and bottom graph show a cumulative frequency distribution of the YFP and CFP signals across the population. In all three panels the fluorescence intensity is shown in arbitrary units; 100 cells were scored. The legend applies to all three graphs. (EPS)

**Table S1** *Bacillus subtilis* strains used in this work. (PDF)

**Table S2** Oligonucleotide primers used in this work. (PDF)

**Text S1** Supporting Materials and Methods, Results and Discussion. (DOC)

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**Author Contributions**

Conceived and designed the experiments: MS CPM AOH. Performed the experiments: MS GR JS. Analyzed the data: MS GR JS JC CPM AOH. Wrote the paper: MS AOH.

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