A New Way of Sensing: Need-Based Activation of Antibiotic Resistance by a Flux-Sensing Mechanism

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ABSTRACT Sensing of and responding to environmental changes are of vital importance for microbial cells. Consequently, bacteria have evolved a plethora of signaling systems that usually sense biochemical cues either via direct ligand binding, thereby acting as “concentration sensors,” or by responding to downstream effects on bacterial physiology, such as structural damage to the cell. Here, we describe a novel, alternative signaling mechanism that effectively implements a “flux sensor” to regulate antibiotic resistance. It relies on a sensory complex consisting of a histidine kinase and an ABC transporter, in which the transporter fulfills the dual role of both the sensor of the antibiotic and the mediator of resistance against it. Combining systems biological modeling with in vivo experimentation, we show that these systems in fact respond to changes in activity of individual resistance transporters rather than to changes in the antibiotic concentration. Our model shows that the cell thereby adjusts the rate of de novo transporter synthesis to precisely the level needed for protection. Such a flux-sensing mechanism may serve as a cost-efficient produce-to-demand strategy, controlling a widely conserved class of antibiotic resistance systems.

IMPORTANCE Bacteria have to be able to accurately perceive their environment to allow adaptation to changing conditions. This is usually accomplished by sensing the concentrations of beneficial or harmful substances or by measuring the effect of the prevailing conditions on the cell. Here we show the existence of a new way of sensing the environment, where the bacteria monitor the activity of an antibiotic resistance transporter. Such a “flux-sensing” mechanism allows the cell to detect its current capacity to deal with the antibiotic challenge and thus precisely respond to the need for more transporters. We propose that this is a cost-efficient way of regulating antibiotic resistance on demand.
tion is regulated by two-component systems whose HKs lack discernible ligand-binding domains and instead form a sensory complex with the transporter (9, 10). The signaling process is best understood in *Bacillus subtilis*, where the two-component system BceRS and its associated ABC-transporter BceAB together sense and counteract the deleterious effects of bacitracin and several other antimicrobial peptides interfering with the lipid II cycle of cell wall biosynthesis, by triggering a 500-fold increase in the expression of the *bceAB* transporter operon (5, 9, 11) (Fig. 1a).

To characterize the regulatory role of the transporter, here we took a systems approach, combining mathematical modeling with experiments probing the time-resolved, dose-dependent response of the Bce system to its substrate bacitracin. We show that signaling within the Bce system operates by a flux-sensing mechanism, monitoring the activity of individual transporters. Our model allowed us to derive a unique response signature for a flux sensor, which was experimentally validated. Moreover, the model was able to predict the antibiotic sensitivity of cells depending on transporter expression, leading us to propose that flux sensing serves as a novel produce-to-demand strategy to control antibiotic resistance in changing environments.

**RESULTS**

ABC transporter production rapidly adapts to a wide range of bacitracin inputs. To obtain detailed quantitative information on the regulatory dynamics of the Bce system, we first studied the relationship between the external antibiotic concentration and the transcriptional response of the target promoter $P_{bceA}$. To this end, exponentially growing SGB073 cells (wild-type *B. subtilis* carrying a chromosomally integrated $P_{bceA}$-*luxABCDE* reporter) were exposed to sublethal concentrations of bacitracin. At virtually all bacitracin concentrations tested, luciferase activity initially rose rapidly upon antibiotic addition, before leveling off to reach a plateau 20 to 30 min after induction (Fig. 2A). A plot of the plateau level against antibiotic concentration revealed that the system's response quickly adapted to a wide dynamic range of antibiotic

FIG 1  Schematic of conceivable sensory scenarios employed by the BceRS-BceAB system. In an external sensing scenario (a), the ABC transporter BceAB might act as a scaffold that keeps the histidine kinase BceS in an active conformation, which would allow BceS to perceive the extracellular concentration of bacitracin (red symbols). Since up-regulation of BceAB is not expected to change the extracellular concentration of bacitracin, the rate of gene expression should be independent of the BceAB level in this scenario (no feedback). In an internal sensing scenario (b), BceAB might be required to translocate bacitracin into the cytoplasm where BceS could sense its abundance. Here, up-regulation of BceAB should lead to an increased rate of bacitracin influx, which would in turn lead to further up-regulation of BceAB expression (positive feedback). In a flux-sensing scenario (c), BceAB itself is the true sensor, which directly signals its transport activity to BceS. In such a scenario, up-regulation of BceAB would reduce the load experienced by each individual transporter and thereby reduce signaling via BceS (negative feedback). (d) Schematic depiction of the expected impact of different levels of the BceAB transporter (low, red curves; high, green curves) on dose-dependent $P_{bceA}$ activity.
input (0.1 to 100 µg/ml bacitracin) (Fig. 2B). Such gradual, homeostatic control of target gene expression is often found in regulatory systems that exploit negative-feedback mechanisms, while positive-feedback regulation frequently enables switch-like or even hysteretic responses (12). The presence of a negative feedback mechanism was also suggested by our observation that the P\textsubscript{bceA} promoter activity reached its steady-state value within a short time (20 to 30 min) (Fig. 2A) relative to the cell doubling time of ~70 min (see Fig. S1 in the supplemental material), as negative-feedback control is known to reduce the response time of genetic circuits (13).

To elucidate the source of this apparent feedback effect, we considered three plausible roles of the transporter in the regulatory pathway. (i) In the simplest scenario, the transporter acts as a "hydrophobic vacuum cleaner" (17), conferring resistance by clearing the target from the inhibitory grip of the antibiotic (Fig. 1c) (7, 18). In such a scenario, increasing BceAB copy numbers should alleviate the load experienced by individual transporters (Fig. 1c), resulting in a negative feedback of BceAB on its own expression. Thus, qualitatively, a flux-sensing scenario best reflects the observed dynamics of P\textsubscript{bceA} activation.

The behavior of the wild-type system is compatible with a mathematical model for relative flux sensing. To test if the proposed flux-sensing mechanism can quantitatively explain the regulatory dynamics in the Bce system, we developed a mathematical model, incorporating signal transduction via such a mechanism. Bacitracin is known to bind to its membrane-associated target molecule undecaprenyl-pyrophosphate (UPP), thus blocking the dephosphorylation and recycling of UPP in the lipid II cycle of cell wall biosynthesis (19). If we suppose that the ABC transporter BceAB catalyzes the release of bacitracin from UPP with Michaelis-Menten enzyme kinetics, the time-dependent concentration of the bacitracin-bound form of UPP, UPP-bac, can be described by a differential equation of the form

\[
\frac{d}{dt} [\text{UPP-bac}] = k^{\text{on}} [\text{bac}] [\text{UPPtot} - [\text{UPP-bac}]] - k^{\text{off}} [\text{UPP-bac}] - \frac{v_{\text{max}}}{K_m + [\text{bac}]}/K_m
\]

Here, [bac] is the externally applied bacitracin concentration, \(k^{\text{on}}\) and \(k^{\text{off}}\) are the spontaneous on and off rates for the binding of bacitracin to UPP, \(v_{\text{max}}\) is the total UPP level in the cell, \(J_{\text{bac}} = [\text{UPP-bac}]/(K_m + [\text{UPP-bac}])\) is the relative bacitracin load per BceAB transporter, and \(v_{\text{max}}\) and \(K_m\) are the maximal transport rate and Michaelis-Menten constant of BceAB, respectively (see Tables S1 and S2 in the supplemental material).

To implement the proposed flux-sensing mechanism in our model, we took into account that the expression of the two-component system operon bceRS is constitutive (see Fig. S2 in the supplemental material) and also that the interaction between the histidine kinase BceS and the BceAB transporter is bacitracin independent (9). Moreover, we verified that the overproduction of BceS did not significantly affect the MIC of a strain with constitutive BceAB expression (see Fig. S3 in the supplemental material), indicating that the transport activity of BceAB is not affected by the formation of the sensory complex with BceS in vivo. Thus, as long as BceAB molecules outnumber BceS molecules, so that BceS is the limiting component in complex formation, there should be a constant number of functional BceS-BceAB sensory complexes in the cell, while the number of free BceAB transporters should change with increasing total transporter levels. Under inducing conditions this is a safe assumption, because we can readily detect the presence of BceA, but not of BceS, using Western blotting or

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\text{Luciferase activity [RLU/OD]}
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\text{Bacitracin [g/ml]}
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fluorescent protein fusions (our unpublished observations). Under noninducing conditions, both proteins are below our current detection limit and therefore not accessible to quantification. Based on the relative promoter strengths of \( P_{\text{bceA}} \) (see Fig. S2 in the supplemental material) and \( P_{\text{xylA}} \) (Fig. 2A), it could well be that uninduced cells possess more kinases than transporters. Nevertheless, within our mathematical model we assume that the number of sensory complexes does not change over time and thus that BceS always monitors the activity of a fixed number of transporters. While this assumption might be inaccurate in the early phase of induction, BceAB levels are expected to quickly exceed those of BceS such that the model should well reflect the experimental conditions shortly after induction.

Based on these considerations, we assume within our model that BceS signals the load of individual transporters to the response regulator BceR, such that the level of the active (phosphorylated) form of BceR is proportional to the bacitracin load per transporter, \( J_{\text{bac}} \). Following a thermodynamic model for transcriptional regulation (20), activation of gene expression from the \( P_{\text{bceA}} \) promoter by phosphorylated BceR can then be formulated in terms of \( J_{\text{bac}} \), such that the dynamic equations for \( bceA \) mRNA concentration, \( [m] \), and BceAB protein level, \([BceAB]\), read

\[
\frac{d}{dt}[m] = \alpha \frac{1 + \omega (J_{\text{bac}}/\kappa)^n}{1 + (J_{\text{bac}}/\kappa)^n} - \lambda [m] \tag{2}
\]

\[
\frac{d}{dt}[\text{BceAB}] = \beta [m] - \delta [\text{BceAB}] \tag{3}
\]

Here, \( \alpha \) is the basal transcription rate, \( \omega \) is the ratio of maximal to basal promoter activity, \( \lambda \) is the mRNA degradation rate, and \( \kappa \) is a measure of the relative flux at which \( P_{\text{bceA}} \) is activated. The Hill exponent \( (n) \) in turn reflects all forms of cooperativity in stimulus perception and signal transduction, as well as in BceR-DNA binding and recruitment of RNA polymerase. Finally, \( \beta \) is the translation rate and \( \delta \) is the protein dilution rate due to cell doubling. The dynamic equations for luciferase reporter expression were formulated analogously to equations 2 and 3 and are given in Materials and Methods.

We then asked whether the data in Fig. 2 were in quantitative agreement with our mathematical model. To this end, all known and measured model parameters were fixed to their physiological values (see Table S1 in the supplemental material), the remaining ones were confined to physiological intervals (see Table S2 in the supplemental material), and then the model was fitted to the experimental dose-response in Fig. 2B (see Materials and Methods for details of the fitting procedure). Overall, we found that the dynamic behavior of the model closely resembled the rapid adaptation kinetics observed in the experimental time series (Fig. 2A). Likewise, the model adequately captured the gradual increase of the experimental dose-response characteristics over a wide range of input levels (Fig. 2B). These findings provided the first quantitative indication that the Bce system does in fact implement a flux-sensing mechanism that monitors the bacitracin load per BceAB transporter. The agreement between theory and experiment in the early phase (0 to 15 min) after induction further demonstrates that the model assumption of a constant number of sensory complexes per cell was reasonable: if BceAB were initially less abundant than BceS, the number of sensory complexes should increase upon induction of BceAB production, which should result in a positive feedback on signaling. Such a positive feedback should cause a lag in the response while the number of sensory complexes is still very low, followed by a rapid increase in signaling and more complex forms are formed. Such an effect is not visible in our data (Fig. 2A), showing that the window in which the number of sensory complexes is not constant is short and cannot be resolved by the luciferase reporter.

Predicting the signature of a relative flux sensor. One key feature of the proposed flux sensor model is that up-regulation of BceAB leads to a reduction of the bacitracin load per transporter, which ultimately down-regulates transcription of \( bceA \). Hence, if the model was correct, disabling this negative autoregulation of BceAB should abolish the graded response to bacitracin. Consequently, constitutively supplying the cell with a fixed number of transporter molecules should provide an alternative means of distinguishing between the three different signaling scenarios detailed above. For a relative flux-sensing mechanism, in cells with few transporters, the load per transporter should be saturated at low bacitracin concentrations, leading to a highly sensitive response (Fig. 1d, right). Conversely, cells with many transporters should respond more sluggishly (Fig. 1d, right), because more bacitracin is required to produce a high load per transporter. For an intracellular sensing mechanism, the opposite behavior is expected: cells with a high level of BceAB should respond more sensitively than those with few transporters, as the total amount of bacitracin translocated increases with the number of transporters present (Fig. 1d, center). Last, for an extracellular-concentration-sensing mechanism, the dose-response behavior should not be affected by alterations in the level of the transporter (Fig. 1d, left). In fact, this last situation was recently reported for the DctA/DcuS sensor complex of \( E. coli \) (21), in which the transporter DctA merely acts as an activity switch for the HK DcuS.

When we modified our mathematical model to accommodate constitutive production of the transporter, the predicted dose-response behavior was altered in two respects. First, the elimination of autoregulation of the level of BceAB results in a more switch-like response of the \( P_{\text{bceA}} \) promoter to increasing bacitracin concentrations (Fig. 3a). This sharp response is due to the fact that the fit to the data for the wild type in Fig. 2 yielded a Hill exponent \( (n) \) of 7.5 ± 0.2, suggesting that signal transduction and regulation of \( P_{\text{bceA}} \) exhibit a high degree of cooperativity. Second, when the copy number of the transporter is changed, the model predicts a shift in the dose-response curves consistent with the signature of a flux sensor: in cells that constitutively express low levels of BceAB, the promoter is triggered by low bacitracin concentrations (Fig. 3a), while much higher concentrations of the antibiotic are required to activate \( P_{\text{bceA}} \) in cells that synthesize large amounts of BceAB (Fig. 3a).

In order to test these predictions experimentally, we constructed a strain (SGB218) in which the endogenous \( bceA \) locus had been deleted, and replaced by a chromosomally integrated construct driven by the xylose-inducible promoter \( P_{\text{xylA}} \). In addition, this strain carries the \( P_{\text{xylA}}-\text{luxABCDE} \) reporter used above. We previously quantified the dose-response characteristics of \( P_{\text{xylA}} \) (22). It showed a basal transcription level ~30-fold higher than that driven by \( P_{\text{bceA}} \) and could be activated up to ~100-fold by increasing the xylose concentration in the medium (Fig. 3b). Based on these data, we selected five xylose concentrations (0%, 0.005%, 0.01%, 0.03%, and 0.2%) that resulted in markedly different \( P_{\text{xylA}} \) activities. Incorporation of these promoter activities into our mathematical model led to distinct BceAB protein levels
for each xylose concentration and thus also to the parameter-free predictions for the shifts in the activation threshold of $P_{bceA}$ discussed above (Fig. 3a).

Figure 3c shows the bacitracin-dependent $P_{bceA}$ activity of SGB218 cells grown in the presence of the selected xylose concentrations. Strikingly, we found that both the theoretically predicted abrupt onset of activation and the shift in induction threshold with increasing xylose concentration were quantitatively reflected in our experimental results. The latter becomes manifest, for instance, when EC10 values (the bacitracin concentration at which the dose-response curves in panel c reach 10% of their maximal activity) are shown as a function of xylose concentration (red symbols). (c) Experimental $P_{bceA}$-luxABCDE dose-response curves in strain SGB218, in which the endogenous chromosomal bceAB locus has been deleted and transporter expression is constitutively driven from a chromosomally integrated xylose-dependent $P_{xylA-bceAB}$ construct (colored symbols). The wild-type dose-response curve (black symbols) was derived from strain SGB073. (d) Data from panels a and c with the x axis rescaled by the respective EC10 values. For details, see the text.
occupied by a dimer of BceR, indicating that a total of four BceR molecules are required for promoter induction, which could further enhance cooperativity in signaling.

The model successfully predicts inhibitory concentrations of bacitracin. Bacitracin acts by binding to the lipid carrier UPP and preventing its dephosphorylation (19). Due to its essentiality for cell growth, a certain minimal fraction of free lipid carrier is needed to maintain cell wall biosynthesis at a given growth rate, and blocking a larger fraction of UPP is thus lethal. Intuitively, expression of the BceAB transporter is expected to release UPP from the inhibitory grip of bacitracin and thereby keep a significant fraction of UPP bacitracin free. Hence, BceAB expression should directly affect the bacitracin-bound UPP levels in the cell and, with that, the cellular sensitivity to inhibition by bacitracin.

To analyze the physiological implications of the flux-sensing mechanism, we first calculated the fraction of bacitracin-bound UPP in the cell using our mathematical model. For the wild-type strain employing bacitracin-dependent feedback regulation of bceAB expression, the fraction of bacitracin-bound UPP first increases rapidly with the applied concentration of the antibiotic (Fig. 4a). As soon as BceS detects a significant bacitracin flux via the BceAB transporter (at ca. 0.3 µg/ml bacitracin), transporter production is up-regulated and the rate of accumulation of bacitracin-bound UPP is slowed. Based on the bacitracin concentration needed to inhibit the growth of the wild type (ca. 200 µg/ml), we calculated the lethal fraction of bacitracin-bound UPP to be 90% (Fig. 4a). In the absence of BceAB transporters, our model predicted that the fraction of bacitracin-bound UPP increases rapidly with the applied bacitracin concentration and reaches the lethal 90% threshold at 2 µg/ml bacitracin (Fig. 4a). This is slightly below the experimentally determined MIC of 8 to 16 µg/ml for a strain with bceAB deleted. However, the difference is not surprising given that the model does not take into account residual bacitracin resistance caused, e.g., by the UPP phosphatase BccC and other members of the σM, σX, and σW regulons involved in the response of B. subtilis to cell envelope stress (24–26). In contrast to the homeostatic control seen in the wild type, for the strain with constitutive bceAB expression, the model predicted the binding curve to be of the same shape as in the absence of BceAB. However, the curves were shifted to ever-higher bacitracin concentrations the more transporter was present in the cell (Fig. 4a). Hence, the model also predicted that the higher the level of BceAB, the greater the antibiotic concentration required for killing (Fig. 4a).

To confront these predictions with experimental data, we assayed the reporter strains for growth inhibition by bacitracin. For this, growth rates were determined after addition of a range of bacitracin concentrations to exponentially growing cultures producing different levels of transporter. For each culture, increasing the added concentration of bacitracin first led to a significant decrease in growth rate (Fig. 4b) and eventually to complete cessation of growth or cell lysis, with higher concentrations being required to inhibit cells expressing bceAB at higher levels. Prediction of the lethal threshold concentration by the model approximately reproduced the observed relationship between growth inhibition and bceAB expression (dashed line in Fig. 4b). The steeper decline of the theoretical curve compared to the experimental data at low levels of BceAB can again be explained by the presence of alternative resistance determinants in B. subtilis, as discussed above. When we adjusted the model to the background resistance of a bceAB deletion-containing strain (here, 15 µg/ml), it accurately described the correlation between BceAB expression levels and inhibitory bacitracin concentration (solid line in Fig. 4b).

Our model does not distinguish between the cellular concentration of UPP-bacitracin complexes (i.e., the assumed transport substrate) and the true transport flux as input parameters, because binding kinetics and transport activity are mathematically equivalent in the Michaelis-Menten equation employed. This consideration becomes important in light of the possibility that BceAB might serve as a sensor without actually translocating any of its substrate. However, if BceAB were transport deficient, the concentration of UPP-associated bacitracin should always be proportional to the extracellular antibiotic concentration, regardless of the number of functional transporters in the cell. This is entirely inconsistent with the shifts in dose-response curves observed in cells expressing different amounts of BceAB (Fig. 3). Furthermore,
the good fit between observed growth inhibition by bacitracin and predicted lethal threshold at different transporter expression levels (Fig. 4) showed that the transporter indeed had an impact on the fraction of bacitracin-bound UPP and thus must be able to translocate its substrate.

Taken together, our theoretical and experimental data clearly indicate that a combination of relative flux sensing and concomitant negative feedback provides efficient homeostatic control over the level of bacitracin-bound UPP, allowing it to be maintained below the lethal concentration threshold over a range of antibiotic concentrations covering at least two orders of magnitude.

**DISCUSSION**

Bacteria can perceive their environment either directly, by monitoring the concentration of a relevant substance, or indirectly, by monitoring the effects on cellular physiology caused by a particular condition. We show here that sensing of transport flux of antimicrobial substances through a resistance pump presents a third and novel sensing strategy, by which the cell can directly monitor and respond to its current detoxification capacity. Through quantitative, time-resolved analysis of the dose-response dynamics, combined with mathematical modeling of the regulatory pathway, we obtained evidence that the Bce system of *B. subtilis* implements such a flux sensor, where the parameter monitored by the signaling system is the activity of individual BceAB transporters. This elegant mechanism permits continual assessment of the most critical parameter of antibiotic resistance, i.e., the cell’s current capacity to deal with the inhibitory effects of the applied drug. From a systems perspective, this parameter is far more relevant to the cell than the present concentration of the antibiotic; as long as the cell’s transport capacity is sufficient to detoxify the drug, there is no need for a further response even at high antibiotic concentrations. We therefore propose that flux sensing is a very cost-efficient regulatory strategy to control antibiotic resistance. To our knowledge, this is the first report of such a regulatory mechanism in any physiological context.

Over 200 Bce-like systems can currently be found in protein databases, and their components were shown to have coevolved (23). Combined with experimental confirmation of the transporter’s sensory role in all systems studied to date (8, 11, 27–29), this tight evolutionary correlation suggests conservation of the signaling mechanism. Flux sensing may therefore be a widespread regulatory principle in antimicrobial peptide resistance. Because this mechanism relies on the intricate process of communicating transport flux between proteins, it should, conceivably, be easy to disrupt and thus might constitute a prime drug target to counteract resistance in pathogenic bacteria possessing Bce-like systems, such as *S. aureus*, *E. faecalis*, *Listeria monocytogenes*, and *Clostridium difficile* (8, 23, 27, 30).

Our modeling approach not only has provided evidence for a flux-sensing mechanism but also has given access to important system variables that are difficult to quantify experimentally, most notably the fraction of bacitracin-bound UPP. Analysis of such “hidden” parameters can lead to highly relevant predictions for bacterial physiology, such as our calculation of the dependence between the bacitracin concentration required to inhibit growth and the expression level of the resistance determinant. Ultimately, such an approach may have important implications for the treatment of infectious disease caused by drug-resistant bacteria. Importantly, Bce-like systems have been shown to respond to a large variety of peptide antibiotics that interfere with different stages of cell wall synthesis, including lantibiotics such as nisin, but also the clinically relevant glycopeptides vancomycin and teicoplanin (6, 31, 32).

In summary, we report the first observation of transport flux sensing as an elegant way of implementing adaptation via negative feedback regulation. We propose that this represents a highly cost-efficient mode of gene regulation, finely adjusted to the current physiological needs of the cell. In the case of antibiotic resistance mediated by Bce-like systems, this need is an increased demand for detoxification. Future exploration of further systems employing transporters to control a signaling pathway will show if this mechanism can also be found in other physiological contexts.

**MATERIALS AND METHODS**

**Bacterial strains and growth conditions.** All strains used in this study are listed in Table S3 in the supplemental material. Strains were routinely propagated in Luria-Bertani (LB) medium. For all functional assays, *B. subtilis* was grown in chemically defined CSE medium (33), in which the carbon source was modified to provide constant growth rates over an extended period of time [3.3 g/liter (NH₄)₂SO₄, 29 mM KH₂PO₄, 70 mM K₂HPO₄, 1 × III’ salts (100× III’ salts is 0.232 g/liter MnSO₄·4H₂O, 12.3 g/liter MgSO₄·7H₂O), 50 mg/liter tryptophan, 22 mg/liter ammonium ferric citrate, 0.8% (wt/vol) potassium glutamate, 0.6% (wt/vol) sodium succinate, 2.5% (wt/vol) fructose]. Selective medium for *B. subtilis* contained kanamycin (10 mg/liter), chloramphenicol (5 mg/liter) or erythromycin (1 mg/liter) in combination with lincomycin (25 mg/liter) for macrolide-lincosamide-streptogramin B resistance (MLS’). Selective medium for *E. coli* contained ampicillin (100 mg/liter). Solid medium additionally contained 1.5% (wt/vol) agar.

**Construction of plasmids and strains.** All cloning was performed according to BioBrick standard RFC10 (http://hdl.handle.net/1721.1/45138) or RFC25 (http://hdl.handle.net/1721.1/45140). Plasmids, strains, and primer sequences are listed in Table S3 in the supplemental material. The *bceAB* operon of *B. subtilis* was adapted to the BioBrick standard by addition of prefix and suffix sequences according to a modified RFC25 standard (22) using PCR (primers TM2577 and TM2578). All internal PstI sites were changed from CTGCAG to CTTCAG and EcoRI sites from GAA TTC to GAGTTC by PCR overlap extension mutagenesis (34). Point mutations were chosen so to avoid any change in the encoded protein sequence. Cloning of the resulting fragment into the EcoRI and SpeI sites of pSB1A3 resulted in pNTSB103. The Pₚ₀₄ region of Pₓ was adapted for BioBrick cloning by the addition of RFC10 prefix and suffix sequences via PCR (primers iGEM134 and iGEM135) and cloning into the EcoRI and SpeI sites of pSB1A3, to generate pNTSB104. Subsequently, the *bceAB* operon was placed under the transcriptional control of Pₚᵧ by BioBrick assembly of the pNTSB103 and pNTSB104 inserts into the vector pSBSE (22), resulting in pNT2E01. To quantify target promoter activities, wild-type *B. subtilis* W168 was transformed with a transcriptional Pₚᵧ-luxABCD reporter construct, pSLux101 (35), producing strain SGB073. Introduction of the same reporter together with pNT2E01 into the *bceAB*: Kan deletion strain TMB035 produced strain SGB218.

**Luciferase assays.** Luciferase activities were assayed using a Synergy2 multimode microplate reader from BioTek (Winoski, VT) controlled by the software Gen5. Aliquots of culture (100 μl) were added to 96-well plates (black walls, clear bottoms; Greiner Bio-One, Frickenhausen, Germany), which were incubated at 37°C with medium-intensity agitation. Cell growth was monitored by measuring optical density at 600 nm (OD₆₀₀). For each individual sample, the OD₆₀₀ and relative luminescence units (RLU) (endpoint reads; 1-s integration time; sensitivity, 200) were background corrected by subtracting the respective values measured for wells containing 100 μl of CSE medium. RLU/OD₆₀₀ values were calculated for individual measurements. Means and standard deviations

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The text provided is a scientific discussion on the sensing of transport flux in bacterial resistance mechanisms, specifically focusing on the Bce system of *B. subtilis*. The authors highlight the importance of flux sensing as a regulatory mechanism that allows for continual assessment of the cell's ability to detoxify antibiotics, which is critical for antibiotic resistance. The study utilizes a combination of theoretical modeling and experimental data to support the hypothesis that flux sensing is a widespread regulatory strategy in bacterial physiology. The implications of this mechanism are discussed in the context of its potential use in understanding and treating antibiotic resistance in clinical settings.
of RLU/OD600 values were determined from at least three biological replicates.

To synchronize cultures, 10 ml of CSE medium in a 125-ml flask was inoculated with 0.2 ml of an overnight culture and incubated at 37°C with agitation (200 rpm) to an OD600 of 0.2 to 0.5. Cultures were then diluted in fresh CSE medium to an OD600 of 0.05 and transferred to 96-well plates. OD600 and luminescence were monitored every 10 min, and at an OD600 of ~0.1 (corresponding to an OD600 of ~0.4 in cuvettes with a 1-cm light path length), 5 μl of Zn2+ bacitracin was added to give the final concentrations indicated in the figure legends. Incubation was continued, and OD600 and luminescence were monitored every 5 min for 1 h. For controlled expression of bceAB in strain SGB218, xylose was added to all growth media at the final concentrations indicated in the figure legends.

Bacitracin sensitivity assays. The MIC of bacitracin for B. subtilis grown in CSE medium was determined by a broth dilution technique. Cultures were grown to stationary phase in CSE medium and then diluted (1:500) into fresh CSE medium containing different concentrations of Zn2+ bacitracin. Following 20 to 24 h of incubation at 37°C with agitation, the MIC was scored as the lowest concentration at which no growth was observed. Inhibition of growing cultures (Fig. 4b) was determined as follows. Cells of strain SGB218 were cultured with the indicated xylose concentrations and challenged with the final concentrations of Zn2+ bacitracin indicated in the figure legends as described for the luciferase assays above. Average growth rates (γ) were estimated from an exponential fit to the growth curve (OD600) from 0 h (bacitracin addition) to 1 h for each experimental condition. Growth inhibition was calculated as 1 – (γ/γmax), where γmax is the maximal growth rate at a given xylose concentration.

Mathematical model and parameter estimation. The minimal model for the dynamics of the bceAB operon in the wild-type strain SGB073 is described by equations 1 to 3. In constructing this model we made the simplifying assumption that the maximal amount of UPP in a cell, UPₚₑᵣₙ, is given by the sum of all intermediate forms of the lipid carrier molecule present in the cell (see Table S1 in the supplemental material for parameter values). Binding of bacitracin to UPP then leads to the accumulation of the bacitracin-bound form of UPP, UPP-bac, to the maximal amount (UPPₚₑᵣₙ). To model the constitutive expression of bceAB in strain SGB218, the flux-dependent transcription rate in equation 2 was replaced by a temporally constant transcription rate, which is determined solely by the concentration of externally supplied xylose:

\[ \frac{d}{dt} m_{xylose} = \alpha_{xylose} - \lambda m_{xylose} \]  

(4)

The xylose-dependent rate of bceAB transcription driven by Pxylose was modeled as \( \alpha_{xylose} = \alpha \times f(xylose)/bacitracin = 1 \), where \( \alpha \) is the rate of Pbac-controlled transcription in the absence of bacitracin and f(xylose) and g(bacitracin) are the experimental dose-response curves for Pxylose (Fig. 3b) and PBac (Fig. 2B), respectively. In addition, expression of the luxABCDE reporter genes in all strains is under the control of an ectopically integrated PBac promoter, which is assumed to follow the same transcriptional kinetics as the promoter at its native genomic locus (cf. equation 2):

\[ \frac{d}{dt} m_{lux} = \frac{1 + \frac{m_{bac}}{K + [bac]}}{1 + \frac{m_{bac}}{K + [bac]}} - \lambda_{lux} m_{lux} \]  

(5)

Here, \( m_{lux} \) is the luxABCDE mRNA, \( \lambda_{lux} \) is the associated degradation rate, and all other parameters are the same as in equation 2. Assuming that one of the proteins in the lux operon is rate limiting for light production, its dynamics is modeled by

\[ \frac{d}{dt} Lux = \beta m_{lux} - \delta_{lux} Lux \]  

(6)

where \( \beta \) is the translation rate and \( \delta_{lux} \) is the corresponding protein half-life. In addition, a multiplicative scaling factor, \( \sigma \), was introduced to relate the Lux protein level to the experimentally measured luminescence output.

To fit the model to our experimental data, the parameters were fixed to physiological values whenever possible (see Table S1 in the supplemental material) and constrained to physiologically reasonable intervals in all other cases (see Table S2 in the supplemental material). Then, a trust-region-reflective Newton method (MatLab; The MathWorks, Inc.) was used to minimize the value of \( \chi^2 \) between the dose-response curve in Fig. 2B and the model. To account for the presence of local optima and to quantify the uncertainty in the estimated parameters, 100 independent fits were performed with randomly chosen initial parameter sets (see Fig. S4 and S5 in the supplemental material for correlation graphs between \( \chi^2 \) and estimated parameters). Confidence intervals for the fitted parameters (see Table S2) were obtained as previously described (36). The prediction of the dose-response curves for strain SGB218 was based on the parameter set from strain SGB073, but calculated using equation 4 instead of equation 2.

SUPPLEMENTAL MATERIAL

Supplemental material for this article may be found at http://mbio.asm.org/lookup/suppl/doi:10.1128/mbio.00975-15/-DCSupplemental.

Figure S1, EPS file, 0.5 MB.
Figure S2, EPS file, 0.1 MB.
Figure S3, TIF file, 2.3 MB.
Figure S4, EPS file, 0.8 MB.
Figure S5, EPS file, 2 MB.
Table S1, DOCX file, 0.1 MB.
Table S2, DOCX file, 0.1 MB.
Table S3, DOCX file, 0.02 MB.

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G.F. performed all mathematical modeling; S.D., N.S.T., and J.R. performed the experiments; S.G. coordinated experimental work; T.M., U.G., G.F., and S.G. designed the study; G.F. and S.G. wrote the manuscript; all authors approved the manuscript.

REFERENCES

7. Gebhard S. 2012. ABC transporters of antimicrobial peptides in Firmic-


