Double trouble: *Bacillus* depends on a functional Tat machinery to avoid severe oxidative stress and starvation upon entry into a NaCl-depleted environment

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ABSTRACT

The widely conserved twin-arginine translocases (Tat) allow the transport of fully folded cofactor-containing proteins across biological membranes. In doing so, these translocases serve different biological functions ranging from energy conversion to cell division. In the Gram-positive soil bacterium *Bacillus subtilis*, the Tat machinery is essential for effective growth in media lacking iron or NaCl. It was previously shown that this phenomenon relates to the Tat-dependent export of the heme-containing peroxidase EfeB, which converts Fe^{2+} to Fe^{3+} at the expense of hydrogen peroxide. However, the reasons why the majority of *tat* mutant bacteria perish upon dilution in NaCl-deprived medium and how, after several hours, a sub-population adapts to this condition was unknown. Here we show that, upon growth in the absence of NaCl, the bacteria face two major problems, namely severe oxidative stress at the membrane and starvation leading to death. The *tat* mutant cells can overcome these challenges if they are fed with arginine, which implies that severe arginine depletion is a major cause of death and resumed arginine synthesis permits their survival. Altogether, our findings show that the Tat system of *B. subtilis* is needed to preclude severe oxidative stress and starvation upon sudden drops in the environmental Na^{+} concentration as caused by flooding or rain.

1. Introduction

Bacterial twin-arginine translocation (Tat) pathways can translocate fully folded cargo proteins across the cytoplasmic membrane [1,2,89]. Cargo proteins that are to be translocated by Tat must contain a twin-arginine “RR”-motif in the N-terminal region of their signal peptide for specific recognition by the Tat translocase [3,4]. The *Bacillus* Tat translocation system is composed of so-called TatA and TatC subunits. TatC is the larger of the two, representing an integral membrane protein with six transmembrane domains. The smaller TatA subunit has a single N-terminal transmembrane spanning domain [5]. According to current models for protein translocation via the Tat pathway in bacteria and the thylakoidal membrane of chloroplasts, the TatA and TatC subunits of *Bacillus* collectively form a docking complex for cargo proteins [1]. The translocation process is initiated when a protein with the correct RR-signal peptide interacts with this docking complex. During the initial interaction, the docking complex proofreads the signal peptide and inserts the substrate into the membrane, which requires the recruitment of additional TatA subunits. These may either form a transmembrane pore or weaken the membrane, thereby facilitating translocation of the cargo protein [6,7]. The energy to drive the subsequent cargo translocation across the bacterial and thylakoidal membranes is provided by the proton-motive force [5,8–10]. Once the translocation process has been initiated, the signal peptide is proteolytically removed from the cargo.
protein by signal peptidase [11–13], allowing release of the translocated protein at the trans side of the membrane [14].

Of note, the genes for three TatA and two TatC subunits have been identified in the B. subtilis genome. The tatAy-tatCy and tatAd-tatCd genes are organized in operons at different genomic loci, and the tatAc gene is independently expressed from a third genomic locus [15]. Comprehensive expression studies have shown that the tatAyCy operon is constitutively expressed across many different conditions, and the same is true for tatAc [16]. In contrast, the tatAdCd operon is expressed only under conditions of phosphate limitation [15,17]. The operon-encoded Tat subunits assemble into two distinct Tat translocases: TatAyCy and TatAdCd. Each pathway works independently from the other and translocates its own cargo proteins [11,15]. While TatAdCd translocates only the phosphodiesterase PhoD, TatAyCy is known to translocate the heme-containing Dyp-type peroxidase EfeB [11,18], the Rieske iron-sulfur protein QcrA [19], and the metallo-phosphoesterase YkuE [16,19,20]. The third TatA protein, TatAc, is a dispensable component of the TatAyCy translocase, which enhances this translocase’s efficiency when the function of TatAy is compromised [19]. Based on these previous observations, it has been concluded that TatAyCy represents the core Tat translocase of Bacillus.

While the Tat system is not essential for B. subtilis under most growth conditions, we observed previously that TatAyCy is very important for growth in Lysogeny Broth (LB) lacking NaCl [21,22]. When grown in LB without NaCl, mutant strains lacking tatAy, tatCy or both these tat genes will initially start growing. However, in the early exponential growth phase, the mutant bacteria will stop growing and lyse. Nonetheless, part of the population of mutant bacteria will adapt to the salt-deprived condition and resume growth. The severity of this growth defect depends on the degree at which TatAyCy function is affected in the export of its main substrate EfeB, as was previously shown by investigations on TatAy proteins with site-specific mutations [5]. Accordingly, efeB mutant B. subtilis cells show exactly the same phenotype in LB without NaCl as tatAyCy mutant cells.

The peroxidase EfeB is a subunit of the elemental iron transport complex EfeUOB in B. subtilis (Fig. 1), where it oxidizes ferrous iron to ferric iron at the expense of hydrogen peroxide. The lipoprotein EfeO binds the ferric iron and transfers it to the ferric iron permease EfeU in the membrane [18]. Although the need for TatAyCy-dependent translocation of EfeB across the membrane for unimpairment of growth of B. subtilis in LB without NaCl was previously documented, the reason(s) why the tatAyCy or efeB mutant cells start to lyse in this growth condition remained unclear. In addition, it remained unclear how the surviving cells manage to recover from the lysis phase as depicted in Fig. 2. Of note, previous research had shown that the recovery of tat or efeB mutant bacteria reflects an adaptation rather than the emergence of suppressor mutations, because the cells that had resumed growth showed exactly the same lysis-recovery pattern when used to inoculate fresh LB medium without NaCl [5,21,22].

The objective of the present study was to elucidate the reasons why tat mutant bacteria start to lyse in the absence of NaCl, and how they manage to adapt to this condition. To address these questions, we followed an initial transcriptomics approach combined with subsequent functional verification. In brief, the results unveil a scenario where oxidative stress in the cell membrane of tat-deficient cells hinders the uptake of nutrients, causing the cells to starve, which ultimately leads to cell lysis. The surviving cells recover by catalyzing amino acid pools in the cell, especially arginine, and by upregulating various mechanisms to counteract the oxidative stress.

2. Materials and methods

2.1. Bacterial strains, media and basic growth conditions

Bacterial strains used in this study are listed in Supplementary Table S1. Lysogeny Broth (LB) was composed of 1% tryptone and 0.5% yeast extract with or without 1% NaCl. Bacteria were grown in LB broth.

![Fig. 1. Schematic representation of the EfeUOB elemental iron transport system and the Tat translocase in the membrane of B. subtilis. The cartoon depicts the Tat-dependent export of the ferrous iron peroxidase EfeB, which catalyzes the conversion of Fe2+ to Fe3+ at the expense of hydrogen peroxide. The newly formed Fe3+ is bound by the lipoprotein EfeO and transferred to the Fe3+ permease EfeU for uptake by the cell. EfeB and EfeO are associated with EfeU [18].](#)

![Fig. 2. Growth of the B. subtilis wild-type (WT) strain 168 and a total-tat mutant (Δtat) derivative strain in LB with or without 1% NaCl as monitored in a microtiter plate reader. In LB without NaCl, the Δtat strain displays a lysis-recovery phenotype, which is typical for the growth of all tat-deficient B. subtilis strains [21,22]. Note that the bacteria grow to a lower OD600 in 96-well microtiter plates than in shake flasks (Fig. S1).](#)
at 37 °C under vigorous shaking, or on LB agar plates at 37 °C. Growth in LB broth was recorded by optical density readings at 600 nm (OD_{600}). When appropriate the cultures were supplemented with antibiotics: 10 μg/mL tetracycline (Tc), 4 μg/mL pheleomycin (Pl), 20 μg/mL kanamycin (Km) or 100 μg/mL spectinomycin (Sp) or combinations thereof.

### 2.2. Live/dead staining and fluorescence confocal microscopy

To monitor the viability of wild-type and tat mutant strains, they were first cultured overnight in 2 mL of LB with 1% NaCl and the appropriate antibiotics. The overnight cultures were diluted 50-fold into fresh 10 mL LB with 1% NaCl and grown till mid-exponential phase (approximately 3 h). A final 50-fold dilution was made in 75 mL LB without NaCl in a 250 mL conical shake flask. During growth samples were withdrawn from the cultures for OD_{600} readings. B. subtilis strains equivalent to an OD_{600} of 1 were harvested at different time points and stained with the LIVE/DEAD BacLight™ Bacillary Viability Kit (ThermoFisher®) for 15 min according to the manufacturer’s instructions. Essentially, this kit contains two dyes: the green-fluorescent nucleic acid stain SYTO9 that penetrates both viable and non-viable bacteria, and the red-fluorescent nucleic acid stain propidium iodide that penetrates only non-viable bacteria shifting the emitted fluorescence to red. LIVE/DEAD-stained bacteria were washed 1× with PBS to remove unbound dye and fixed in 4% formaldehyde for 10 min. Cells were spotted on a glass slide for microscopy. Image acquisition was performed with a Leica TCS SP8 fluorescence confocal microscope (Leica Microsystems, Germany). Images were processed using LAS X Life Science and ImageJ software (National Institutes of Health). Cells imaged in the two fluorescence channels were counted using the threshold and analyze particles ImageJ software plugins.

### 2.3. RNA extraction

For RNA extraction, the bacteria were cultured as described in Section 2.2. Total RNA was isolated from three independent cultures of wild-type or tat mutant B. subtilis cells, respectively, according to the method described by Eymann et al. with some modifications [16,23]. Briefly, bacterial cells equivalent to 15 OD_{600} units were harvested by centrifugation for 3 min at 4 °C after addition of 1/5 volume of ice-cold killing buffer (20 mM Tris/HCl [pH 7.5], 5 mM MgCl_{2}, 20 mM NaN_{3}) to the culture sample. After discarding the supernatant, cell pellets were frozen in liquid nitrogen and stored at −80 °C. For mechanical cell disruption, the pellets were resuspended in 200 μL of ice-cold killing buffer, immediately transferred to a Teflon disruption vessel (precooled and filled with liquid nitrogen), and then disrupted in a Mikro-Dismembrator S (Sartorius) for 2 min at 2600 rpm. The resulting frozen powder was resuspended in 4 mL of lysis solution prewarmed at 50 °C (4 M guanidine thiocyanate, 25 mM sodium acetate [pH 5.2], 0.5% N-laurylsarcosinate 40 [wt/vol]) by repeated pipetting. Afterwards, 1 mL aliquots of the lysate were transferred to microcentrifuge tubes and immediately frozen in liquid nitrogen. Total RNA was isolated by acid-phenol extraction. The samples were extracted twice with an equal volume of acid phenol/chloroform/isoamyl alcohol (25:24:1, [pH 4.5]) and once with chloroform/isoamyl alcohol (24:1). After adding 1/10 volume of 3 M sodium acetate (pH 5.2), RNA was precipitated with isopropanol, washed with 70% ethanol and dissolved in 100 μL of RNase free water. For transcriptome analysis, 35 μg RNA were DNase-treated using the RNase-Free DNase Set (Qiagen) and purified using the RNA Clean-Up and Concentration Kit (Norgen). The RNA concentration was measured using a NanoDrop spectrophotometer, and the quality of the RNA preparations was assessed using an Agilent 2100 Bioanalyzer according to the manufacturer’s instructions.

### 2.4. Expression arrays

After quality control, 5 μg aliquots of the purified RNA were used for microarray analysis. Prior to cDNA synthesis, ten different in vitro synthesized transcripts derived from the One-Color RNA Spike-In kit (Agilent Technologies) were added in equal amounts to each total RNA sample [24]. The subsequent synthesis and fluorescent labeling of cDNA followed a strand-specific method using the FairPlay III Microarray Labeling Kit (Agilent Technologies) and actinomycin D (Calbiochem) [16]. 100 ng of Cy3-labeled cDNA were hybridized to the microarray following Agilent’s hybridization, washing and scanning protocol (One-Color Microarray-based Gene Expression Analysis, version 5.5). Data were extracted and processed using the Feature Extraction software (version 11.5.1.1). For each gene, the median of the individual probe intensities was calculated and gene-level intensities were scaled, based on the intensity values of the ten different in vitro synthesized spike-in transcripts that hybridize to complementary control probes on the array. The average difference of the control signal intensities between different arrays was used to scale the intensities of each individual array in order to account for technical variation associated with sample processing. Further data analysis was performed using GeneSpring GX 14.8 software (Agilent Technologies) and R 3.5.2 [96]. The microarray data set is available from NCBI’s Gene Expression Omnibus (GEO) database (accession number GSE149595). The scaled mRNA expression data are available as supplemental material (Supplementary Table S2, sheets 1 and 2). Voronoi treemap visualizations were generated after exporting the expression data to MS-Excel (MS-Office, Microsoft) using regulon information provided by the online resource SubtiWiki ([25,26]; http://subtiwiki.uni-goettingen.de/) [94] and the Voronoi treemap software (Decodon GmbH). In the treemaps thus generated, each individual cell represents an individual gene transcript and the color denotes the transcript level ratios between the wild-type and tat mutant bacteria.

### 2.5. Bacterial strain construction

B. subtilis IIG-Bs3 was made competent in Spizizen medium as previously described [27]. To introduce the tatAyCy:spc mutation in this strain, genomic DNA of B. subtilis 168 tatAyCy:spc was used as a template, and the tatAyCy:spc region was amplified by PCR with primers YdiG_F/YdiG_R that hybridize to the flanking regions of tatAyCy (Supplementary Table S3). Subsequently, the amplified DNA was used to transform competent cells of B. subtilis IIG-Bs3 and transformants were selected on plates with Sp.

### 2.6. Growth of B. subtilis in microtiter plates

Strains were cultured overnight in 2 mL of LB with 1% NaCl and the appropriate antibiotics. The overnight cultures were diluted 50-fold into fresh 10 mL LB with 1% NaCl and grown till mid-exponential phase (approximately 3 h). A final 50-fold dilution was made into 100 μL of LB without NaCl in wells of a 96-well microtiter plate (Greiner), which was subsequently incubated in a Bioteck Synergy II plate reader (37 °C, with shaking). OD_{600} readings were recorded at 10 min intervals for 24 h. For the growth studies with glucose supplementation, LB without NaCl containing 2% glucose was prepared by adding glucose from a 50% stock solution. For the growth studies with amino acid supplementation, stocks of 0.5 M of the amino acids arginine, glutamate or histidine were prepared in LB without NaCl and then filter-sterilized using a 0.2 μm membrane. The medium was then supplemented with the appropriate concentration of each amino acid.

### 2.7. LDS-PAGE and Western blotting

The cultures equivalent to 2.0 OD_{600} units were collected at two time points. A first sample was collected at the onset of lysis when the OD_{600} started to decline (OD_{600} ~ 0.9). Samples from parallel cultures of the B. subtilis 168 wild-type control strain growing in LB without NaCl were collected at essentially the same OD. The second time point of sampling was in the recovery phase when the OD_{600} of the cultures with tat...
mutant or wild-type bacteria was ~2. The samples were centrifuged for 5 min at 14,000 rpm at 4 °C and then kept on ice. The supernatant was transferred to a separate eppendorf tube and proteins in this fraction were collected by precipitation with 10% trichloroacetic acid (TCA). To this end, the supernatant fractions were incubated with TCA on ice for 1 h. Subsequently, the precipitated proteins were collected by centrifugation for 10 min at 14,000 rpm, 4 °C. The supernatant was discarded and the pellet was washed with 500 μL of ice-cold acetone and centrifuged for 5 min at 14,000 rpm, 4 °C. Upon removal of the acetone supernatant, the protein pellet was dried at 60 °C for 10 min. Finally, 100 μL of lithium dodecyl sulphate (LDS) sample buffer with reducing agent (Life technologies) was added and the samples were incubated for 10 min at 95 °C. The collected cell pellets were resuspended in LDS sample buffer and, subsequently, the cells were disrupted with glass beads in a Precellys®24 homogenizer (3 × 30 s at 6500 rpm with 30 s intermittences). The samples were then heated to 95 °C for 10 min. Subsequently, samples with cellular or secreted proteins were separated by LDS-PAGE using pre-cast Bis-Tris NuPAGE gels (Invitrogen). The separated proteins were stained in the gel with SimplyBlueTM Safe Stain. Alternatively, the proteins separated by LDS-PAGE were semi-dry blotted (75 min at 1 mA/cm²) onto a nitrocellulose membrane (Protran®, Schleicher & Schuell), and the presence of EfeB, FeuA, QcrA, Thioredoxin A (TrxA) and LiaH was detected with specific polyclonal antibodies raised in rabbits. Visualization of bound antibodies was performed with fluorescent IgG secondary antibodies (IRDye 800 CW goat anti-rabbit from Licor Biosciences) in combination with the Odyssey® Infrared Imaging System (Licor Biosciences).

2.8. ICPMS

Wild-type and tat mutant bacteria were cultured in LB without NaCl as indicated above. Cells were harvested by centrifugation and the collected cell pellets were resuspended in Tris-HCl buffer (10 mM, pH 7.4) to 8 μL per OD₆₀₀ per mL. After transfer of the sample to screw-capped micro tubes (Sarstedt, made from PP) filled with 0.5 mL glass beads (Sartorius, 0.1 mm diameter), the cells were disrupted by 6 cycles in a FastPrep-24 instrument (MP-Biomedicals; 30 s per cycle, 6.5 m/s, 4 min cooling on ice between the cycles). Glass beads and cell debris were removed by two subsequent centrifugation steps at 5000 × g for 5 min and at 20,000 × g for 10 min, and the supernatant from the last centrifugation step was stored at ~20 °C in aliquots until further processing. Using size-exclusion chromatography (column: Superose 6 Increase 3.2 × 300, eluent: 10 mM Tris-HCl pH 7.4, flow rate: 100 μL/min, isocratic elution), aliquots from each sample were separated and the flow-through was directly injected into a 7500c ICP-MS (Agilent, plasma operated a 1460 W) to monitor the intensities for several elemental isotopes over a period of 100 min. The recorded chromatograms for each isotope were corrected for sensitivity drifts by a smoothed ¹³C baseline, and the manufacturer provided natural isotope abundance using R scripts. Peak fitting and integration were performed with the program Fityk (version 1.3.1, [28]) and peak areas were normalized to the protein content of the sample as determined by Bradford assay using BSA as external calibrant.

3. Results and discussion

As shown in Fig. 2, tat-deficient B. subtilis cells that are introduced into LB without NaCl start to lyse after several hours of growth in LB lacking NaCl. To pinpoint the stage at which the bacteria actually start dying, we collected samples at different time points after diluting cells of the B. subtilis Δtat mutant or the wild-type strain 168 in LB without NaCl. Cells in the collected samples were then stained with the fluorescent dyes SYTO9 and propidium iodide, which distinguishes living and dead cells by their green and red fluorescence, respectively (Fig. 3). The results obtained by confocal fluorescence microscopy showed that the tat mutant bacteria remained viable during the early time points after dilution into LB without NaCl, and that substantial numbers of dead bacteria were only detectable when the OD₆₀₀ of the cultures with tat mutant bacteria started to decline at the entry into the lysis phase. In contrast, no dead bacteria were detectable when the wild-type bacteria were diluted into LB without NaCl (Fig. 3). Importantly, a fraction of the tat mutant bacteria remained viable during the lysis phase in LB without NaCl. Upon recovery, the tat mutant bacteria resumed growth and dead bacteria were no longer detectable.

To gain insights into the physiological state of tat mutant bacteria that start to lyse during growth in LB without NaCl, we recorded the growth of B. subtilis Δtat in shake flasks and collected samples for RNA isolation at the moment when the OD₆₀₀ of the cultures started to decline (OD₆₀₀ ~ 0.9; Supplementary Fig. S1). Samples from parallel cultures of the B. subtilis 168 wild-type control strain in LB without NaCl were
collected for RNA extraction at essentially the same OD. Upon process-
ing of the RNA samples and appropriate quality control, transcript
profiling was performed using expression arrays that represent all cod-
ing and non-coding genes of B. subtilis [16,29]. Further, we used spike-in
normalization of in vitro synthesized RNA transcripts [24] for detailed
comparisons of mRNA levels in the tat mutant bacteria and the wild-type
control. This revealed a striking reorganization of the transcriptome in
the tat mutant bacteria (Supplementary Table S2). As visualized through
the Voronoi treemaps in Fig. 4 and Supplementary Fig. S2, the expres-
sion of many genes was strongly reduced in the tat mutant bacteria (depicted in blue) with only a specific subset of genes being upregulated
(depicted in red). The upregulated genes relate to a limited number of
regulons (Fig. 4B). The striking global downregulation observed in the
tat mutant bacteria may relate to reduced transcription at the time point
of sampling as the mutant bacteria had already ceased growth. The
strong growth effect is also supported by a significant reduction in the
expression of genes subject to the stringent response (Fig. 4B; Supple-
mentary Fig. S2B).

3.1. Upregulation of oxidative stress-responsive genes in the lysis phase

The RNA polymerase sigma factor SigB is a key transcription factor
that responds to various stress stimuli [30]. Upregulation was essentially
only observed for the SigB-regulon in the tat mutant bacteria upon
entering the lysis phase, which indicates exposure to severe stress. The
strong 23-fold induction of the PerR-controlled katA gene encoding the
major vegetative catalase that detoxifies H₂O₂, is in turn indicative of
peroxide stress [31,95]. This view is supported by the 10-fold elevated
transcript level of the katE gene for a second catalase of B. subtilis [32].
Likewise, the transcription of ohrB and cypC, two other SigB-controlled
general stress genes, was also upregulated in the tat mutant bacteria. OhrB
is known to confer hydroperoxide resistance in B. subtilis [33,34].
CypC is a long chain-fatty acid beta-hydroxylating cytochrome P450
that hydroxylates myristic acid to beta-hydroxymyristic acid by utilizing
H₂O₂, and it is required for the protection against paraquat stress
[35,36]. Altogether, the upregulation of katA, katE, ohrB and cypC at the
start of the lysis phase is indicative of an accumulation of H₂O₂ and other
reactive oxygen species (ROS) in the tat mutant bacteria. This is fully
consistent with our previously reported observation that the TatAyCy-
dependently exported EfeB protein consumes H₂O₂ for the conversion
of ferric to ferrous iron, thereby also setting a limit to the unwanted
production of reactive oxygen species by ferric iron-activated Fenton
chemistry [18]. It thus seems likely that the increased oxidative stress
in the absence of TatAyCy or EfeB leads to the oxidation of phospholipids,
which will affect membrane permeability and fluidity and ultimately
leads to leakage and lysis of the cell [57]. Importantly, this view is
consistent with the data presented in Fig. 3, where the increased
membrane permeability is evidenced by the staining of tat mutant
bacteria with the membrane-impermeable dye propidium iodide.

To verify the defective EfeB secretion at the onset of the lysis phase,
Western blotting experiments were performed (Fig. 5). Indeed, at the
beginning of the lysis phase, EfeB was not detectably secreted by the
tat mutant bacteria, whereas the wild-type bacteria displayed low-level
secretion of EfeB. Conversely, the tat mutant cells contained higher
levels of EfeB than the wild-type cells, consistent with the previously
reported EfeB secretion defect in the absence of a functional Tat ma-
chinery [11]. It thus seems that the tat mutant bacteria upregulated
SigB-controlled genes for proteins that detoxify H₂O₂ in various ways,
in order to mitigate the detrimental accumulation of H₂O₂ at the extrac-
ytoplasmic side of the membrane due to the absence of the peroxidase
activity of EfeB. However, the Tat-deficiency may also elicit the pro-
duction of ROS in other ways. For instance, one of the four known
B. subtilis Tat substrates is the Rieske iron-sulfur protein QcrA. This
protein is an integral component of the cytochrome bc₁ complex, which
faces the extracellular side of the cytoplasmic membrane and serves as a
menaquinone:cytochrome c reductase [38]. It is thus conceivable that the
absence of QcrA from the cytochrome bc₁ complex leads to imbalances
in the respiratory chain and the formation of ROS. However, as shown
by Western blotting (Fig. 5), the QcrA protein is barely expressed in
growing wild-type B. subtilis at OD600 values equivalent to the lysis phase
of the Δtat mutant bacteria. Thus, it seems less likely that QcrA plays a
role in the onset of the lysis phase.

3.2. Starvation responses upon entry of tat mutant bacteria into the lysis
phase

The Voronoi treemaps of genome-wide gene expression in the lysis
phase portray a global downregulation in the transcription of almost all
systems in the tat mutant bacteria (Fig. 4). This includes many genes
for nutrient uptake and central carbon metabolism, which could lead to
starvation of the tat mutant bacteria due to an inability to acquire and
utilize sugars. This view would be supported by the observation that
the mutant bacteria substantially increased the expression of genes for
amino acid catabolism in order to meet their energy demands. Indeed,
the tat mutant bacteria seemed to utilize the cellular and extracellular
arginine pools, as evidenced by a ~ 2.3- to 9-fold upregulation of the
rocGABC operons encoding proteins involved in catabolizing arginine to 2-oxaloglutarate [39]. Of note, the strong
upregulation of the roc genes occurred despite the fact that expression
of SR1, a small regulatory RNA that inhibits ahrC translation [40,41],
was highly upregulated in the tat mutant bacteria. AhrC is a transcriptional
regulator of the ArgR family, which represses the arg genes for arginine
biosynthesis and activates the roc genes for arginine catabolism possibly
via RocR and SigL [42-44].

The view that the tat mutant bacteria were starving and forced to
utilize alternative sources for energy is further supported by the
observed upregulation of CcpN-controlled pckA and gapB genes, which
are both involved in gluconeogenesis. Also, the derepression of part of
the CcpA regulon (e.g. acoABC, licBCAH, malA and glpFK) indicates that
the mutant cells experienced glucose limitation. In this respect, it should
be noted that LB medium contains low amounts of glucose and other
catabolite-repressing sugars, leading to repression of CcpA-dependent
B. subtilis 168 genes especially in the exponential growth phase and
the transition to stationary phase [16,45]. To verify the idea that the tat
mutant bacteria were starving, we included 2% glucose in the LB me-
dium without NaCl. As shown in Fig. 6, the lysis phenotype of the tat-
mutant bacteria was suppressed by the glucose supplementation.
Fig. 4. (continued).
To understand how the tat mutant cells overcame the problem imposed by impaired Tat-dependent protein translocation in the absence of NaCl, we also investigated the recovery phase by transcript profiling with expression arrays. The results are presented in Supplementary Table S2 and graphically depicted in Figs. 4C, D and Supplementary Figs. S2C, D. Contrary to the lysis phase, in the recovery phase the general downregulation of gene expression was no longer observed (Fig. 4), which is in agreement with the observation that the mutant cells overcame the problem (Fig. 2). Interestingly, the LiaH levels in the mutant bacteria grown in regular LB without NaCl were also slightly elevated compared to the wild-type bacteria at the entry into the lysis phase, despite the fact that in this phase a difference in liaH expression by the mutant and wild-type bacteria was not clearly evident by transcript profiling (Fig. 5). This is different from the situation observed when *B. subtilis* is grown in regular LB with 1% NaCl, where the expression of LiaH is not influenced by the absence of a functional Tat system [6] and where no lysis-recovery growth phenotype is presented by tat-deficient bacteria (Fig. 2).

### 3.3. Oxidative stress is overcome in the recovery phase

Further, particular genes and regulons were upregulated, but these were mostly different from those in the lysis phase. A first important conclusion that can be reached from these observations is that the tat mutant bacteria no longer displayed the SigB- and PerR-dependent oxidative stress responses, despite the fact that EleB most likely does not contribute to *H₂O₂* detoxification in absence of a functional Tat translocase. There are various possible explanations for the alleviated oxidative stress response. For instance, the *spa* gene was upregulated, which is known to confer resistance to paraquat stress [46,57]. Likewise, the observed induction of *hp* is suggestive of Hp-mediated dimerization of ribosomes, which is a known resistance mechanism against paraquat-induced oxidative stress [36,48,49]. Also, the observed upregulation of the *lia* and *liaH* genes may possibly facilitate LiaH-mediated mitigation of membrane damage caused by the oxidative stress in absence of a functional Tat system. LiaH is a homologue of the phage shock protein A (PspA) of *E. coli* and the IM30 (VIPPI) protein of thylakoid-harboring organisms. Proteins of the PspA/IM30 family bind and stabilize distorted membrane regions [50–52]. The expression of LiaH is upregulated via the LiaRS two-component regulatory system upon cell envelope stresses elicited by antibiotics and antimicrobial peptides [53,54], secretion of certain heterologous proteins [95], and overexpression of the TatAyCy translocase to which it can bind [6]. Indeed, Western blotting showed that, in the recovery phase, the LiaH protein was upregulated in the tat mutant bacteria compared to the wild-type bacteria where LiaH was barely detectable (Fig. 5). This is different from the situation observed when *B. subtilis* is grown in regular LB with 1% NaCl, where the expression of LiaH is not influenced by the absence of a functional Tat system [6] and where no lysis-recovery growth phenotype is presented by tat-deficient bacteria (Fig. 2). Interestingly, the LiaH levels in the tat mutant bacteria grown in LB without NaCl were also slightly elevated compared to the wild-type bacteria at the entry into the lysis phase, despite the fact that in this phase a difference in liaH expression by the mutant and wild-type bacteria was not clearly evident by transcript profiling. In this respect, one has to bear in mind that mRNA levels in general were decreased in the tat mutant bacteria, thus likely facilitating increased translation of the remaining mRNA molecules present at similar levels as in the wild-type. Altogether, these findings imply that severe oxidative stress in the cell envelope due to the absence of a functional Tat system is a primary cause of the observed lysis phenotype of tat mutant *B. subtilis* cells upon growth in LB medium without NaCl, and that this stress is overcome in the recovery phase by various stress-mitigating systems. Further, membrane damage, as indicated by the upregulation of LiaH, would explain why the bacteria show symptoms of starvation upon entry into the lysis phase and start to utilize alternative energy sources.
3.4. Increased potential for uptake and biosynthesis of amino acids upon recovery

During the lysis phase, genes for catalobizing arginine and redirecting the metabolites for gluconeogenesis were significantly upregulated in the tat mutant bacteria. This was reversed in the recovery phase and, instead, the artPQR genes for uptake of arginine were upregulated 95- to 155-fold (Fig. 4), which encode a high-affinity arginine binding ABC transporter [55,56]. Alongside the enhanced potential for uptake of arginine, the capacity for biogenesis of arginine was also dramatically upregulated as implied by increased expression of the CodY-regulated arg (argBCDFGHJ) and car (carAB) gene families [42,55,57,58]. Conversely, the roc genes for arginine utilization were downregulated [39,59]. All of this implies that the tat mutant cells had consumed their available arginine supply to survive the lysis phase and had started to replenish their arginine pool via increased uptake and biosynthesis of this amino acid. Furthermore, the gltAB genes for the biosynthesis of glutamate were also (~30-fold) upregulated in the recovery phase of the tat mutant cells, whereas in the wild-type cells rocG was more strongly expressed leading to low levels of gltAB expression [60,61]. Lastly, the utilization and uptake of histidine was apparently upregulated in the recovering tat mutant bacteria, as indicated by the ~30-fold upregulation of the hutPHUIGM genes [62,63].

3.5. Iron starvation response during recovery

Despite the fact that the EfeUBV uptake system is unable to facilitate the utilization of ferric iron in tat-deficient B. subtilis, we did not observe an iron starvation response in the lysis phase (Fig. 4). However, a Fur-dependent iron starvation response was clearly evident in the recovery phase of the tat mutant cells, consistent with the impaired export of EfeB via the Tat pathway. This implies that, at the onset of lysis, the mutant bacteria still contained sufficient elemental iron, but that the cellular iron pool was rapidly depleted when the bacteria resumed growth. In particular, upon recovery the ykuN and ykuP genes were upregulated, both encoding FMN-binding flavodoxins. These proteins replace ferredoxin under conditions of iron limitation [64,65]. Likewise, systems for iron siderophore synthesis and uptake were also upregulated. For instance, the dhbABCD genes involved in synthesis of the siderophore bacillibactin were upregulated. Also, the transcriptional activator btr and its target, the feuABC operon for siderophore uptake, were upregulated [64,66–68]. The strong upregulation of feuA was confirmed by Western blotting, which showed that compared to the wild-type bacteria, indeed, the production of FeuA was strongly upregulated in the tat mutant bacteria upon recovery (Fig. 5). However, also in this case, the Western blotting detected upregulation of the FeuA levels in the tat mutant bacteria upon entry into the lysis phase, despite the fact that similar feuA mRNA levels were detected in the mutant and wild-type bacteria. Again, these data suggest that, due to the general depletion of mRNA in the mutant, similar feuA mRNA levels in the mutant and the wild-type bacteria gave raise to higher protein levels in the mutant bacteria, because the feuA mRNA was preferentially translated due to a lack of competition for ribosomes. Additionally, expression of fbpB, encoding a basic protein that acts as an RNA chaperone for the regulatory FsrA RNA in response to iron limitation was upregulated in the recovery phase, as was the case for the FsrA RNA itself [64,69,70]. All these adaptations seem to enable the tat mutant cells to overcome the iron limitation resulting from defective biogenesis of EfeB via Tat. However, quite remarkably, in the recovery phase we noticed the Tat-independent secretion of FeuB by tat mutant bacteria to levels that were comparable to the EfeB secretion by the wild-type bacteria (Fig. 5). Possibly, this Tat-independent secretion of FeuB relates to the fact that the expression level of genes for heme biosynthesis at the onset of the lysis phase was downregulated 20- to 30-fold. It is thus conceivable that the tat mutant cells that recovered from the lysis phase were depleted for heme and that there was insufficient heme to be bound by all EfeB molecules synthesized. As a result, the heme-deficient FeuB could become a substrate for the Sec pathway, which is known to accept loosely folded proteins for translocation [71]. This explanation would be supported by the finding that, despite the Tat-independent export of FeuB, the tat mutant cells displayed a strong induction of Fur-regulated genes in the recovery phase, which implies that FeuB was secreted in an inactive form. Likewise, we have previously shown that heterologous or hybrid Tat substrates were Sec-dependently secreted in B. subtilis, probably due to their inefficient folding in the cytoplasm and inadequate ‘Sec-avoidance’ [72,73]. However, it remains to be demonstrated whether the observed Tat-independent secretion of EfeB in the recovery phase is indeed facilitated by the Sec pathway.

3.6. Competition for nutrients induces genes for sibling killing and ICEBs genes during recovery

Amongst the most highly upregulated genes in the recovery phase of the tat mutant bacteria were the sibling killing genes skfABC (between 8- to 22-fold), the alb genes involved in production of the bacteriocin subtilosin (between 25- to 100-fold), and genes belonging to the so-called Integrative and Conjugative Elements of B. subtilis (ICEBs1) cluster (between 436- to 2000-fold). The upregulation of both the skf and alb genes was previously reported to occur upon increased competition for nutrients in a B. subtilis population [74,75]. Thus, the upregulation of the skf and alb genes in the recovery phase could be a consequence of the apparent starvation of the tat mutant bacteria upon entry into the lysis phase. The ICEBs1 cluster consists of several genes regulated by ImmR, and it is involved in the transfer of mobile genetic elements [76–78]. In particular, the massive up to 2000-fold upregulation of the ICEBs1 genes suggested that these genes might somehow be responsible for the recovery of the tat mutant bacteria. To investigate
whether induction of the ImmR regulon and the ICEBs1 genes was responsible for recovery, the tatAyCy genes were deleted in a strain of B. subtilis lacking the ICEBs1 genes. The mutant bacteria lacking both the tatAyCy and the ICEBs1 genes (IIG-Bs3 ΔtatAyCy) still showed the lysis phenotype upon growth in LB without NaCl, whereas the mutant lacking just the ICEBs1 genes (IIG-Bs3) grew similar to the wild-type (Fig. 7). Nevertheless, the mutant bacteria lacking both the ICEBs1 genes and tatAyCy did not recover to the same extent as the tat mutant bacteria. These results indicate that the observed hyper-induction of ICEBs1 genes was not a primary cause of recovery but, rather, that the ICEBs1 genes may somehow assist the bacterial recovery.

3.7. Changes in the expression of several ABC transporters

While many transporter genes were downregulated at the entry into the lysis phase, the genes for various ABC transporters facilitating the uptake of nutrients and exchange of ions were found to be upregulated in the tat mutant bacteria during recovery. For instance, the CodY-
regulated frbONMD genes for fructose uptake and utilization were upregulated [79]. Thus, it seems that the internalized fructose is being converted to Glucose-6-Phosphate to be utilized as an energy source in the growing cells. Similarly, the amyC and amyD transcripts for melibose and rafinose transport were also upregulated upon recovery of the tat mutant bacteria [68]. Moreover, the dct operon involved in the uptake of other carbon sources, such as succinate, fumarate and oxaloacetate, was upregulated upon recovery of the tat-deficient cells. These observations are fully in line with the fact that the recovered cells were growing rapidly for which an adequate supply of nutrients is crucial.

3.8. Suppressed lysis phenotype upon arginine supplementation

As described above one of the most striking features displayed by tat mutant bacteria upon entry into the lysis phase was an extreme upregulation of the roc genes for arginine utilization, most likely as a starvation response due to oxidative damage of the cell membrane. Conversely, during the recovery phase the roc genes were no longer expressed at elevated level, whereas the genes for transport and synthesis of arginine were upregulated. These observations led us to investigate the effects of supplementation of the growth medium with this amino acid. To this end, LB medium without NaCl was supplemented with different amounts of L-arginine and the growth of the tat-deficient and wild-type bacteria on these supplemented media was recorded. Indeed, when the tat-deficient bacteria were supplemented with 25 mM L-arginine in LB without NaCl the lysis phenotype was completely suppressed (Fig. 8A). In fact, the growth of the tat-deficient bacteria was close to identical to that of the wild-type. Upon reduction of this amino acid against the lysis of the tat-deficient and wild-type bacteria on these supplemented media was recorded. Indeed, when the tat-deficient bacteria were supplemented with 25 mM L-arginine in LB without NaCl the lysis phenotype was completely suppressed (Fig. 8A). In fact, the growth of the tat-deficient bacteria was close to identical to that of the wild-type. Upon reduction of the L-arginine concentration to 12.5 mM, the protective effect of L-arginine against the lysis of the tat-deficient mutants in LB without NaCl was lost (Fig. 8A). In contrast to the supplementation with L-arginine, supplementation of LB with the control amino acid l-lysine did not alter the growth phenotype of the tat mutant bacteria on LB without NaCl (Figs. 8B). These results show that the availability of arginine modulates the growth behavior of tat mutant bacteria such that they do not display the typical lysis phase as observed upon growth in LB without NaCl. This finding supports the view that it is the consumption of arginine that is most important for survival of the lysis phase by a fraction of the tat mutant bacterial population. To obtain further evidence for the view that the elevated amino acid synthesis by the tat mutant bacteria in LB without NaCl contributes to their survival of the lysis phase, we inspected also their survival upon supplementation of this medium with L-glutamate or L-histidine. Indeed, when the tat-deficient bacteria received additional L-glutamate, there was a clear delay in the onset of the lysis phase and upon recovery.

As shown in Fig. 9, the tat mutant bacteria contained more intracellular Na⁺ ions compared to the wild-type upon entry into the lysis phase. Consistent with this finding, the mprABCDDEF genes, which encode the major Mrp sodium extrusion system of B. subtilis [80], were severely downregulated in the lysis phase. However, during recovery this difference in the cellular Na⁺ concentration was ameliorated. Further, the expression of the Na⁺/H⁺ antiporter nhaC was consistently lower in the tat-deficient bacteria compared to the wild-type when grown in LB without NaCl [80,81]. Together, these observations suggest that the tat-deficient bacteria were less efficient compared to the wild-type in releasing the intracellular Na⁺ when transferred from LB with 1% NaCl to LB medium without NaCl. Reducing the expression of nhaC when facing Na⁺-deplete conditions is arguably an energetically favorable response, as the exchange of Na⁺ against H⁺ would result in a lowered proton-motive force (pmf) and, consequently, reduced generation of ATP by the pmf-dependent ATP synthase. During the recovery phase, the Na⁺ concentrations in the tat-deficient and wild-type bacteria were comparable, in line with the view that the mutant bacteria had adapted to the absence of NaCl. Here, it is noteworthy that there was no significant change in the expression profiles of the genes involved in managing the bacterial Na⁺ homeostasis upon recovery. In particular, the expression of the mpr and nhaC genes, and that of the naAB and nhaC genes for ATP-dependent Na⁺ export systems showed no significant changes during the onset of lysis and the subsequent recovery phase [82,83]. This most likely means that, eventually, the remaining expression level of the Mrp and NaHc sodium transporters was sufficient to equilibrate the Na⁺ level of the tat mutant bacteria to a similar extent as in the wild-type bacteria, or that there are other Na⁺ transporters active in B. subtilis that remain to be discovered.

In contrast to the elevated Na⁺ level, the tat mutant bacteria showed a lowered cellular K⁺ concentration compared to the wild-type bacteria when entering the lysis phase. In agreement with this finding, upon entry into the lysis phase, expression of the ydaO riboswitch-controlled ktrAB and the recently discovered kimA genes for high-affinity K⁺ uptake was severely downregulated (~25–30-fold) in the tat mutant bacteria compared to the wild-type [84,85]. Along with the ktrAB and kimA genes, the ktrCD genes encoding a low-affinity K⁺ transporter and the khtUT genes encoding a K⁺/H⁺ antiporter were also slightly downregulated (~3-fold) in the tat mutant bacteria compared to the wild-type [80,85–88]. This suggests that, compared to the wild-type, the mutant bacteria...
bacteria were less competent for K⁺ intake upon entry into the lysis phase, which would lead to the lowered cellular K⁺ concentration as observed.

Altogether, a depletion of the pmf in the tat mutant bacteria would provide a plausible explanation for the observed downregulation of most energy-consuming systems upon entry into the lysis phase. This view is in fact supported by the results of live/dead-staining, which showed that the membrane of a substantial part of the bacterial population entering the lysis phase had become permeable for propidium iodide (Fig. 3). In any case, in the surviving tat mutant cells that manage to recover from the lysis phase, the cellular Na⁺ and K⁺ concentrations are again comparable to those of the wild-type bacteria.

4. Conclusions

Altogether, our present findings show that tat mutant B. subtilis cells that are diluted into a NaCl-free growth medium have to face two major problems. Firstly, because they cannot secrete the heme peroxidase EfeB and perhaps also due to the mis-localization of the Rieske protein QcrA, these mutant cells suffer from severe oxidative stress at the membrane as evidenced by a strong upregulation of genes required for the detoxification of H₂O₂. This leads to their second major problem, namely the inability to take up nutrients, whereupon the cells start to starve. In response to this starvation, the tat mutant bacteria catabolize arginine and glutamate, leading to a further depletion of their intracellular nutrient pools and, ultimately, death of the largest part of the population. However, a sub-population manages to recover, probably because the respective cells are able to overcome severe oxidative stress at the membrane. Possibly, this sub-population mounts an adequate response earlier than the dying bacteria, allowing them to replenish their intracellular arginine and glutamate pools before starving to death. This view is supported by the observation that the lysis phase can be prevented by feeding the tat mutant bacteria arginine right from the moment when they are diluted into the NaCl-free medium. This observation focuses attention on the critical role played by arginine as a source of energy to overcome severe carbohydrate starvation. The idea that severe carbohydrate starvation is a major cause of death of a large part of the tat mutant population is strengthened by the observation that the lysis phase can be suppressed by the addition of an excess amount of glucose.

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Author contributions

B.P., U.M. and J.M.v.D. conceived and designed the experiments.
B.P., M.B.C., M.L.A., M.S., J.B., H.R., L.S., and U.M. performed experiments and analyzed the data.
B.P. and J.M.v.D. wrote the manuscript.
All authors have read and approved the manuscript.

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Declaration of competing interest

The authors declare that they have no known competing financial interests or personal relationships that could have appeared to influence the work reported in this paper.

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Data availability

The microarray data set is available from NCBI’s Gene Expression Omnibus (GEO) database (accession number GSE149595).


