Evidence for a Proton–Protein Symport Mechanism in the Anthrax Toxin Channel

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The toxin produced by Bacillus anthracis, the causative agent of anthrax, is composed of three proteins: a transloca
tive heptameric channel, (PA63)7, formed from protective antigen (PA), which allows the other two proteins, lethal
and edema factors (LF and EF), to translocate across a host cell’s endosomal membrane, disrupting cellular
homeostasis. It has been shown that (PA63)7 incorporated into planar phospholipid bilayer membranes forms
a channel capable of transporting LF and EF. Protein translocation through the channel is driven by a proton
electrochemical potential gradient on a time scale of seconds. A paradoxical aspect of this is that although LFN
(the N-terminal 263 residues of LF), on which most of our experiments were performed, has a net negative charge, it is
driven through the channel by a cis-positive voltage. We have explained this by claiming that the (PA63)7 channel
strongly disfavors the entry of negatively charged residues on proteins to be translocated, and hence the aspartates
and glutamates on LFN enter protonated (i.e., neutralized). Therefore, the translocated species is positively
charged. Upon exiting the channel, the protons that were picked up from the cis solution are released into the
trans solution, thereby making this a proton–protein symporter. Here, we provide further evidence of such a
mechanism by showing that if only one SO3-, which is essentially not titratable, is introduced at most positions in
LFN, through the reaction of an introduced cysteine residue at those positions with 2-sulfonato-ethyl-methanethio-
sulfonate, voltage-driven LFN translocation is drastically inhibited. We also find that a site that disfavors the entry
of negatively charged residues into the (PA63)7 channel resides at or near its Φ-clamp, the ring of seven phenyla-
nines near the channel’s entrance.

INTRODUCTION

The toxin produced by Bacillus anthracis, the causative agent of anthrax, has proved to be a promising model
system to study the molecular driving forces that govern protein translocation across biological membranes. It is
composed of three separate monomeric proteins: protective antigen (PA; 83 kD), named for its effectiveness
in inducing protective antibody-mediated immunity against anthrax, and two enzymes, lethal factor (LF; 90 kD) and
edema factor (EF; 89 kD). The three proteins may be produced recombinantly in soluble form and studied independently (for a review of anthrax toxinn see Young and Collier, 2007). Toxin action is initi-
ated by a self-assembly process. First, PA binds to a cell surface receptor, where it is activated by a furin family
pro tease that cleaves off a 20-kD N-terminal fragment. The remaining 63-kD receptor-bound portion (PA63)
self-assembles into a ringshaped homoheptamer, called the prepore. The prepore may then form complexes
with up to three molecules of EF and/or LF. These complexes are endocytosed and delivered to an acidic
vesicle compartment, where the prepore undergoes an acidic pH-dependent conformational rearrangement to
form a cation-selective, ionconducting channel. The (PA63)7 channel spans the membrane as an extended,
14-stranded β barrel (Benson et al., 1998; Nassi et al., 2002; Nguyen, 2004; Katayama et al., 2008) that serves
as the conduit for LF and EF into the cytosol. Once in the cytosol, LF, a Zn2+-protease, specifically cleaves and
inactivates MAP kinase kinases (Pannifer et al., 2001), and EF, a Ca2+-calmodulin-dependent adenylyl cyclase,
increases cAMP levels (Drum et al., 2002); both activi-
ties benefit invading B. anthracis by suppressing the host’s immune functions (Young and Collier, 2007).

A model of the (PA63)7 14-strand β barrel reveals that its lumen is ~15-Å wide and is able to accommodate sec-
dondary structure only as large as an α-helix (Krantz et al., 2004). Translocation through the lumen thus re-
quires the substrates to unfold. Thermodynamic analysis

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Abbreviations used in this paper: EF, edema factor; LF, lethal factor; MTS-ACE, 2-amino-carboxyl-ethyl-methanethiosulfonate; MTS-ES, 2-sulfon-
ato-ethyl-methanethiosulfonate; MTS-ET, 2-trimethylammonium-ethyl-
methanethiosulfonate; PA, protective antigen; PEG, polyethylene-glycol;
WT, wild-type.

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of the conformational stabilities of the homologous ~250-residue amino-terminal domains of LF and EF (LFN and EFN, respectively) indicates that acidic conditions encountered in the endosome are sufficient to destabilize the native structures of these proteins (Krantz et al., 2004). When added to planar lipid bilayer membranes, (PA63)7 forms channels with a unitary conductance of ~55 pS in 100 mM KCl at pH 5.5 (Krantz et al., 2005); at pM concentrations, several thousand channels can be incorporated into the membrane (Blaustein et al., 1989). It has been demonstrated that these channels are capable of translocating LF and EF across planar lipid bilayers (Krantz et al., 2006), where the amino terminus precedes the carboxy terminus into the pore (Zhang et al., 2004a), and the driving force comes from the gradient of the electrochemical potential of H+ (Zhang et al., 2004b; Krantz et al., 2006). However, translocation is more complicated than acid-induced unfolding, followed by electrophoresis through a passive pore (Finkelstein, 2009). Both the second law of thermodynamics and the laws of electrostatics require that the translocated species have a net positive charge, given that a cis-positive voltage drives translocation, yet LFN has a net negative charge. (LFN contains 54 acidic side chains [19 aspartates and 35 glutamates] and 47 basic side chains [5 arginines, 9 histidines, and 33 lysines] [Bragg and Robertson, 1989]. If the pKs of the side chains are the same as those of their respective free amino acids, LFN bears a net negative charge of ~7 at pH 5.5 and ~12 at pH 6.5, a symmetric pH at which LFN translocation can still be driven by voltage [Krantz et al., 2006]. Thus, unless the average pKs of the aspartates and glutamates on LFN are shifted 1.5 units or more above their free amino acid values, LFN bears a net negative charge at at least some of the pHs at which its translocation has been studied.) The simplest mechanism to achieve a positive charge on the translocated species is for the carboxyl groups of the aspartic and glutamic acid residues to be largely neutralized, i.e., protonated. Thus, these carboxyls on LFN must pick up protons from the cis solution at some point during their entrance into the channel, and then discharge them into the trans solution as they exit the channel. In other words, the (PA63)7 channel functions as a proton–protein symporter (Krantz et al., 2006; Finkelstein, 2009). At all times, the portion of LFN that lies within the channel bears a net positive charge.

At pH 5.5, a carboxyl on LFN spends ~97% of its time in its ionized, negatively charged form (assuming the pKs of the aspartates and glutamates on LFN are approximately the same as those of the free amino acids). Why, then, should its minority, protonated neutral form be
the one that enters the channel? It can be argued that the channel’s significant (although not ideal [Blaustein et al., 1989; Blaustein and Finkelstein, 1990]) cation selectivity implies that it strongly disfavors entry of negatively charged side chains into the channel. Here, we provide further evidence for the importance of the protonation of the carboxyls on LF by showing that if only one SO$_3^-$, which is essentially not titratable, is introduced at most positions in LF (through the reaction of an introduced cysteine residue at those positions with 2-sulfonato-ethyl-methanethiosulfonate [MTS-ES]), LF translocation is drastically inhibited.

**MATERIALS AND METHODS**

**Protein Purification and Labeling with MTS Reagents**

Wild-type (WT) PA (83 kD), its F427A mutant, LF$_N$ (residues 1–263 of LF, containing the N-terminal Novagen His$_6$-tag), and its cysteine mutants (Fig. 1) were expressed recombinantly and purified as described previously (Krantz et al., 2004, 2005; Pimental et al., 2004; Zhang et al., 2004b). The heptameric prepore form of PA$_{63}$ was prepared by nicking PA$_{63}$ with trypsin and purifying the PA$_{63}$ heptamer from the smaller 20-kD fragment using anion-exchange chromatography (Cunningham et al., 2002). The MTS-labeling reaction of LF$_S$ cysteine mutants was performed by incubation of 100 μl LF$_S$ (2 mg/ml) with 3 μl of MTS reagents (20 μg/μl; Toronto Research Chemicals) for 30 min at room temperature in degassed 150 mM NaCl and 20 mM NaPO$_4$, pH 7.2.

**Planar Lipid Bilayers**

Bilayers were formed by the brush technique (Mueller et al., 1963) across a 350-μm diameter aperture in a Teflon partition. Membranes separated two compartments of 3.5 ml containing symmetric buffered solutions of 100 mM KCl, 5 mM potassium succinate, and 1 mM EDTA, pH 5.5, which could be stirred by small magnetic bars. Agar salt bridges (3 M KCl, 3% agar) linked Ag/AgCl and 1 mM EDTA, pH 5.5, which could be stirred by small magnetic buffered solutions of 100 mM KCl, 5 mM potassium succinate, and 1 mM EDTA, pH 5.5. Bilayers were formed by the brush technique ([Mueller et al., 1963]) cation exchange chromatography (Cunningham et al., 2002). The MTS-labeling reaction of LF$_S$ cysteine mutants was performed by incubation of 100 μl LF$_S$ (2 mg/ml) with 3 μl of MTS reagents (20 μg/μl; Toronto Research Chemicals) for 30 min at room temperature in degassed 150 mM NaCl and 20 mM NaPO$_4$, pH 7.2. The reaction was stopped by dialyzing out the MTS reagents at 4°C. To confirm that virtually all of the protein was labeled, MTS-reacted and unreacted protein were incubated with 600 μM maleimide 5,000 polyethylene-glycol (PEG; Sigma-Aldrich) for 30 min at 30°C and then run on an SDS non-reducing acrylamide gel. The unreacted protein suffers a shift on the gel, whereas the MTS-reacted LF$_S$ is unaffected (Fig. 2); WT LF$_S$, which has no native cysteines, is also unaffected (not depicted).

**Figure 2.** Example of an SDS non-reducing acrylamide gel of an LF$_S$ cysteine mutant (I77C) reacted with MTS reagents, followed by incubation with maleimide 5,000 PEG. Lane 1, 177C; lane 2, I77C plus maleimide PEG; lane 3, 177C reacted with MTS-ES, followed by maleimide PEG; lane 4, 177C reacted with MTS-ET, followed by maleimide PEG; lane 5, I77C reacted with MTS-ACE, followed by maleimide PEG. Note the gel shift in lane 2 caused by the reaction of the maleimide PEG with the cysteine on I77C; the virtual absence of any such shift in lanes 3–5 indicates that almost all the 177C had reacted with the MTS reagent.
RESULTS

LF₅ translocation is driven by a gradient of the electrochemical potential of H⁺, which can be established by either applying a ΔΨ or a ΔpH (or both) across the membrane (see Finkelstein, 2009). Although pH-driven translocation is physiologically more relevant than voltage-driven translocation (Krantz et al., 2006), our concern here is strictly with the biophysics of voltage-driven translocation.

Effect of an Introduced SO₃⁻ on LF₅ Translocation

Despite LF₅ having a net negative charge of approximately −7 at pH 5.5, it is driven through the (PA₆₃)₇ channel by cis-positive voltages (Zhang et al., 2004b). We have argued that this can occur because the carboxyls on the aspartates and glutamates of LF₅ are, for the most part, in their protonated form within the channel (Krantz et al., 2006), and that this is because the channel strongly disfavors the entry into it of negative charges (anions) (Finkelstein, 2009). If this is so, one might expect that the introduction into LF₅ of essentially non-titratable negative charges would have a detrimental effect on its rate of translocation. And indeed, introducing only one SO₃⁻ at five arbitrarily chosen positions within its sequence had a profound effect on its rate of translocation. Namely, normally under

Figure 3. The effect of introducing one SO₃⁻ (by reacting an LF₅ cysteine mutant with MTS-ES) on the translocation rate of LF₅. The panels show the normalized rise of conductance (a reflection of translocation of LF₅ through the (PA₆₃)₇ channel) that occurred when, after the perfusion of the indicated MTS-reacted LF₅ cysteine mutant out of the cis compartment, the voltage was stepped from +20 to +55 mV. Note the very slow translocation of the MTS-ES-reacted LF₅ (red). In contrast, the translocation rates of the MTS-ET-reacted (blue) and the MTS-ACE-reacted LF₅ (black) were essentially the same as that of WT LF₅ (which is not shown in the panels for clarity), with a half-time of ~5 s.

Figure 4. Partial recovery of the translocation rate of MTS-ES–reacted LF₅ (red) when positively charged lysines are flanking the introduced SO₃⁻. The experiments were performed as described in Fig. 3. The rate of translocation of MTS-ACE–reacted LF₅ E126C, T199C, and N242C (black) was the same as that of WT LF₅ and the unreacted lysine mutants (not depicted). Note that one lysine adjacent to the SO₃⁻ (orange in E126C and N242C, and purple in T199C) increased the rate of translocation, and two lysines, one on either side of the SO₃⁻ (green in E126C), produced an even greater increase in the rate of translocation, although still considerably short of the rate of translocation of WT LF₅.
our experimental conditions (symmetric pH 5.5, ΔΨ = +55 mV) the translocation half-time of LF_N (with the N-terminal Novagen His6-tag) was ∼5 s. However, after attaching a S-(CH_2)_2SO_3^- at residue K14C, A59C, E126C, T199C, or N242C, we obtained ≤20% translocation even after 45 or 100 s (Figs. 3 and 4). (As expected, if LF_N that had reacted with MTS-ES was subsequently treated with DTT to remove the SO_3^- , its translocation rate was restored to normal [not depicted].) This slow translocation time is most certainly a consequence of the introduced negative charge on SO_3^-, because attaching the similarly sized groups S-(CH_2)_2CONH_2 or S-(CH_2)_2N(CH_3)_3+ (by reacting with 2-aminocarbonyl-ethyl-methanethiosulfonate [MTS-ACE] or 2-trimethylammonium-ethyl-methanethiosulfonate [MTS-ET], respectively) had virtually no effect on the translocation rate (Fig. 3).

In support of this “electrostatic” mechanism of translocation inhibition, we found that introducing one positive charge (Lys+) adjacent to the SO_3^- -bearing cysteine residue at position 126, 199, or 242 increased the rate of translocation, and introducing two positive charges (Lys+) flanking the SO_3^- at 126 (one at residue 125 and one at residue 127) further increased the rate of translocation (Fig. 4). Interestingly, the electrostatic barrier to SO_3^- entry into the channel is so large that even with positively charged lysines flanking the SO_3^- at residue 126, the half-time was considerably slower than that of WT (36 instead of 5 s; Fig. 4).

Exceptions
Whereas introducing an SO_3^- at most positions in LF_N drastically slowed translocation, we found two exceptions to this: introducing SO_3^- at either the C terminus (residue 263) or the N terminus (residue 1) had no effect on the translocation rate (Fig. 5). One can rationalize the former by saying that unlike an interior residue that is followed by another residue, the C-terminal residue is followed by water, which via its higher dielectric constant reduces the electrostatic barrier to entry of the SO_3^- into the channel. One cannot, however, make the same argument for the N-terminal residue 1 and say that it is preceded by water, because our experiments were done with the 20-residue His6-tag attached at the N terminus. Thus, residue 1 is as much an interior residue as 14, 59, 126, 199, and 242, which, when reacted with MTS-ES, had a profound effect on translocation (Fig. 3).

Sequence gazing reveals that the neighborhood of residue 1 differs from that of the other residues we had examined in two respects: (1) it is followed by two glycines, and (2) there are positively charged residues (histidines) nearby on either side of it (at positions +2 and +4) (Fig. 1). Either one of these features could account for the failure of the introduced SO_3^- at position 1 to significantly slow translocation. Thus, because of their small size, the glycines could leave space for water to follow the residue; alternatively, the nearby charged residues could provide electrostatic shielding of the SO_3^- , just as was done by the introduced lysines on either side of residue 126 (Fig. 4). A similar situation exists in the neighborhood of residue 77; namely, it too is followed by two glycines and has nearby positively charged residues (in this case lysines) on either side of it (at positions 75 and 80) at exactly the same distances as exist for residue 1. We therefore examined this position and found that if residue 77 was mutated to a cysteine and

Figure 5. Introducing an SO_3^- at residues 1, 77, or 263 (by reacting the corresponding LF_N cysteine mutant with MTS-ES; red) had very little or no effect on the translocation rate of LF_N. The experiments were performed as described in Fig. 3. Note that if the nearby lysines were mutated to glutamates at positions K75E and K80E (green), an SO_3^- at position 77 greatly retarded LF_N translocation as in Fig. 4. The glutamate mutations alone did not affect the translocation rate (not depicted). (For unknown reasons, the rate of translocation of LF_NA1C reacted with MTS-ES, MTS-ET, or MTS-ACE [half-time of 10 s] was half that of WT LF_N [half-time of 5 s].)
then reacted with MTS-ES, the translocation rate was barely affected (Fig. 5). It appears that of the two possible factors that we have speculated could be the cause of this, the two glycines or electrostatic shielding, it is the latter that accounts for this at position 77, because when the lysines at positions 75 and 80 were mutated to glutamates, the introduction of an SO$_3^-$ at position 77 now severely slowed translocation (Fig. 5). Unfortunately, mutating the histidines at positions $-2$ and $+4$ to aspartates had no effect on the translocation of the MTS-ES-reacted cysteine at position 1 (not depicted). Thus, why an SO$_3^-$ at position 1 does not slow translocation remains an unexplained exception.

A Site of Negative Charge Exclusion from the Channel
Where within the channel is the negative charge exclusion of SO$_3^-$ occurring? The (PA$_63$)$_7$ channel is a mushroom-like structure with a long stem and a cap that contains the binding site for LF$_N$ (Fig. 6 B) (Krantz et al., 2005; Katayama et al., 2008). Near the junction of the cap with the stem lies residue F427, which forms a ring of seven phenylalanines that plays an important role in protein translocation, and which we have dubbed

Figure 6. The effect of replacing phenylalanine with alanine at residue 427 of PA$_63$ on the rate of translocation of LF$_N$. (A) The experiments were performed as described in Fig. 3. For the WT channel, as shown in Fig. 3 and reproduced here, the introduction of an SO$_3^-$ at residue 59 (red) drastically reduced the rate of LF$_N$ translocation from that of MTS-ACE–reacted LF$_N$ (black), which was the same as that of WT LF$_N$ (not depicted). Mutating the phenylalanine at residue 427 to alanine in the (PA$_63$)$_7$ channel dramatically increased the rate of translocation of LF$_N$ with an attached SO$_3^-$ (orange) and decreased the rate of translocation of MTS-ACE–reacted LF$_N$ (gray), which was the same as that of WT LF$_N$ (not depicted). (B) Cartoon of the (PA$_63$)$_7$ channel with LF$_N$ being translocated through it. The constriction near the junction of the vestibule with the stem is the $\Phi$-clamp, which is formed by seven F427s. We envision that for negatively charged residues (aspartates or glutamates) on LF$_N$ to get past the $\Phi$-clamp, they must be neutralized; that is, they pick up protons from the cis solution. This proton is subsequently discharged into the trans solution after the residue has traversed the channel. If a non-titratable SO$_3^-$ is introduced into LF$_N$, it is retarded at the $\Phi$-clamp. Mutation of F427 to alanine alters the constriction and now more readily allows a negatively charged group such as SO$_3^-$ to get past it.
K⁺ over Cl⁻. We see in Fig. 7 that the (PA_{63}F427A)₇ channel, although still cation selective, is less so than is the WT channel.

**Discussion**

Because LF₅ translocation from the cis to the trans solution through (PA₆₃)₇ channels is driven by cis-positive voltages, even though LF₅ bears a net negative charge, we have argued that LF₅’s aspartates and glutamates must be transported in their protonated (neutralized) form (see Krantz et al., 2006; Finkelstein, 2009). That is, negatively charged residues are largely excluded at some point from entering the channel. The experiments reported here support this argument in that (with specific exceptions discussed below) the introduction of SO₃⁻/H₁₁₀₀²⁻ among the residues D₂₇₆, E₃₀₂, E₃₀₈, D₃₁₅, D₃₃₅, and E₃₄₃ (with specific exceptions discussed below) the introduction of SO₃⁻/H₁₁₀₀²⁻ among the residues D₂₇₆, E₃₀₂, E₃₀₈, D₃₁₅, D₃₃₅, and E₃₄₃

![Figure 7](image)

**Figure 7.** The effect of mutating F427 to an alanine on the ion selectivity of the (PA_{63})₇ channel. The experiments were started with the membrane (diphytanoyl-phosphatidylcholine) separated by symmetric solutions of 100 mM KCl, 5 mM potassium succinate, and 1 mM EDTA, pH 5.5. After treating the membrane with KCl nolate, and 1 mM EDTA, pH 5.5. After treating the membrane with the membrane (diphytanoyl-phosphatidylcholine) separated by symmetric solutions of 100 mM KCl, 5 mM potassium succinate, and 1 mM EDTA, pH 5.5. After treating the membrane with KCl nolate, and 1 mM EDTA, pH 5.5. After treating the membrane with KCl nolate, and 1 mM EDTA, pH 5.5. After treating the membrane with KCl nolate, and 1 mM EDTA, pH 5.5. After treating the membrane with KCl nolate, and 1 mM EDTA, pH 5.5. After treating the membrane with KCl nolate, and 1 mM EDTA, pH 5.5. After treating the membrane with KCl nolate, and 1 mM EDTA, pH 5.5. 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of WT LF_N (Fig. 6 A). This is to be expected, because insofar as ionized glutamates and aspartates on LF_N are allowed to enter the channel, they will act to retard its (positive) voltage-driven translocation. At this time, it is not clear to what extent the slower voltage-driven translocation of LF_N through the (PA_{63}F427A)^{7+} channel is a consequence of its allowing negatively charged glutamates and aspartates to enter the channel, or to its effect on the unfolding of LF_N (Krantz et al., 2005).

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