The Prodomain of *Bordetella* **FhaB, a Prototypical Two-Partner Secretion Pathway Protein, Remains Intracellular yet Affects the Conformation of the**

Extracellularly-Located Mature C-terminal Domain

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SUPPLEMENTARY INFORMATION

Supplemental Figure Legends

Supplemental Figure 1

Model of the FhaB/FhaC Two-Partner Secretion (TPS) system. (A) FhaB translocation across the *Bordetella* outer membrane. The FhaB preproprotein (labeled) is exported into the periplasm by the general secretory system (not shown). It is not known if the entire polypeptide is translocated into the periplasm before translocation through FhaC occurs. In this figure, the peptidoglycan layer and cytoplasmic membrane are not shown for simplicity. Also note that this figure was drawn to scale, as best as possible. Residue numbers of the FhaB proprotein are indicated. The FhaB TPS domain (orange) interacts with FhaC (purple) to initiate outer membrane translocation of FhaB as a hairpin. Upon extracellular exposure, the C-terminal portion of the TPS domain folds into a β-helix, nucleating folding of the β-helical shaft (blue) in an N- to C-terminal direction. At this point, FHA biogenesis could proceed by two routes, depending on the localization of the prodomain. (B) Possibility that the prodomain remains intracellular. After the MCD (light green) has reached the cell surface, SphB1 (yellow) and an unidentified protease (dark

green) cleave the intracellular prodomain (red) from FhaB and the prodomain is rapidly degraded. Mature FHA (labeled) can be either surface-associated or released. The mechanism for release is unknown. (C) Possibility that the prodomain reaches the extracellular space. In this scenario, prodomain cleavage and degradation would both occur extracellularly.

Supplemental Figure 2

The FhaB prodomain comprises distinct subdomains. At top is a schematic of *B. bronchiseptica* FhaB showing domain locations. At bottom, WebLogo 3.1 display of homology shared amongst TpsA proteins to the ~125 aa *B. bronchiseptica* FhaB prodomain N-terminus (PNT).

Supplemental Figure 3

Insertion of an HA epitope tag before the FhaB proline-rich region (PRR) does not affect FHA maturation or function. (A) Schematic of FhaB proteins used in experiment. Domain layout is the same as that of Figure 1A. The PRR in front of which the HA tag was introduced is labeled for the HAPRR strain. (B) Anti-MCD and anti-HA immunoblot of whole-cell lysates and concentrated supernatants. Introducing an HA tag at the Cterminus of FhaB causes instability of full-length FhaB. Moving the epitope upstream of the PRR does not affect the integrity or maturation of full-length FhaB. FHA release into the supernatants is unaffected by either location of the HA tag.

Supplemental Figure 4

Introduction of an HA tag to the FhaB prodomain suggests an intracellularly-localized prodomain. (A) Schematic of FhaB proteins used in experiment. Domain layout is the same as that of Figure 1A. (B) At the top, anti-MCD and anti-HA immuno-dot-blot of HAPRR and RBX11 strains. Normalized amounts of whole cells and boiled lysates were applied. Below, illustrations of immuno-stained samples. Layout of these illustrations is as described in Figure 5B.

Supplemental Figure 5

A small amount of prodomain is released from *B. bronchiseptica* with a deletion of the MCT. (A) Schematic of FhaB proteins used in experiment. Domain layout is the same as that of Figure 3A. (B) Anti-MCD and anti-HA immunoblot of concentrated supernatants. On the left is a merge showing release of prodomain from HA-ΔCS, HA-ΔMCT, and HA-ΔPNT strain. On the right is an image of the same immunoblot, with the 700 nm (red) channel isolated and enhanced to facilitate the visualization of prodomain bands released into the supernatant of the ΔMCT strain.

Strain list

Plasmid list

Strain construction

RBX11Δ*sphB1* was constructed by performing allelic exchange on RBX11 using plasmid pEG7SΔ*sphB1* as described (Martínez de Tejada *et al*, 1996). The strain was confirmed to be constructed as intended by PCR and nucleotide sequence analysis.

HAPRR and HAPRRΔ*sphB1* were constructed by performing allelic exchange on RBX11 and RBX11Δ*sphB1*, respectively, using plasmid pSS4245-HAPRR as described (Inatsuka *et al*, 2010). The strains were confirmed to be constructed as intended by PCR and nucleotide sequence analysis.

HA-ΔCS and HA-ΔCSΔ*sphB1* were constructed by performing allelic exchange on HAPRR and HAPRRΔ*sphB1*, respectively, using plasmid pSS4245-ΔCS. The strains were confirmed to be constructed as intended by PCR and nucleotide sequence analysis.

HA-ΔMCT and HA-ΔMCTΔ*sphB1* were constructed by performing allelic exchange on HAPRR and HAPRRΔ*sphB1*, respectively, using plasmid pSS4245-ΔMCT. The strains were confirmed to be constructed as intended by PCR and nucleotide sequence analysis.

HA-ΔPNT and HA-ΔPNTΔ*sphB1* were constructed by performing allelic exchange on HAPRR and HAPRRΔ*sphB1*, respectively, using plasmid pSS4245-ΔPNT. The strains were confirmed to be constructed as intended by PCR and nucleotide sequence analysis.

BPSMAQ was constructed by performing allelic exchange on BPSM using plasmids pSORTP1-Bp MCI/Y1871/AcTEV and pSORTP1-SS Template/Q72His7. The strains were confirmed to be constructed as intended by PCR and nucleotide sequence analysis

BPSMAQT-N was constructed by introducing pEG7-FI1a/C&R-N into BPSMAQ by conjugation and selecting co-integrates on BG-Sm-Gm agar as described (Akerley *et al*, 1995) Integration of plasmids at the correct site in the chromosome was confirmed by PCR.

CTHA was constructed by introducing pEG7-CTHA into RBX11 by conjugation and selecting co-integrates on BG-Sm-Gm agar. Integration of the plasmids at the correct site in the chromosome was confirmed by PCR.

JS26, JS55, JS27, JS56, JS28, JS57, JS48, JS58, JS52, JS59, JS49, JS60, JS51, JS61, JS50, JS62, JS53, JS63, JS54, and JS64 were constructed by introducing pJB51, pJB127, pJB52, pJB128, pJB53, pJB129, pJB87, pJB130, pJB93, pJB131, pJB88, pJB132, pJB89, pJB133, pJB90, pJB134, pJB94, pJB135, pJB95, and pJB136, respectively, into JS20 by conjugation and selecting co-integrates on BG-Sm-Gm agar. Integration of the plasmids at the correct site in the chromosome was confirmed by PCR.

Plasmid construction

pJB28 is a pCR2.1 derivative that contains a PCR-amplified 2.0 kb fragment of RBX11 *fhaB* (corresponding to codons 1814 through 2470).

The following plasmids are pEG7 derivatives used to construct co-integrate strains. Sequences cloned into this plasmid between the gentamicin resistance gene and ampicilin resistance gene are described.

pJB48 contains PCR-amplified 2.0 kb, and 3.8 kb fragments of RBX11 *fhaB* (corresponding to codons 1814 through 2470 and codons 2471-3710 followed by a STOP codon) from RBX11 ligated together.

pJB101 contains PCR-amplified 2.0 kb, and 350 bp fragments of RBX11 *fhaB* (corresponding to codons 1814 through 2470 and codons 2471-2588 followed by a STOP codon) from RBX11 ligated together.

pJB51, pJB52, pJB53, pJB87, pJB93, pJB88, pJB89, pJB90, pJB94 and pJB95 contain PCR-amplified 2.0 kb, and 3.8 kb fragments of RBX11 *fhaB* (corresponding to codons 1814 through 2470 and codons 2471-3710 followed by a STOP codon) from RBX11 ligated together with a QuickChange mutagenesis of the residues specified in plasmid list.

pJB127, pJB128, pJB129, pJB130, pJB131, pJB132, pJB133, pJB134, pJB135 and pJB136 contain PCR-amplified 2.0 kb, and 350 bp fragments of RBX11 *fhaB* (corresponding to codons 1814 through 2470 and codons 2471-2588 followed by a stop codon) from RBX11 ligated together with a QuickChange mutagenesis of the residues specified in plasmid list.

pEG7-CTHA contains PCR-amplified 0.6 kb (corresponding to codons 3429 through 3703) and 0.5 kb fragments of RBX11 *fhaB* (corresponding to codon 3703 extending to

457 bp 3' of STOP codon) ligated together with nucleotides encoding an HA epitope following codon 3703.

The following plasmids are pSS4245 derivatives used for allelic exchange in *B. bronchiseptica*. Sequences cloned into this plasmid between the I-SceI cleavage site and the tetracycline resistance gene are described.

pSS4245-HAPRR contains PCR-amplified 0.5 kb (corresponding to codons 3208 through 3375) and 0.6 kb fragments of RBX11 *fhaB* (corresponding to codons 3375 through 3567) ligated together with nucleotides encoding an HA epitope following codon 3375.

pSS4245-ΔCS contains PCR-amplified 0.5 kb (corresponding to codons 2048 through 2216) and 0.5 kb fragments of RBX11 *fhaB* (corresponding to codons 2648 through 2808) ligated together.

pSS4245-ΔMCT contains PCR-amplified 0.5 kb (corresponding to codons 2048 through 2216) and 0.5 kb fragments of RBX11 *fhaB* (corresponding to codons 2472 through 2640) ligated together.

pSS4245-ΔPNT contains PCR-amplified 0.5 kb (corresponding to codons 2295 through 2471) and 0.5 kb fragments of RBX11 *fhaB* (corresponding to codons 2648 through 2808) ligated together.

The following plasmids are pSORTP1 derivatives used for allelic exchange in *B. pertussis*. Sequences cloned into this plasmid between the gentamicin resistance gene and ampicilin resistance gene are described.

pSORTP1-Bp MCI/Y1871/AcTEV contains PCR-amplified 600 bp fragments flanking the codon for Y1871 of RBX11 *fhaB* with nucleotides encoding an AcTEV cleavage site inserted following Y1871.

pSORTP1-SS Template/Q72His7 contains PCR-amplified 600 bp fragments flanking the codon for Q72 of RBX11 *fhaB* with nucleotides encoding a His7 epitope inserted following Q72.

References

- Akerley BJ, Cotter PA & Miller $[F(1995)$ Ectopic expression of the flagellar regulon alters development of the Bordetella-host interaction. *Cell* 80: 611–620
- Inatsuka CS, Xu Q, Vujkovic-Cvijin I, Wong S, Stibitz S, Miller JF & Cotter PA (2010) Pertactin is required for Bordetella species to resist neutrophil-mediated clearance. *Infect. Immun.* **78:** 2901–2909
- Julio SM & Cotter PA (2005) Characterization of the filamentous hemagglutinin-like protein FhaS in Bordetella bronchiseptica. *Infect. Immun.* **73:** 4960–4971
- López CM, Rholl DA, Trunck LA & Schweizer HP (2009) Versatile dual-technology system for markerless allele replacement in Burkholderia pseudomallei. *Appl. Environ. Microbiol.* **75:** 6496–6503
- Martínez de Tejada G, Miller JF & Cotter PA (1996) Comparative analysis of the virulence control systems of Bordetella pertussis and Bordetella bronchiseptica. *Mol. Microbiol.* **22:** 895–908
- Mazar J & Cotter PA (2006) Topology and maturation of filamentous haemagglutinin suggest a new model for two-partner secretion. *Mol. Microbiol.* 62: 641–654

Miller VL & Mekalanos JJ (1988) A novel suicide vector and its use in construction of insertion mutations: osmoregulation of outer membrane proteins and virulence determinants in Vibrio cholerae requires toxR. *J. Bacteriol.* **170:** 2575-2583

A

B

A

B

Supernatant

Supernatant