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1 **Structure-function analysis of the TssL cytoplasmic domain reveals a new**
2 **interaction between the Type VI secretion baseplate and membrane**
3 **complexes.**

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26

27 **Running head:** TssL structure-function analysis

28

1 Abstract

2 The Type VI secretion system (T6SS) is a multiprotein complex that delivers toxin effectors
3 in both prokaryotic and eukaryotic cells. It is constituted of a long cytoplasmic structure - the
4 tail - made of stacked Hcp hexamers and wrapped by a contractile sheath. Contraction of the
5 sheath propels the inner tube capped by the VgrG spike protein towards the target cell. This
6 tubular structure is built onto an assembly platform - the baseplate - that is composed of the
7 TssEFGK-VgrG subunits. During the assembly process, the baseplate is recruited to a trans-
8 envelope complex comprising the TssJ outer membrane lipoprotein and the TssL and TssM
9 inner membrane proteins. This membrane complex serves as docking station for the
10 baseplate/tail and as channel for the passage of the inner tube during sheath contraction. The
11 baseplate is recruited to the membrane complex through multiple contacts including
12 interactions of TssG and TssK with the cytoplasmic loop of TssM, and TssK interaction with
13 the cytoplasmic domain of TssL, TssL_{Cyto}. Here, we show that TssL_{Cyto} interacts also with the
14 TssE baseplate subunit. Based on the available TssL_{Cyto} structures, we targeted conserved
15 regions and specific features of TssL_{Cyto} in enteroaggregative *Escherichia coli* (EAEC). By
16 using bacterial two-hybrid and co-immunoprecipitation, we further show that the disordered
17 L3-L4 loop is necessary to interact with TssK, that the L6-L7 loop mediates the interaction
18 with TssE, whereas the TssM cytoplasmic loop binds the conserved groove of TssL_{Cyto}.
19 Finally, competition assays demonstrated that these interactions are physiologically important
20 for EAEC T6SS function.

21

22 **Keywords:** Type VI secretion, protein-protein interaction, membrane complex, baseplate
23 complex, loops, crevice, cleft.

24

1 Introduction

2 Bacteria have evolved strategies to survive within difficult environment or to
3 efficiently colonize a specific niche. When nutrients become limiting or when conditions are
4 defavorable, most Gram-negative Proteobacteria delivers anti-bacterial toxins into
5 competitors. One of the main mechanisms for toxin delivery into prokaryotic cells is a
6 multiprotein machinery called Type VI secretion system (T6SS).¹⁻⁶ The T6SS resembles a ~
7 600-nm long cytoplasmic tail-like tubular structure anchored to the cell envelope, and works
8 as a nano-crossbow.^{2,7,8} The T6SS tail shares structural and functional homologies with
9 contractile tail particles such as R-pyocins or bacteriophages.⁷⁻¹⁰ The cytoplasmic tubular
10 structure is constituted of an inner tube made of stacked Hcp hexamers organized head-to-tail
11 and wrapped by a contractile sheath.^{7,9,11-17} Contraction of the sheath propels the inner tube
12 towards the target cell, allowing toxin delivery and target cell lysis.^{7,18-20} This tubular
13 structure is tipped by a spike, composed of a trimer of the VgrG protein and of the PAAR
14 protein, which serves as puncturing device for penetration inside the target cell.^{9,21} Toxin
15 effectors are preloaded and different mechanisms of transport have been proposed, including
16 cargo models in which effectors directly or indirectly binds on VgrG, PAAR or within the
17 lumen of Hcp hexamers.^{3,6,21-29}

18 The T6SS tail polymerizes on an assembly platform or baseplate complex (BC), which
19 is also broadly conserved in contractile particles.³⁰⁻³⁴ The composition of the T6SS baseplate
20 has been recently revealed and is constituted of five proteins: TssE, TssF, TssG and TssK that
21 assemble a complex together with the VgrG spike.^{32,33,35} Once assembled in the cytoplasm,
22 the BC is recruited and stabilized by a trans-envelope complex, or membrane complex (MC),
23 constituted of TssJ, TssL and TssM subunits.^{32,36,37} The structure and assembly of the MC are
24 well known. TssJ is an outer membrane lipoprotein with a tranthyretin fold^{38,39}, whereas
25 TssM and TssL are both anchored to the inner membrane. TssM is constituted of three trans-
26 membrane helices (TMH) that delimitate a cytoplasmic loop between TMH2 and TMH3 and
27 a large periplasmic domain downstream TMH3.⁴⁰ This periplasmic domain could be
28 segmented into four sub-domains, the C-terminal one mediating contacts with TssJ.^{37,39} By
29 contrast, TssL has a single TMH located at its extreme C-terminus, and thus the majority of
30 the protein protrudes into the cytoplasm.⁴¹ The structures of the TssL cytoplasmic domains of
31 enteroaggregative *E. coli* (EAEC), *Francisella tularensis* and *Vibrio cholerae* have been
32 reported: they are composed of 7 helices grouped in two bundles, with an overall shape

1 resembling a hook.⁴²⁻⁴⁴ The biogenesis of the MC starts with TssJ at the outer membrane and
2 progresses with the sequential addition of TssM and TssL.³⁷ Ten copies of this heterotrimeric
3 complex then combine to assemble a 1.7-MDa trans-envelope complex that serves both as
4 docking station for the BC/tail structure and as channel for the passage of the inner tube
5 during sheath contraction.^{32,37,45} Recruitment of the BC to the MC is mediated by multiple
6 interactions including interactions of TssG and TssK with the cytoplasmic domain of TssM,
7 and of TssK with the cytoplasmic domain of TssL.^{32,46}

8 Here, we conducted a structure-function analysis of the TssL cytoplasmic domain,
9 TssL_{Cyto}. We first demonstrate that, in addition to making contacts with the cytoplasmic
10 domain of TssM and TssK, TssL_{Cyto} interacts with the TssE baseplate component.
11 Comparison of the EAEC, *F. tularensis* and *V. cholerae* TssL_{Cyto} structures highlighted the
12 presence of a cleft at the interface of the two-helix bundles with conserved negative charges.
13 In addition, the two loops connecting helices 3-4 and 6-7 display significantly different shapes
14 and/or flexibility. Site-directed mutagenesis coupled to protein-protein interaction studies
15 demonstrated that the L3-4 and L6-7 loops mediate contact with the baseplate components
16 TssK and TssE respectively, whereas the central cleft accommodates the TssM cytoplasmic
17 domain. Finally, anti-bacterial assays showed that all these contacts are necessary for proper
18 function of the Type VI secretion apparatus.

19 **Results**

20 **The TssL cytoplasmic domain, TssL_{Cyto}, interacts with itself, the cytoplasmic loop of** 21 **TssM and the TssE and TssK baseplate components.**

22 Previous studies have demonstrated that the cytoplasmic domain of the
23 enteroaggregative *Escherichia coli* TssL protein (EC042_4527; Genbank accession (GI):
24 **284924248**) forms dimers and interacts with the TssM and TssK proteins.^{40,42,46} To gain
25 further insights onto the interaction network of TssL_{Cyto}, we performed a systematic bacterial
26 two-hybrid (BACTH) analysis (Fig. 1A). As previously shown, we detected TssL_{Cyto}
27 interaction with itself, with TssK and with the cytoplasmic domain of TssM, TssM_{Cyto}. In
28 addition, this analysis revealed the interaction between TssL_{Cyto} and the baseplate component
29 TssE (Fig. 1A). The TssL_{Cyto}-TssE interaction was further validated *in vitro* by using Surface
30 Plasmon Resonance using purified proteins. TssE was covalently bound to the sensorchip and
31 recordings were monitored after injection of increasing concentrations of TssL_{Cyto} (Fig. 1B

1 and 1C). The sensorgrams confirmed the BACTH results and demonstrated that the two
2 proteins interact with an affinity estimated to $55 \pm 1.3 \mu\text{M}$ (Fig. 1B and 1C).

3

4 **Structure analyses of TssL cytoplasmic domains.**

5 The crystal structures of the EAEC, *F. tularensis* and *V. cholerae* TssL cytoplasmic
6 domains are available (PDB IDs: **3U66**⁴², **4ACL**⁴³ and **4V3I**⁴⁴). All structures share common
7 features (Fig. 2A; Supplementary Fig. S1): TssL_{Cyto} is composed of 7 α -helices organized in
8 two bundles constituted of helices α 1-4 and α 5-7. The α 5-7 bundle is made of shorter helices
9 in average, making an overall hook-like structure delimiting a cleft comprising conserved
10 charged residues including aspartate 74 and glutamate 75 (Supplementary Fig. S1A).
11 However, the three structures also highlighted significant differences, notably in loops L3-L4
12 and L6-L7. TssL_{Cyto} loop L3-L4 is disordered in *F. tularensis* whereas comprises a small
13 additional α -helix, α A, in EAEC and *V. cholerae*. In addition, part of the L3-L4 loop
14 structure could not be solved in the EAEC TssL_{Cyto}, suggesting that this loop exhibits
15 structural flexibility. TssL_{Cyto} loop L6-L7 comprises an additional α -helix, α B, in *V. cholerae*,
16 whereas adopts different conformations in EAEC and *F. tularensis* (Supplementary Fig. S1).
17 These two loops having distinct structures, conformations or flexibility, they could be
18 considered as interesting binding sites to confer specificity.

19

20 **Mutagenesis of the charged cleft and L3-L4 and L6-L7 loops unveils contact zones with** 21 **TssM_{Cyto}, TssK and TssE.**

22 To gain information on the role of the conserved cleft and of the L3-L4 and L6-L7
23 loops, we engineered amino-acid substitutions in these different regions (Fig. 2B and Table
24 1): (i) two charged residues (Glu-81 and Asp-84) within loop L3-L4 were converted to
25 opposed charges (GluAsp-to-LysLys mutant, called hereafter EKDK) (orange arrows in Fig.
26 2), (ii) small (Gly-137), aromatic (Phe-138) and charged (Asp-74 and Glu-75) chains within
27 the cleft were substituted to yield Gly-to-Glu (GE), Phe-to-Glu (FE), GlyPhe-to-GluGlu
28 (GEFE), Asp-to-Arg (DR), Glu-to-Arg (ER) and AspGlu-to-ArgArg (DRER) mutants (green
29 arrows in Fig. 2), and (iii) three hydrophilic/charged residues within loop L6-L7 (Gln-145,

1 Asp-146 and Asp-147) were substituted with Lysine residues (GlnAspAsp-to-LysLysLys,
2 QKDKDK) (blue arrows in Fig. 2).

3 These substitutions were first introduced into the TssL_{Cyto}-T18 and pIBA-TssL_{Cyto}
4 vectors to test their impact on the interaction with TssE, TssK and the cytoplasmic loop of
5 TssM, TssM_{Cyto}, using bacterial two-hybrid and co-immunoprecipitation (Fig. 3). Two-hybrid
6 analyses showed that none of these substitutions break the oligomerization of TssL_{Cyto} (Fig.
7 3A), in agreement with a previous study showing that TssL_{Cyto} oligomerization is mediated by
8 contacts between helices α 1.⁴² These results also suggest that each mutant variant is properly
9 produced and does not present large structural changes compared to the wild-type TssL_{Cyto}
10 domain. The assay also revealed that most mutations within the TssL_{Cyto} central cleft prevent
11 formation of the TssL_{Cyto}- TssM_{Cyto} complex whereas substitutions within loops L3-L4 and
12 L6-L7 abolish interaction with TssK and TssE, respectively (Fig. 3A).

13 These two-hybrid results were validated by co-immuno-precipitation analyses. Soluble
14 lysates of cells producing the C-terminally FLAG-tagged wild-type TssL cytoplasmic domain
15 and its substitution variants were combined with lysates containing VSV-G-tagged TssE,
16 TssK and TssM_{Cyto}. TssL_{Cyto}-containing complexes were immobilized on agarose beads
17 coupled to the monoclonal anti-FLAG antibody. Figure 3B shows that the wild-type TssL_{Cyto}
18 domain co-precipitates TssE, TssK and TssM_{Cyto}. Each TssL_{Cyto} variant is produced and
19 immuno-precipitated at levels comparable to the wild-type TssL_{Cyto} domain. Mutation of the
20 Glu-Asp (EKDK mutant) and Gln-Asp-Asp (QKDKDK mutant) motifs within the L3-L4 and
21 L6-L7 loops prevented interaction with TssK and TssE respectively, whereas most
22 substitutions within the conserved groove abolished interaction with the TssM cytoplasmic
23 domain (Fig. 3B).

24

25 **TssL_{Cyto} interactions with TssE, TssK and TssM_{Cyto} are critical for proper function of**
26 **the Type VI secretion apparatus.**

27 The EAEC Sci-1 T6SS is involved in inter-bacterial competition by delivering Tle1, a
28 toxin with phospholipase activity into competitor cells.²⁷ We therefore tested whether
29 substitutions that abolish TssL_{Cyto} complexes formation impact the function of the T6SS. The
30 substitutions were introduced into the pOK-TssL vector, that encodes the full length TssL
31 protein and previously shown to fully complement the Δ tssL phenotypes.⁴¹ The anti-bacterial

1 activity was tested against a competitor strain engineered to constitutively express the GFP
2 and to resist kanamycin. The fluorescence levels of mixture containing the EAEC and
3 competitor strains at a 4:1 ratio, which is proportional to the number of competitor cells was
4 measured after 4 hours of contact. In addition, the survival of the competitor strain was
5 measured by counting fluorescent colony-forming units (cfu) after plating serial dilutions of
6 the mixture on plates supplemented with kanamycin. The results represented in Figure 4 show
7 that the growth of the competitor strain was inhibited by the $\Delta tssL$ strain producing the wild-
8 type TssL protein, at a level comparable to that of the wild-type strain. By contrast, the $\Delta tssL$
9 strain did not cause growth inhibition of competitor cells. With the exception of the FE
10 mutant strain, all the TssL variants were unable to complement the anti-bacterial defects of
11 the $\Delta tssL$ strain, demonstrating the formation of TssL_{Cyto}-TssE, TssL_{Cyto}-TssK and TssL_{Cyto}-
12 TssM_{Cyto} complexes is necessary for proper assembly and function of the EAEC Sci-1 T6SS.

13

14 Discussion

15 In this study, we have used a systematic bacterial two-hybrid approach to define the
16 partners of the T6SS TssL cytoplasmic domain. In addition to the known interacting subunits,
17 TssM⁴⁰ and TssK⁴⁶, we have found an additional contact with the TssE protein, a component
18 of the baseplate. This interaction was confirmed *in vitro* using surface plasmon resonance.
19 With the identification of TssM_{Cyto}-TssG, TssM_{Cyto}-TssK and TssL_{Cyto}-TssK contacts^{32,46,47},
20 the interaction of TssL_{Cyto} with TssE corresponds to the fourth interaction between the T6SS
21 membrane and baseplate complex. The cytoplasmic domain of TssL is located at the base of
22 the TssJLM complex³⁷, a location compatible with the position of the baseplate *in vivo*.^{7,32,48}
23 Although these interactions are of low affinity between isolated molecules (the dissociation
24 constant measured *in vitro* for the TssL_{Cyto}-TssE interaction is ~ 50 μ M), the avidity should
25 increase within the secretion apparatus by the number of interactions and the local
26 concentration. Furthermore, the existence of four contacts likely stabilizes the recruitment of
27 the baseplate to the membrane complex. These multiple contacts are probably important to
28 properly position the baseplate onto the membrane complex and to maintain the baseplate
29 stably anchored when the sheath contracts. In addition, it has been shown that the
30 bacteriophage T4 baseplate is subjected to large conformational changes during sheath
31 contraction^{33,49}, and a similar situation is likely to occur in the case of the T6SS.^{30,32} Therefore

1 it might be critical to have a multitude of contacts between the baseplate and membrane
2 complexes as several interactions might be broken during the conformational transition.

3 TssL dimerizes and interacts with three proteins of the secretion apparatus (Fig. 5). In
4 enteroaggregative *E. coli*, TssL dimerization occurs mainly by the trans-membrane segment
5 with contribution of residues from helix $\alpha 1$. In this study, we provided further molecular
6 details on the TssL interaction by conducting a structure-function analysis. First, using
7 sequence alignment, we defined that a number of residues share high level of conservation.
8 Interestingly, most of these residues locate at the interface between the two-helix bundles and
9 delimitate a cleft. Second, by comparing the three available crystal structures of TssL
10 cytoplasmic domains (from EAEC, *F. tularensis* and *V. cholerae*), we targeted two loops,
11 loops L3-L4 and L6-L7, which present different shapes, distinct secondary structures
12 (addition of short helices) and are highly degenerated. Substitutions were introduced in the
13 cleft as well as in loops L3-L4 and L6-L7 and were tested for their impact on the interactions.
14 None of these mutations disrupted the oligomerization of TssL_{Cyto} suggesting that their impact
15 on TssL_{Cyto} folding was null or moderated. Our data show that the cleft is required for proper
16 interaction with TssM_{Cyto}, whereas loops L3-L4 and L6-L7 are putative binding sites for TssK
17 and TssE respectively. The conservation of the charged crevice in TssL proteins suggests that
18 the mode of binding of TssL/TssM proteins might be conserved. It is worthy to note that the
19 T6SS-associated TssL and TssM proteins share homologies with IcmH/DotU and IcmF, two
20 subunits of the *Legionella pneumophila* Type IVb secretion system (T4bSS).^{8,42} Interestingly,
21 IcmH/DotU also possesses charged residues in the putative cleft position, suggesting that this
22 cleft might also be important for binding to IcmF. By contrast, the variability of the L3-L4
23 and L6-L7 loops might confer specificity between TssL proteins and the baseplate complex,
24 notably when different T6SS are produced simultaneously in a bacterium. However, while our
25 results demonstrate that these regions are necessary for these interactions, it remains to be
26 defined whether these regions are sufficient. Swapping experiments between TssL proteins
27 from different bacteria would be an interesting extension of this study. Finally, these data are
28 interesting for the development of inhibitors that will target the assembly of the membrane
29 complex or the recruitment of the baseplate. Specifically, crevices such as the cleft that
30 accommodates the TssM cytoplasmic domain are interesting targets for drugs, while mimetic
31 peptides might be used to prevent interaction of the baseplate components with the TssL
32 loops.

1

2 MATERIALS and METHODS

3 **Bacterial strains and media.** The *Escherichia coli* K-12 DH5 α , BTH101, W3110 and BL21(DE3)
4 pLysS strains were used for cloning procedures, bacterial two-hybrid analyses, co-
5 immunoprecipitations and protein production, respectively. Strain W3110 pUA66-*rrnB* (Kan^R,
6 constitutively expressing the Green Fluorescent Protein [GFP])^{50,51} was used as prey in anti-bacterial
7 competition experiments. Enteroaggregative *E. coli* (EAEC) strain 17-2 has been used as source of
8 DNA for PCR amplification, and for phenotypic analyses. The Δ *tssL* 17-2 derivative mutant strain has
9 been previously described.³⁶ Cells were grown in Lysogeny broth (LB), Terrific Broth (TB) or Sci-1-
10 inducing medium (SIM)⁵² as specified. Plasmids were maintained by the addition of ampicillin (100
11 μ g/mL), chloramphenicol (40 μ g/mL) or kanamycin (50 μ g/mL for *E. coli* K-12 and 100 μ g/mL for
12 EAEC). Expression of genes cloned into pOK12, pASK-IBA37+, pBAD33 and pETG20A vectors
13 were induced by the addition of isopropyl-thio- β -D-galactopyranoside (IPTG; 50 μ M in liquid, 10
14 μ M on agar plates), anhydrotetracyclin (AHT; 0.1 μ g/mL), L-arabinose (0.2%) and IPTG (0.5 mM),
15 respectively.

16 **Plasmid construction.** Plasmids used in this study are listed in Supplemental Table S1. Polymerase
17 Chain Reactions (PCR) were performed using a Biometra thermocycler using the Q5 high fidelity
18 DNA polymerase (New England BioLabs). Custom oligonucleotides, listed in Supplemental Table S1,
19 were synthesized by Sigma Aldrich. Enteroaggregative *E. coli* 17-2 chromosomal DNA was used as a
20 template for all PCRs. The amplified DNA fragments correspond to the full-length or the cytoplasmic
21 domain (TssL_{Cyto}, residues 1-184)⁴¹ of TssL (EC042_4527, GI: 284924248), the full-length TssK
22 (EC042_4526, GI: 284924247) and TssE (EC042_4545, GI: 284924266) proteins, and the
23 cytoplasmic domain (TssM_{Cyto}, residues 62-360) of the TssM protein (EC042_4539, GI: 284924260).
24 The pOK-TssL plasmid, producing the full-length TssL proteins fused to a C-terminal HA epitope and
25 plasmids pETG20A-TssL_{Cyto} and pETG20A-TssE have been previously described.^{41,42,45} pASK-
26 IBA37+, pBAD33 plasmid derivatives were engineered by restriction-free cloning⁵³ as previously
27 described.³⁶ Briefly, genes of interest were amplified with oligonucleotides introducing extensions
28 annealing to the target vector. The double-stranded product of the first PCR was then been used as
29 oligonucleotides for a second PCR using the target vector as template. Codon substitutions have been
30 obtained by site-directed mutagenesis using complementary oligonucleotides bearing the nucleotide
31 modifications. All constructs have been verified by restriction analysis and DNA sequencing
32 (Eurofins, MWG).

33 **Bacterial two-hybrid assay.** The adenylate cyclase-based bacterial two-hybrid technique⁵⁴ was used
34 as previously published.⁵⁵ Briefly, compatible vectors producing proteins fused to the isolated T18 and

1 T25 catalytic domains of the *Bordetella* adenylate cyclase were transformed into the reporter BTH101
2 strain and the plates were incubated at 30°C for 24 hours. Three independent colonies for each
3 transformation were inoculated into 600 µL of LB medium supplemented with ampicillin, kanamycin
4 and IPTG (0.5 mM). After overnight growth at 30°C, 10 µL of each culture were spotted onto LB
5 plates supplemented with ampicillin (100 µg/mL), kanamycin (50 µg/mL), IPTG (0.5 mM) and
6 bromo-chloro-indolyl-β-D-galactopyrannoside (40 µg/mL) and incubated for 16 hours at 30 °C. The
7 experiments were done at least in triplicate from independent transformations and a representative
8 result is shown.

9 **Co-immunoprecipitations.** W3110 cells producing the protein of interest were grown to an $A_{600} \sim 0.4$
10 and the expression of the cloned genes were induced with AHT (0.1 µg/mL) or L-arabinose (0.2%) for
11 1 hour. 10^{10} cells were harvested, and the pellets were resuspended in 1 mL of LyticB buffer (Sigma-
12 Aldrich) supplemented with lysozyme 100 µg/mL, DNase 100 µg/mL and protease inhibitors
13 (Complete, Roche) and incubated for 20 min at 25°C. Lysates were then clarified by centrifugation at
14 $20,000 \times g$ for 10 min. 250 µL of each lysate were mixed, incubated for 30 min on a wheel and the
15 mixture was applied on anti-FLAG M2 affinity gel (Sigma-Aldrich). After 2 hours of incubation, the
16 beads were washed three times with 1 mL of 20 mM Tris-HCl pH 7.5, 100 mM NaCl, resuspended in
17 25 µL of Laemmli loading buffer, boiled for 10 min and subjected to SDS-PAGE and
18 immunodetection analyses.

19 **Anti-bacterial competition assay.** Antibacterial competition growth assays were performed as
20 previously described in Sci-1-inducing conditions²⁷, except that cultures were supplemented with
21 IPTG 50 µM, and that IPTG (10 µM) was added on the competition plates. The wild-type *E. coli*
22 strain W3110 bearing the kanamycin-resistant GFP⁺ pUA66-*rrnB* plasmid⁵¹ was used as prey. After
23 incubation on plates for 4 hours, cells were scratched off and the fluorescence levels were measured
24 using a TECAN infinite M200 microplate reader. The number of surviving prey cells was measured
25 by counting fluorescent colonies on kanamycin plates.

26 **Protein purification.** The TssE protein and TssL cytoplasmic domain produced from pETG20A
27 derivatives are fused to an N-terminal 6×His-tagged thioredoxin (TRX) followed by a cleavage site for
28 the Tobacco etch virus (TEV) protease. Purifications of TssE and TssL_{Cyto} have been performed as
29 previously described.^{42,45} Briefly, *E. coli* BL21(DE3) pLysS cells carrying the pETG20A plasmid
30 derivatives were grown at 37°C in TB medium (1.2% peptone, 2.4% yeast extract, 72 mM K₂HPO₄,
31 17 mM KH₂PO₄, and 0.4% glycerol) and expression of the cloned genes was induced at $A_{600} = 0.6$ with
32 0.5 mM IPTG for 18 hours at 16°C. Cells were then resuspended in lysis buffer (50 mM Tris-HCl pH
33 8.0, 300 mM NaCl, 1 mM EDTA, 0.5 mg/mL lysozyme, 1mM phenylmethylsulfonyl fluoride),
34 submitted to four freeze-thawing cycles and sonicated after the addition of 20 µg/mL DNase and 20

1 mM MgCl₂. The soluble fraction obtained after centrifugation for 30 min at 16,000 × g was loaded onto a 5-mL Nickel column (HisTrap™ FF) using an ÄKTA Explorer apparatus (GE healthcare) and the immobilized proteins were eluted in 50 mM Tris-HCl pH8.0, 300 mM NaCl supplemented with 250 mM imidazole. The protein solution was desalted on a HiPrep 26/10 column (Sephadex™ G-25, Amersham Biosciences), and untagged proteins were obtained by cleavage using 2 mg of TEV protease for 18 hours at 4°C and collected in the flow-through of a 5-mL Nickel column. The proteins were concentrated using the centricon technology (Millipore, 10-kDa cut-off). After concentration, the soluble proteins were passed through a Sephadex 200 26/60 column pre-equilibrated with 25 mM Tris-HCl pH7.5, 100 mM NaCl, 5% Glycerol.

10 **Surface Plasmon Resonance (SPR).** Steady state interactions were monitored by SPR using a BIAcore T200 at 25°C, as previously described.³⁹ Briefly, the HC200m sensor chip (Xantech) was coated with purified the thioredoxin-TssE fusion protein immobilized by amine coupling (Δ RU=4000-4300). A control flow-cell was coated with thioredoxin immobilized by amine coupling at the same concentration (Δ RU=4100). Purified TssL_{Cyto} (five concentrations ranging from 5 to 75 μ M) were injected and binding traces were recorded in duplicate. The signal from the control flow cell and the buffer response were subtracted from all measurements. The dissociation constants (K_D) were estimated using the GraphPad Prism 5.0 software on the basis of the steady state levels of Δ RU, directly related to the concentration of the analytes. The K_D were estimated by plotting the different Δ RU at a fixed time (5 s before the end of the injection step) against the different concentrations of TssL_{Cyto}. For K_D calculation, nonlinear regression fit for XY analysis was used and one site (specific binding) as a model which corresponds to the equation $Y = B_{max} * X / (K_d + X)$.

22

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30

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3

4 **Authors contribution**

5 A.Z., A.E. and L.J. constructed the vectors for the *in vivo* studies and performed the BACTH
6 experiments, Chl.C. performed the co-immunoprecipitations and anti-bacterial assays, A.Z.,
7 E.D. and E.C. analysed the TssL structure and identified regions for mutagenesis, B.D.
8 purified TssE and performed SPR experiments E.C. and C.C. supervised the experiments.
9 E.C. wrote the manuscript. Each author reviewed the manuscript prior to submission.

10 **Additional information**

11 **Supplemental information.** The supplemental information contains one Supplemental Table
12 (Strains, Plasmids and Oligonucleotides used in this study) and two Supplemental Figure (S1,
13 Comparison of the EAEC, *F. tularensis* and *V. cholerae* TssL_{Cyto} structures; S2, Sequence
14 alignment of TssL proteins).

15 **Competing financial interests.** The authors declare no competing financial interests.

1 Legend to Figures

2 **Figure 1. TssL_{Cyto} oligomerizes and interacts with TssE, TssK and TssM_{Cyto}.** (A) Bacterial two-
3 hybrid assay. BTH101 reporter cells producing the TssL_{Cyto}-T18 fusion protein and the indicated T6SS
4 proteins fused to the T25 domain of the *Bordetella* adenylate cyclase were spotted on X-Gal-IPTG
5 reporter LB agar plates. Only the cytoplasmic (Cyto) or periplasmic (Peri) domains were used for
6 membrane-anchored proteins. (B and C) Surface plasmon resonance analysis. SPR sensorgrams
7 (expressed as variation of resonance units, Δ RU) were recorded after injection of the increasing
8 concentrations of purified TssL_{Cyto} (from light grey to black: 5, 10, 20, 37.5 and 75 μ M) on TssE-
9 coated HC200m chips (B). The graphs reporting Δ RU as a function of TssL_{Cyto} concentration were
10 used to estimate the dissociation constants of the TssL_{Cyto}-TssE complex (C).

11 **Figure 2. Structure of the EAEC TssL_{Cyto} domain.** (A) Crystal structure of the EAEC TssL_{Cyto}
12 domain. The protein is shown as ribbon and α -helices (α 1- α 7) are indicated. The unstructured L3-L4
13 loop (orange arrow) is shown in dotted line, whereas the L6-L7 loop and the cleft are indicated by blue
14 and green arrows respectively. The figure was made with Chimera.⁵⁶ (B) Sequence of the crystallized
15 TssL_{Cyto} domain, with the same color code that in panel A. The residues substituted in this study are
16 indicated by arrowheads (green, cleft; orange, L3-L4 loop; blue, L6-L7 loop).

17 **Figure 3. Distinct motifs on TssL_{Cyto} mediate interactions with TssE, TssK and TssM_{Cyto}** (A)
18 Bacterial two-hybrid assay. BTH101 reporter cells producing the TssL_{Cyto}-T18 fusion protein variants
19 and the indicated T6SS proteins fused to the T25 domain of the *Bordetella* adenylate cyclase were
20 spotted on X-Gal-IPTG reporter LB agar plates. Only the cytoplasmic (*c*) or periplasmic (*p*) domains
21 were used for membrane-anchored proteins. (B) Co-immunoprecipitation assay. Soluble lysates from
22 3×10^{10} *E. coli* K12 W3110 cells producing WT or mutant FLAG-tagged TssL_{Cyto} (Lc_{FL}) and VSV-G-
23 tagged TssE (TssE_V), TssK (TssK_V) or TssM_{Cyto} (TssMc_V) proteins were subjected to
24 immunoprecipitation with anti-FLAG-coupled beads. The lysates and immunoprecipitated (IP)
25 material were separated by 12.5% acrylamide SDS-PAGE and immunodetected with anti-FLAG
26 (lower panels) and anti-VSV-G (upper panels) monoclonal antibodies. Molecular weight markers (in
27 kDa) are indicated.

28 **Figure 4. TssL_{Cyto} interactions with TssE, TssK and TssM_{Cyto} are required for T6SS anti-**
29 **bacterial activity.** *E. coli* K-12 prey cells (W3110 *gfp*⁺, kan^R) were mixed with the indicated attacker
30 cells, spotted onto Sci-1 inducing medium (SIM) agar plates and incubated for 4 hours at 37°C. The
31 relative fluorescence of the bacterial mixture (in arbitrary unit, AU) is indicated in the upper graph,
32 and the number of recovered *E. coli* prey cells (counted on selective kanamycin medium) is indicated
33 in the graph (in log₁₀ of colony-forming unit (cfu)). The circles indicate values from three

1 independent assays, and the average is indicated by the bar.

2 **Figure 5. Schematic representation of the TssL_{Cyto} interaction network.** Schematic representation
3 of the TssJLM membrane complex (MC) and its interactions with the TssKEFG-VgrG baseplate
4 complex (BC). The TssL (TssL_{Cyto}) and TssM (TssM_{Cyto}) cytoplasmic domains are shown in orange
5 and blue respectively. The interactions defined in this study are indicated by red arrows. Interactions
6 determined previously⁴⁶ or in the accompanying article⁴⁷ are shown in blue dashed arrows.

7

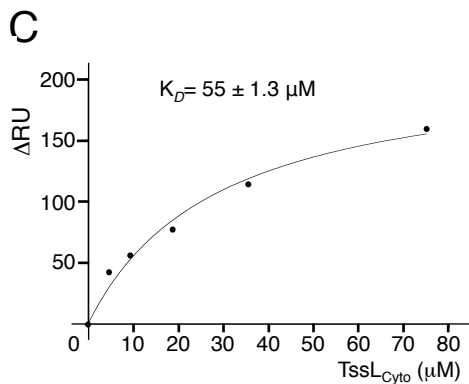
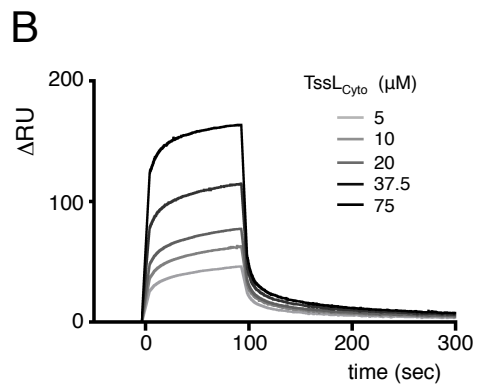
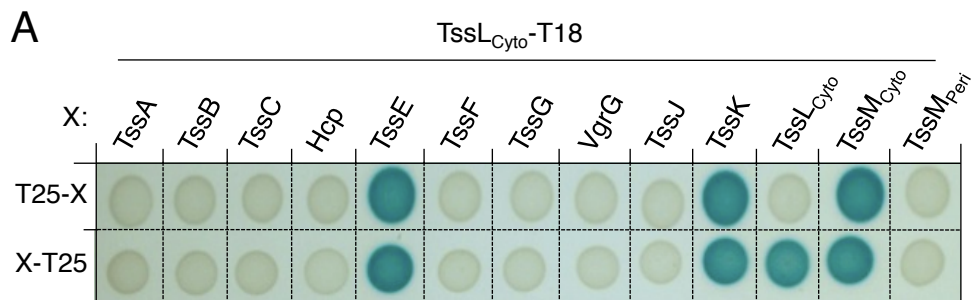
8 **Legend to Supplementary Data**

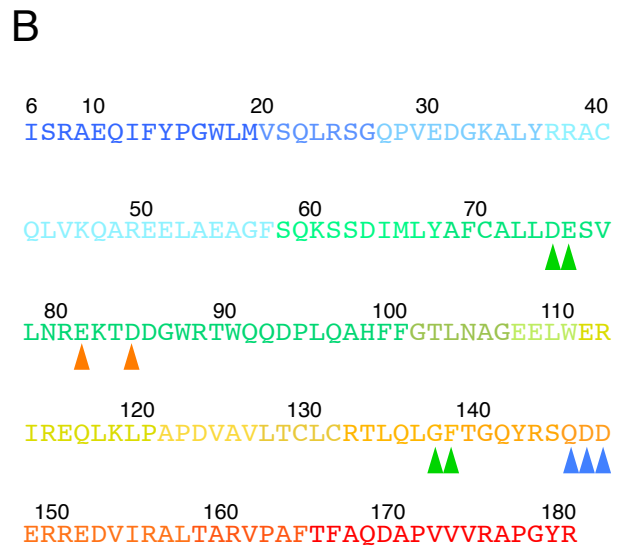
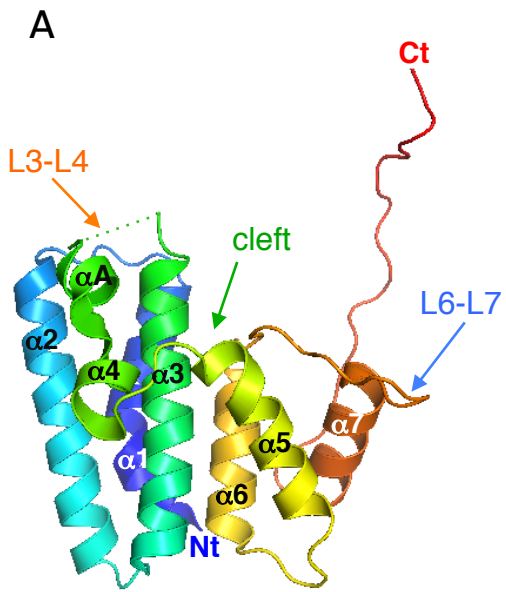
9 **Figure S1. Comparison of the three available TssL_{Cyto} crystal structures.** (A) Sequence alignment
10 of the enteroaggregative *E. coli* (EAEC), *Francisella* and *Vibrio* TssL_{Cyto} sequences. The secondary
11 structures of the EAEC TssL_{Cyto} protein are shown on top whereas conserved residues are shown in
12 red. The residues substituted in this study are indicated by arrowheads (green, cleft; orange, L3-L4
13 loop; blue, L6-L7 loop). (B) Merged crystal structures of the EAEC (PDB: 3U66; green), *Francisella*
14 *tularensis* (PDB: 4ACL, purple) and *Vibrio cholerae* (PDB: 3V3I, blue) TssL_{Cyto} domains. The
15 positions of the cleft, L3-L4 and L6-L7 loops are indicated by green, orange and blue arrows. (C-E)
16 Crystal structures of EAEC (PDB: 3U66; C), *Francisella tularensis* (PDB: 4ACL, D) and *Vibrio*
17 *cholerae* (PDB: 3V3I, E) TssL_{Cyto} domains. Panel C highlights the positions and locations of the
18 residues substituted, as well as helix α A (loop L3-L4) whereas panel E highlights helices α A (loop
19 L3-L4) and α B (loop L6-L7). The figures were made with Chimera.⁵⁶

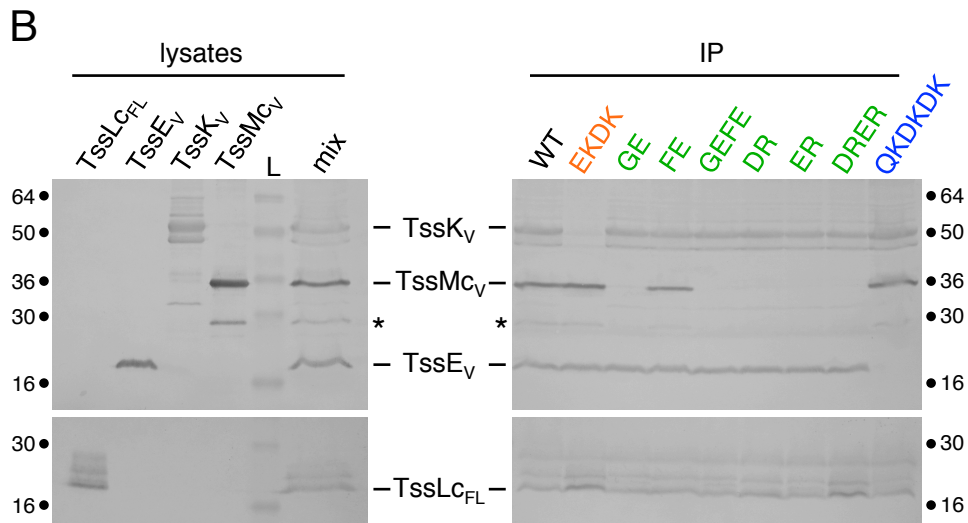
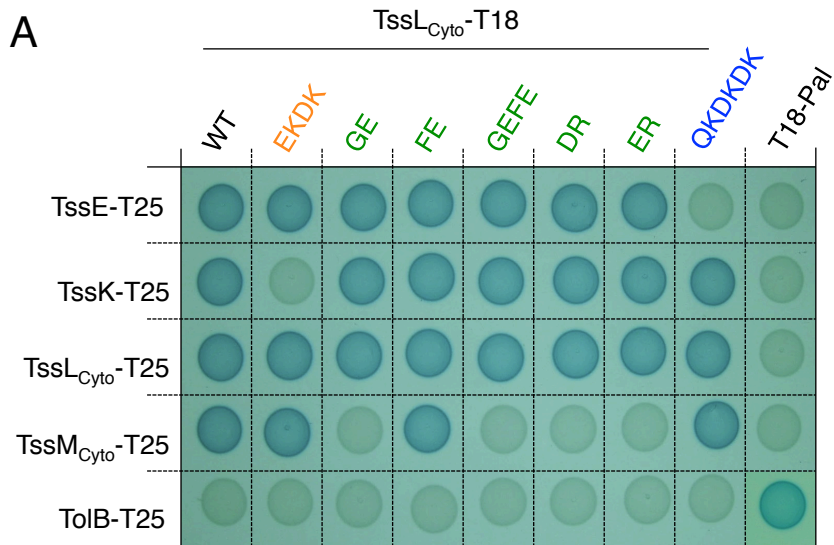
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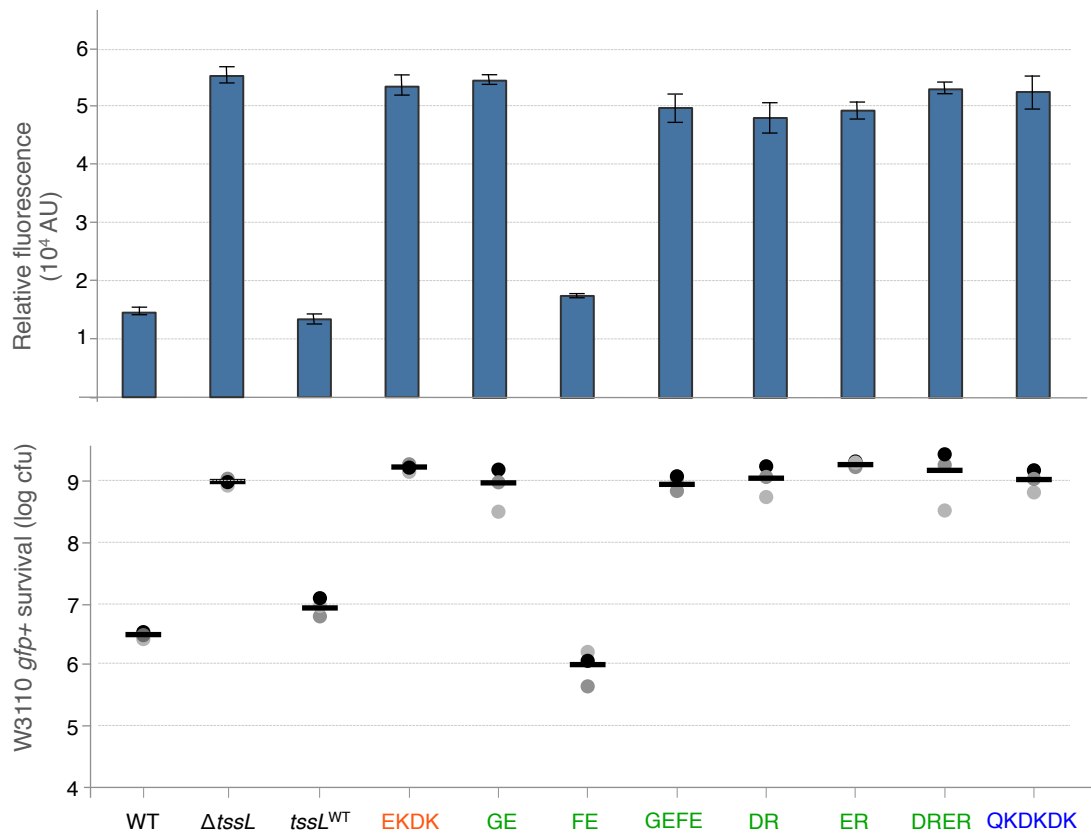
21 **Table S1. Strains, Plasmids and Oligonucleotides used in this study.**

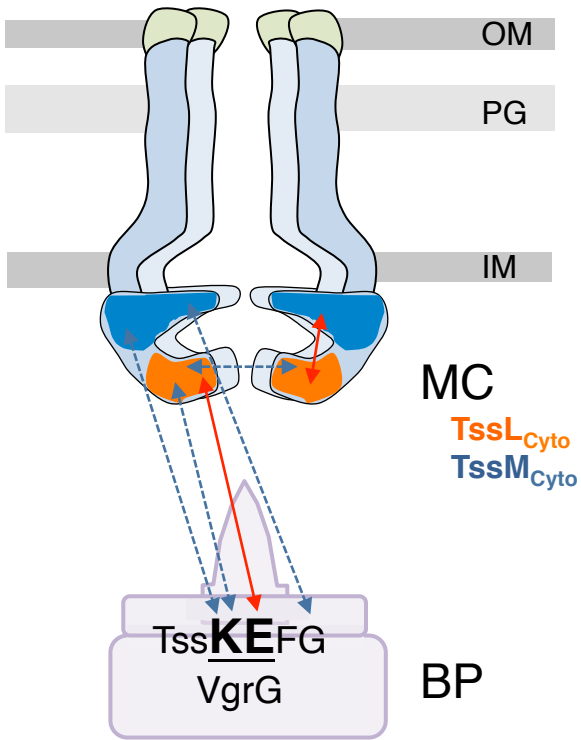
22











SUPPLEMENTAL DATA

Structure-function analysis of the TssL cytoplasmic domain reveals a new interaction between the Type VI secretion baseplate and membrane complexes.

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Supplemental Table S1. Strains, plasmids and oligonucleotides used in this study.

Strains

| Strains | Description and genotype | Source |
|-----------------------------------|---|-------------------------------|
| <i>E. coli</i> K-12 | | |
| DH5 α | F-, Δ (<i>argF-lac</i>)U169, <i>phoA</i> , <i>supE44</i> , Δ (<i>lacZ</i>)M15, <i>relA</i> , <i>endA</i> , <i>thi</i> , <i>hsdR</i> | New England Biolabs |
| W3110 | F-, lambda- IN(<i>rrnD-rrnE</i>)1 <i>rph-1</i> | Laboratory collection |
| BTH101 | F-, <i>cya-99</i> , <i>araD139</i> , <i>galE15</i> , <i>galK16</i> , <i>rpsL1</i> (<i>Str^R</i>), <i>hsdR2</i> , <i>mcrA1</i> , <i>mcrB1</i> . | Karimova <i>et al.</i> , 2005 |
| BL21(DE3) pLys | F-, miniF <i>lysY lacI^f</i> (Cm ^R) / <i>fhuA2 lacZ::T7 gene1 [lon] ompT gal sulA11 R(mcr-73::miniTn10--Tet^S)2 [dcm] R(zgb-210::Tn10-Tet^S) endA1 Δ(<i>mcrC-mrr</i>) 114::IS10</i> | New England Biolabs |
| Enterogaagregative <i>E. coli</i> | | |
| 17-2 | WT enterogaagregative <i>Escherichia coli</i> | Arlette Darfeuille-Michaud |
| 17-2 Δ <i>tssL</i> | 17-2 deleted of the <i>tssL</i> gene of the <i>sci1</i> T6SS gene cluster (EC042_4527) | Aschtgen <i>et al.</i> , 2010 |

Plasmids

| Vectors | Description | Source |
|------------------------|--|-------------------------------|
| Expression vectors | | |
| pUA66- <i>rrnB</i> | <i>P_{rrnB}</i> :: <i>gfpmut2</i> transcriptional fusion in pUA66 | Zaslaver <i>et al.</i> , 2006 |
| pMS600 | cloning vector, pOK12 derivative, P15A origin, <i>Plac</i> , Kan ^R | Aschtgen <i>et al.</i> , 2008 |
| pOK-TssL _{HA} | <i>sci1 tssL</i> (EC042_4527), C-terminal HA tag cloned into pMS600 | Aschtgen <i>et al.</i> , 2010 |
| pOK-TssL-EKDK | Glu81-to Lys and Asp84-to-Lys substitutions introduced into pOK-TssL _{HA} | This study |
| pOK-TssL-GE | Gly137-to-Glu substitution introduced into pOK-TssL _{HA} | This study |
| pOK-TssL-FE | Phe138-to-Glu substitution introduced into pOK-TssL _{HA} | This study |

| | | |
|--------------------------------|---|-------------------------------|
| pOK-TssL-GEFE | Gly137-to-Glu and Phe138-to-Glu substitutions introduced into pOK-TssL _{HA} | This study |
| pOK-TssL-DR | Asp74-to-Arg substitution introduced into pOK-TssL _{HA} | This study |
| pOK-TssL-ER | Glu75-to-Arg substitution introduced into pOK-TssL _{HA} | This study |
| pOK-TssL-DRER | Asp74-to-Arg and Glu75-to-Arg substitutions introduced into pOK-TssL _{HA} | This study |
| pOK-TssL-QKDKDK | Gln145-to-Lys, Asp146-to-Lys and Asp147-to-Lys substitutions introduced into pOK-TssL _{HA} | This study |
| pASK-IBA37(+) | cloning vector, fl origin, <i>Ptet</i> , Amp ^R | IBA technologies |
| pIBA-TssL _{CFL} | <i>scil tssL</i> cytoplasmic domain (amino-acids 1-184; TssL _{Cyto}), C-terminal FLAG tag cloned into pASK-IBA37(+) | Aschtgen <i>et al.</i> , 2012 |
| pIBA-TssL _C -EKDK | Glu81-to-Lys and Asp84-to-Lys substitutions introduced into pIBA-TssL _{CFL} | This study |
| pIBA-TssL _C -GE | Gly137-to-Glu substitution introduced into pIBA-TssL _{CFL} | This study |
| pIBA-TssL _C -FE | Phe138-to-Glu substitution introduced into pIBA-TssL _{CFL} | This study |
| pIBA-TssL _C -GEFE | Gly137-to-Glu and Phe138-to-Glu substitutions introduced into pIBA-TssL _{CFL} | This study |
| pIBA-TssL _C -DR | Asp74-to-Arg substitution introduced into pIBA-TssL _{CFL} | This study |
| pIBA-TssL _C -ER | Glu75-to-Arg substitution introduced into pIBA-TssL _{CFL} | This study |
| pIBA-TssL _C -DRER | Asp74-to-Arg and Glu75-to-Arg substitutions introduced into pIBA-TssL _{CFL} | This study |
| pIBA-TssL _C -QKDKDK | Gln145-to-Lys, Asp146-to-Lys and Asp147-to-Lys substitutions introduced into pIBA-TssL _{CFL} | This study |
| pBAD33 | cloning vector, P15A origin, <i>Para</i> , <i>araC</i> Cm ^R | Guzman <i>et al.</i> , 1995 |
| pBAD33-TssE _{VSV-G} | <i>scil tssE</i> (EC042_4545), C-terminal VSV-G tag cloned into pBAD33 | This study |
| pBAD33-TssK _{VSV-G} | <i>scil tssK</i> (EC042_4526), C-terminal VSV-G tag cloned into pBAD33 | This study |
| pBAD33-TssM _{VSV-G} | <i>scil tssM</i> (EC042_4539) cytoplasmic loop (amino-acids 62-360, TssM _{Cyto}), C-terminal VSV-G tag cloned into pBAD33 | Lauren Logger |
| pETG20A | Gateway [®] expression vector, ColE1 origin, <i>P_{T7}</i> , N-terminal 6xHis-TRX-TEV fusion, Amp ^R | Arie Geerlof |
| pETG20A-TssL _{Cyto} | <i>scil tssL</i> cytoplasmic domain (amino-acids 1-184) cloned into pETG20A | Durand <i>et al.</i> , 2012 |
| pETG20A-TssE | <i>scil tssE</i> cloned into pETG20A | Zoued <i>et al.</i> , 2016 |

Bacterial Two-Hybrid vectors

| | | |
|--------------------------------|---|-----------------------------|
| pT18-FLAG | Bacterial two-hybrid vector, ColE1 origin, <i>Plac</i> , T18 fragment of <i>Bordetella pertussis</i> CyaA, Amp ^R | Battesti & Bouveret, 2008 |
| pT18-Pal | Soluble region of <i>E. coli</i> K-12 Pal cloned downstream T18 in pT18-FLAG | Battesti & Bouveret, 2008 |
| pTssL _C -T18 | <i>scil tssL</i> cytoplasmic domain (amino-acids 1-184) cloned upstream T18 into pT18-FLAG | Durand <i>et al.</i> , 2012 |
| pTssL _C -EKDK-T18 | Glu81-to-Lys and Asp84-to-Lys substitutions introduced into pTssL _C -T18 | This study |
| pTssL _C -GE-T18 | Gly137-to-Glu substitution introduced into pTssL _C -T18 | This study |
| pTssL _C -FE-T18 | Phe138-to-Glu substitution introduced into pTssL _C -T18 | This study |
| pTssL _C -GEFE-T18 | Gly137-to-Glu and Phe138-to-Glu substitutions introduced into pTssL _C -T18 | This study |
| pTssL _C -DR-T18 | Asp74-to-Arg substitution introduced into pTssL _C -T18 | This study |
| pTssL _C -ER-T18 | Glu75-to-Arg substitution introduced into pTssL _C -T18 | This study |
| pTssL _C -DRER-T18 | Asp74-to-Arg and Glu75-to-Arg substitutions introduced into pTssL _C -T18 | This study |
| pTssL _C -QKDKDK-T18 | Gln145-to-Lys, Asp146-to-Lys and Asp147-to-Lys substitutions introduced into pTssL _C -T18 | This study |
| pT25-FLAG | Bacterial two-hybrid vector, P15A origin, <i>Plac</i> , T25 fragment of <i>Bordetella pertussis</i> CyaA, Kan ^R | Battesti & Bouveret, 2008 |

All others BACTH constructs have been described in Zoued *et al.*, 2013.

Oligonucleotides

| Name | Sequence (5' to 3') |
|--|---|
| For site-directed mutagenesis ^a | |
| A-TssL-EKDK | ACGAGAGTGTACTGAACCGCAAAAAAAAACAAAGGATGGCTGGCGCACCTGGC |
| B-TssL-EKDK | GCCAGGTGCGCCAGCCATCCTTTGTTTTTTTTCGCGTTCAGTACACTCTCGTC |
| A-TssL-GE | CTCTGCCGTACGCTTCAGCTCGAGTTTACCGGTCAGTACCGGTCGCAG |
| B-TssL-GE | CTGCGACCGGTACTGACCGGTAACCTCGAGCTGAAGCGTACGGCAGAG |
| A-TssL-FE | CTCTGCCGTACGCTTCAGCTCGGTGAGACCGGTCAGTACCGGTCGCAG |
| B-TssL-FE | CTGCGACCGGTACTGACCGGTCTCACCAGCTGAAGCGTACGGCAGAG |
| A-TssL-GEFE | CTCTGCCGTACGCTTCAGCTCGAGGAGACCGGTCAGTACCGGTCGCAG |
| B-TssL-GEFE | CTGCGACCGGTACTGACCGGTCTCCTCGAGCTGAAGCGTACGGCAGAG |
| A-TssL-DR | GTATGCCTTCTGCGCCCTGCTGCGCGAGAGTGTACTGAACCGCGAAAAAAC |
| B-TssL-DR | GTTTTTTCGCGTTCAGTACACTCTCGCGCAGCAGGGCGCAGAAGGCATAC |
| A-TssL-ER | GTATGCCTTCTGCGCCCTGCTGGACCGGAGTGTACTGAACCGCGAAAAAAC |
| B-TssL-ER | GTTTTTTCGCGTTCAGTACACTCCGGTCCAGCAGGGCGCAGAAGGCATAC |
| A-TssL-DRER | GTATGCCTTCTGCGCCCTGCTGCGCCGGAGTGTACTGAACCGCGAAAAAAC |
| B-TssL-DRER | GTTTTTTCGCGTTCAGTACACTCCGGCGCAGCAGGGCGCAGAAGGCATAC |
| A-TssL-QKDKDK | TTACCGGTCAGTACCGGTCGAAAGAAAAAGGAGCGTCGCGAAGATGTAATAC |
| B-TssL-QKDKDK | GTATTACATCTTCGCGACGCTCCTTTTTCTTCGACCGGTACTGACCGGTAAC |

^a Mutagenized codon in bold

