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## Cell width dictates Type VI secretion tail length

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Running title: T6SS sheath length control

Keywords : Protein transport, protein secretion, contractile injection systems, tail sheath, length regulation, TagA, cell width, molecular ruler, membrane.

## 16 SUMMARY

17 The type VI secretion system (T6SS) is a multiprotein apparatus that injects protein  
18 effectors into target cells, hence playing a critical role in pathogenesis and in microbial  
19 communities [1–4]. The T6SS belongs to the broad family of contractile injection  
20 systems (CIS), such as *Myoviridae* bacteriophages and R-pyocins, that use a spring-like  
21 tail to propel a needle loaded with effectors [5,6]. The T6SS tail comprises an assembly  
22 baseplate on which polymerizes a needle, made of stacked Hcp hexamers, tipped by the  
23 VgrG-PAAR spike complex and wrapped by the contractile sheath made of TssB and  
24 TssC [7–13]. The T6SS tail is anchored to the cell envelope by a membrane complex that  
25 also serves as channel for the passage of the needle upon sheath contraction [14–16]. In  
26 most CIS, the length of the tail sheath is invariable, and is usually ensured by a  
27 dedicated protein called tape measure protein (TMP) [17–22]. Here we show that the  
28 length of the T6SS tail is constant in enteroaggregative *Escherichia coli* cells, suggesting  
29 that it is strictly controlled. By overproducing T6SS tail subunits we demonstrate that  
30 component stoichiometry does not participate to the regulation of tail length. The  
31 observation of longer T6SS tails when the apparatus is relocalized at the cell pole  
32 further shows that tail length is not controlled by a TMP. Finally, we show that tail stops  
33 its elongation when in contact with the opposite membrane, and thus that T6SS tail  
34 length is determined by the cell width.

35

## 36 RESULTS AND DISCUSSION

### 37 T6SS tail sheath length in EAEC.

38 The length of bacteriophage and other CIS tails such as that of anti-feeding prophages is  
39 strictly controlled [17-23]. To determine whether this is also the case for the T6SS, we

40 measured the length of T6SS sheaths in EAEC wild-type cells producing a functional fusion  
41 between the TssB tail subunit and the superfolder-Green Fluorescent Protein (TssB-sfGFP).  
42 The sfGFP-coding sequence was inserted on the chromosome, upstream the *tssB* stop codon.  
43 In this construct, the sfGFP sequence is in frame with the *tssB* gene, and the *tssB-sfGFP*  
44 fusion is under the control of the native *tssB* expression signals. Cells were grown in *scil*  
45 inducing medium (SIM), a defined synthetic medium that avoids batch-to-batch composition  
46 variability and induces the expression of EAEC T6SS genes [24]. In agreement with the  
47 localization of T6SS MC along the cell body with an underrepresentation at the poles [15,25],  
48 we observed that T6SS sheaths assemble from one position on the cell body to the opposite  
49 membrane. To avoid measurements of the length of contracted sheaths or of sheaths under  
50 extension, time-lapse recordings were performed and only sheaths for which the elongation  
51 has been completed (i.e., when the sheath holds >1 min with the same length) were  
52 considered (Figure 1A). The distal extremity of these extended sheaths always co-localized  
53 with the TagA stopper protein (Figure 1B). Quantitative measurements of these T6SS tail  
54 length showed low disparities, with a length mean of  $0.76 \pm 0.11 \mu\text{m}$  ( $n = 150$ ) and a normal  
55 distribution (Figure 1C). We thus concluded that the length of the T6SS sheath is not  
56 randomly distributed, and hence that the arrest of T6SS sheath elongation is controlled. Based  
57 on this conclusion, we hypothesize that T6SS sheath length might be determined by (i) the  
58 number of available T6SS tail subunits, (ii) a tape measure protein, or (iii) the cell width.

59

## 60 **T6SS tail sheath length is not regulated by tube/sheath components stoichiometry**

61 Several reports have demonstrated that the length of some pilus-like structures is limited by  
62 the number of available pilin subunits. For example, the T2SS uses a periplasmic pseudo-  
63 pilus to expel the substrates in the external medium such as a piston or an Archimedes screw

64 [26]. By artificially increasing the number of pseudo-pilins,  $\mu\text{m}$ -long pili can be observed at  
65 the cell surface, suggesting that pseudo-pilus length is determined, in part, by the number of  
66 available subunits [27,28]. A strict control of the number of subunits in the cell by finely  
67 tuned gene expression and protein stability levels would prevent the costly synthesis of  
68 unnecessary subunits. To test whether T6SS sheath length might be controlled by the number  
69 of available tail subunits, we modified the stoichiometry balance by deregulating the levels of  
70 tube/sheath subunits, Hcp, TssB and TssC. TssA, which locates at the distal end of the  
71 growing sheath to coordinate the assembly of the tail tube/sheath [29-31], and the TagA  
72 stopper [31,32] were not included in the study as single TssA and TagA complexes are  
73 responsible for promoting T6SS tail elongation and arrest. *tssB-sfGFP*, and epitope-tagged  
74 *tssC* and *hcp*, were cloned into the pTrc99A vector, under the IPTG-inducible *ptrc* promoter.  
75 Pilot experiments showed that the production of TssB-sfGFP, TssC and Hcp can be tightly  
76 controlled by varying the IPTG inducer concentrations from 0 to 250  $\mu\text{M}$  in the culture  
77 medium. However, although we do not know whether it results from protein aggregation or  
78 stoichiometric unbalance, we noticed that IPTG concentrations higher than 50  $\mu\text{M}$  yielded  
79 non-functional T6SSs, as no dynamic sheath structures were observable by fluorescence  
80 microscopy. Nevertheless, with IPTG concentrations ranging from 0 to 10  $\mu\text{M}$ , we observed  
81 an increase in TssB-sfGFP, TssC and Hcp protein levels up to  $\sim$ 14-18 fold (Figure 2A)  
82 without affecting T6SS sheath formation and dynamics (Figure 2B). However, sheath length  
83 measurement analyses did not reveal striking differences (Figure 2B, 2C and Figure S1).  
84 Collectively, our results therefore argue against a direct correlation between the abundance of  
85 T6SS tail subunits and T6SS sheath length.

86

87 **T6SS sheath length is not regulated by a tape measure protein.**

88 The length of contractile bacteriophage tails is dictated by a tape measure protein (TMP) [18-  
89 20,33,34]. Such a ruler mechanism has been also evidenced or proposed for other CISs such  
90 as antifeeding prophages and *Photorhabdus* virulence cassettes, or non-contractile structures  
91 such as T3SS injectisome needles in *Yersinia*, or the bacterial hook in *Salmonella* [21,22,35-  
92 38]. Although bacterial T6SSs have been shown to be structurally and functionally related to  
93 contractile bacteriophages [6], and contrarily to R-pyocins, AFP, PVC or ACS gene clusters  
94 [21,22,35], no gene encoding a potential TMP can be found within T6SS clusters [39]. In  
95 addition, previous experiments showing T6SS tail sheath extension in *Vibrio cholerae*  
96 spheroplasts [40] and in EAEC and *V. cholerae tagA* mutants [31,32] suggested that longer  
97 tails assemble in the cell, hence arguing against a tape measure-like mechanism. To discard  
98 this hypothesis, we sought to reposition the T6SS at the cell pole to follow the assembly of the  
99 T6SS in the long axis of the cell body. In these conditions, the presence of a TMP would  
100 cause an arrest of tail extension in the cytoplasm, whereas the tail will extend towards the  
101 opposite cell pole or until no tail subunit is available for a TMP-independent mechanism.  
102 T6SS biogenesis starts with the assembly of the membrane complex (MC) [7,15]. The T6SS  
103 MC is composed of the TssJ outer membrane lipoprotein, and TssL and TssM inner  
104 membrane proteins [14]. Its biogenesis starts with the positioning of TssJ and is pursued by  
105 the sequential recruitment of TssM and TssL [15]. The MC initially positions along the cell  
106 body with an underrepresentation at the cell pole [15,25]. To reposition T6SS MCs at the cell  
107 pole, we fused TssM to the *Bacillus subtilis* polar/septal determinant DivIVA. This approach  
108 has been successfully used to relocate the T4SS VirD4 coupling protein to the cell pole in  
109 *Agrobacterium* cells [41]. A fragment encoding the *B. subtilis divIVA* gene was inserted on  
110 the chromosome, downstream the *tssM* ATG start codon and in frame with the *tssM* coding  
111 sequence, to engineer a *divIVA-tssM* fusion. Because TssL is the last component to be  
112 recruited during MC biogenesis [15], we then imaged TssL fused to sfGFP in these cells.

113 Statistical analyses of sfGFP-TssL position, that hence reflects the localization of the fully-  
114 assembled T6SS MC [15], demonstrated that sfGFP-TssL forms ~32% of polar foci in  
115 presence of DivIVA-TssM, by contrast to the wild-type cells, with ~16% of polar foci (Figure  
116 3A, 3B). Introduction of the *divIVA-tssM* fusion into *tssB-sfGFP* EAEC cells showed that few  
117 T6SS tails assemble from the pole suggesting that polar-localized MCs are less functional.  
118 However, the number of tail polymerizations starting from the cell pole was significantly  
119 increased with the relocation of the MC compared to wild-type cells. Statistical analyses  
120 showed that these extensions from the poles lead to significantly longer tails (Figure 3C), with  
121 a mean equal to  $1.05 \pm 0.42 \mu\text{m}$  ( $n = 75$ ). Sheaths that crossed the entire cell body with length  
122 up to  $3.5 \mu\text{m}$  (corresponding to outliers in Figure 3C), and capable of contraction were readily  
123 observed (Figure 3D). Taken together, these data demonstrate that T6SS tails could be  
124 artificially extended by relocalization of the MC at the cell pole, and hence that sheath length  
125 is not regulated by a TMP-mediated ruler mechanism.

126

### 127 **T6SS tail sheath length is dictated by the cell width.**

128 In all the images recorded, we observed that sheaths extend towards and stop when in contact  
129 with the opposite membrane. As the membrane mechanically defines the cell limits, one may  
130 hypothesize that the distance between the two opposite membrane positions is sufficient to  
131 determine sheath length. Indeed, the measure of the distance between the two membranes in  
132 cells analyzed in Figure 1 showed a cell width average of  $0.86 \mu\text{m} \pm 0.07$ , which is  
133 comparable to the sheath length ( $0.76 \mu\text{m} \pm 0.11$ ), specifically if we take into account the  
134 widths of the membranes, of the cytoplasmic portion of the MC, and of the BP [8,9,15,16]. To  
135 further investigate the impact of cell width on T6SS sheath length, we treated EAEC cells  
136 producing TssB-sfGFP with A22, a drug that causes cell shape defects by targeting the

137 cytoskeletal MreB protein. As expected, we observed a significant impact on cell morphology  
138 with a trend to cell rounding (Figure 4A). In these conditions, we observed T6SS sheaths with  
139 length varying from 0.7 to 2  $\mu\text{m}$  (Figure 4A). However, when sheath length was plotted  
140 against cell width, a strict correlation is observed (Kendall's  $\tau = 0.82$ ) (Figure 4B). In addition,  
141 the value of the slope, close to 1 ( $m = 0.92$ ), demonstrates that sheath length is directly  
142 proportional to cell width, which is also confirmed by sheath length/cell width ratio  
143 calculations (Figure 4C). Similarly to wild-type cells [32], the distal extremity of these longer  
144 extended sheaths co-localized with TagA (Figure 4D). We therefore conclude that T6SS  
145 sheath length depends on cell width, and that T6SS sheath polymerization is arrested upon  
146 contact with the opposite membrane, likely by the TagA stopper.

147

#### 148 **Concluding remarks**

149 In this study, we have shown that the T6SS tails in EAEC cells have a defined length. Our  
150 further analyses demonstrated that the length of the T6SS tail is not determined by a tape  
151 measure protein or by the number of available tail tube/sheath subunits, but rather by the  
152 distance between the baseplate and the opposite membrane. This mechanism contrasts with  
153 the TMP-dependent regulation found in most contractile tailed machines. However it is in  
154 agreement with the fact that no putative TMP-encoding genes are encoded on T6SS gene  
155 clusters [5,39]. In TMP-dependent contractile tails, it has been shown that a strict correlation  
156 exists between the number of TMP residues and the length of cognate sheaths [21,22]. An  
157 extrapolation for the T6SS would mean that a sheath of 0.76  $\mu\text{m}$  corresponds to a TMP of ~  
158 5,000 amino-acids. Such a protein is not encoded within T6SS gene clusters. Finally, the  
159 observation that DivIV-mediated relocalisation of the MC to the cell pole yields extra-long  
160 sheath structures demonstrates that no TMP is involved. The assembly of extra-long sheaths

161 also suggests that the number of subunits necessary to assemble a tail tube/sheath is not  
162 limiting in the bacterial cytoplasm, and hence that sheath length is not regulated by the  
163 number of available tail subunits. Indeed, this hypothesis was also discarded by artificially  
164 modulating the levels of T6SS tail subunits, demonstrating that it does not influence tail  
165 sheath length. This results is also in agreement with the recent measurement of T6SS subunits  
166 abundance demonstrating that tail tube/sheath components are not limiting in *Acinetobacter*  
167 *baylyi*, *V. cholerae*, or *P. aeruginosa* cells [42]. All our observations therefore argue for an  
168 arrest of sheath polymerization at the opposite membrane. This hypothesis is likely, as  
169 altering the distance between the two membranes by using A22, an antagonist of the MreB  
170 morphological determinant, showed a strict correlation between membrane width and sheath  
171 length. We conclude that tail tube/sheath polymerization stops when it hits the opposite  
172 membrane. In most cases, the assembly of the T6SS tubular structure starts perpendicular to  
173 the membrane and hence, the length of the sheath correlates with the cell width. However,  
174 when T6SS tail assembly starts non-perpendicularly, its polymerization will proceed until it  
175 touches the opposite membrane boundary. This model is also consistent with the recent  
176 identification of TagA, a membrane-bound protein that binds to the distal extremity of the  
177 growing tail and stops tube/sheath polymerization in EAEC and *V. cholerae* [31,32]. However,  
178 TagA is not a universal stopper as recordings of sheath dynamics of TagA<sup>+</sup> T6SS (*V.*  
179 *cholerae*) or T6SSs lacking TagA (*Acinetobacter baylyi*, *P. aeruginosa* H1, *S. enterica*  
180 Typhimurium, *Francisella novicida*) showed that sheaths extend to and stop at the opposite  
181 membrane [40, 42-45]. It would be interesting to define how T6SS sheath polymerization is  
182 stopped in bacterial species lacking TagA.

183 In conclusion, T6SS has evolved to use a mechanism of tail length control distinct  
184 from other CISs. We thus propose a model in which T6SS tail length is determined by the  
185 distance to the opposite membrane. In EAEC, and likely other TagA<sup>+</sup> species, proper arrest of

186 tail tube/sheath polymerization is mediated by the TagA stopper by binding to the TssA cap  
187 protein once the distal end of the sheath hits the opposite membrane. .

188

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199 interpretation, or the decision to submit the work for publication.

200

## 201 **Authors contributions**

202 Y.G.S. and E.C. designed research; Y.G.S., T.D. and E.C. performed research; Y.G.S.  
203 performed statistical analyses; Y.G.S., T.D., and E.C. analyzed data; L.J. provided expertise  
204 and feedback; Y.G.S. and E.C. wrote the paper with contributions from T.D. and L.J.

205

## 206 **Declaration of interests**

207 The authors declare no competing interests.

208

209 **Legend to Figures**

210 **Figure 1. Statistical measure of the EAEC T6SS sheath length.** (A) Representative  
211 fluorescence micrograph of EAEC cells producing TssB-sfGFP and labelled with FM4-64  
212 (upper panel, phase channel; lower panel, merge of GFP and FM4-64 channels). Scale bar, 1  
213  $\mu\text{m}$ . (B) Representative fluorescence micrograph of EAEC cells producing TssB-CFP and  
214 YFP-TagA, and labeled with FM4-64 (upper panel, phase channel; lower panel, merge of  
215 CFP, YFP, and FM4-64 channels). The open arrowheads point T6SS extended sheaths in  
216 contact with the TagA stopper. Scale bar, 1  $\mu\text{m}$ . (C) Violin plot representation of the sheath  
217 length in wild-type cells. The distribution of the sheath lengths is represented by the outer  
218 shape. The bold horizontal bar represents the median value (median = 0.76  $\mu\text{m}$ ); the lower  
219 and upper boundaries of the internal box plot correspond to the 25th and 75th percentiles  
220 respectively; whiskers extend 1.5 times the interquartile range from the 25th and 75th  
221 percentiles. The number of measured sheaths ( $n=150$ ) is indicated above.

222 **Figure 2. T6SS tail tube/sheath subunits levels do not determine T6SS sheath length.** (A)  
223 Western-blot analyses of tail tube/sheath component abundance.  $2 \times 10^8$  cells of  $\Delta tssBC\Delta hcp$   
224 cells producing TssB-sfGFP (TssB<sub>sfGFP</sub>), 6 $\times$ His-tagged TssC (TssC<sub>6His</sub>) and FLAG-tagged  
225 Hcp (Hcp<sub>FLAG</sub>) from the pTrc-B<sub>GFP</sub>-C<sub>6H</sub>-Hcp<sub>F</sub> grown in presence of 0.4% of glucose or of the  
226 indicated concentration of IPTG were subjected to 12.5% acrylamide SDS-PAGE and  
227 immunodetected with anti-GFP, -His, -FLAG and -EF-Tu monoclonal primary antibodies and  
228 secondary antibodies coupled to AlexaFluor<sup>®</sup> 680. The EF-Tu cytoplasmic elongation factor  
229 is used as loading control. The increased fold values compared to the glucose condition,  
230 measured by densitometric quantification of the band signal intensities and relative to the  
231 loading control, are indicated below. Molecular weight markers (in kDa) are indicated on left.  
232 (B-C) Representative fluorescence microscopy recordings (B) and statistical analyses of  
233 sheath length measurements (C) of  $\Delta tssBC\Delta hcp$  cells producing Hcp<sub>FLAG</sub>, TssB-sfGFP and

234 TssC<sub>6His</sub> in presence of 0.4% glucose or of the indicated concentration of IPTG, and labelled  
235 with FM4-64 (left panels, phase channel; right panels, merge of GFP and FM4-64 channels).  
236 Scale bar, 2  $\mu$ m. In the violin plot representation of the statistical analysis, the distribution of  
237 the sheath length is represented by the outer shape. The bold horizontal bar represents the  
238 median; the lower and upper boundaries of the internal box plot correspond to the 25th and  
239 75th percentiles respectively; whiskers extend 1.5 times the interquartile range from the 25th  
240 and 75th percentiles. Outliers are shown as black dots. Statistical significance from three  
241 independent assays ( $n=100$  for each conditions) relative to the glucose condition is indicated  
242 above the plots (ns, non-significative; \*\*\*,  $p < 0.001$ ; two-tailed Student's  $t$ -test). A  
243 comparison of tail tube/sheath subunits levels and sheath lengths is shown in Figure S1.

244 **Figure 3. Sheath length is not controlled by a tape measure protein.** Representative  
245 fluorescence microscopy recordings of EAEC cells producing sfGFP-TssL in WT (*A*) or  
246 DivIV-TssM (*B*) cells, and labelled with FM4-64 (upper panels, phase channel; lower panels,  
247 merge of GFP and FM4-64 channels). White and blue arrowheads indicate TssL foci with  
248 body or polar localizations, respectively. Scale bar, 2  $\mu$ m. The spatial repartition of sfGFP-  
249 TssL foci is shown on right, as a projection of foci from  $n=152$  and  $n=151$  WT and DivIVA-  
250 TssM cells, respectively, on a single cell (from blue to yellow, see heatmap color chart on  
251 right of panel *A*). The percentage of sfGFP-TssL foci with polar localization is indicated  
252 below. (*C*) Violin plot representation of sheath length measurements in DivIVA-TssM cells  
253 producing TssB-sfGFP (red). An example of a representative microscopy field is shown in the  
254 inset (scale bar, 2  $\mu$ m). The distribution of sheath length in WT cells (shown in Figure 1*B*) is  
255 reported in transparency for comparison (blue). The distribution of the sheath length is  
256 represented by the outer shape. The bold horizontal bar represents the median value (median  
257 = 0.93  $\mu$ m and 0.76  $\mu$ m for DivIVA-TssM and WT cells, respectively); the lower and upper  
258 boundaries of the internal box plot correspond to the 25th and 75th percentiles respectively;

259 whiskers extend 1.5 times the interquartile range from the 25th and 75th percentiles. Outliers  
260 are shown as black dots. The number of measured sheaths ( $n=75$ ) is indicated below.  
261 Statistical significance relative to WT cells is indicated above the plots (\*\*\*,  $p < 0.001$ ; one-  
262 tailed Wilcoxon's  $t$ -test). (D) Fluorescence microscopy time-lapse recordings of DivIVA-  
263 TssM cells producing TssB-sfGFP highlighting polar T6SS sheath assembly (white  
264 arrowhead) and contraction (blue arrowhead). Scale bar, 2  $\mu\text{m}$ .

265 **Figure 4. Cell width dictates T6SS sheath length.** (A) Representative fluorescence  
266 micrographs of EAEC cells producing TssB-sfGFP in absence (upper panel) or in presence of  
267 the MreB inhibitor A22 (lower panel), and labelled with FM4-64 (upper panel, phase channel;  
268 lower panel, merge of GFP and FM4-64 channels). Scale bar, 2  $\mu\text{m}$ . (B) Plot representation  
269 showing the relationship between sheath length and cell width in absence (blue) and presence  
270 of A22 (orange). The dashed line represents the mean of the WT cell width (mean = 0.87  $\mu\text{m}$ ).  
271 Value of the slope ( $m$ ) is indicated on right. Kendall's  $\tau = 0.82$ . (C) Dotplot of the ratios  
272 between sheath length and the width of the corresponding cell from cells grown in absence  
273 (blue) or presence of A22 (orange). Horizontal bars represent the mean in each condition. The  
274 values of the means and standard deviations are indicated above the plots. The number of  
275 analyzed cells ( $n$ ) is indicated below. (D) Representative fluorescence micrograph of EAEC  
276 cells producing TssB-CFP and YFP-TagA in presence of the MreB inhibitor A22, and  
277 labelled with FM4-64 (left panel, phase channel; right panel, merge of CFP, YFP, and FM4-  
278 64 channels). The open arrowheads point T6SS extended sheaths in contact with the TagA  
279 stopper. Scale bar, 2  $\mu\text{m}$ .

280

281 **STAR METHODS**

282

283 **LEAD CONTACT AND MATERIALS AVAILABILITY**

284 Further information and requests for resources and reagents should be directed to and will be  
285 fulfilled by the Lead Contact, Eric Cascales (cascales@imm.cnrs.fr). There are no restrictions  
286 to the availability of reagents.

287

288 **EXPERIMENTAL MODEL AND SUBJECT DETAILS**

289 Strains used in this study are listed in Table S1. *Escherichia coli* DH5 $\alpha$  (New England  
290 Biolabs) or CC118 $\lambda$ pir have been used for cloning procedures. Enteroaggregative *E. coli*  
291 (EAEC) strains used in this work are isogenic derivatives of the wild-type O3:H2 17-2 strain.  
292 The wild-type 17-2 strain and its TssB-sfGFP [46], sfGFP-TssL [15], TssB-CFP/YFP-TagA  
293 (this work), and DivIVA-TssM (this work) derivatives have been used for *in vivo* studies. *E.*  
294 *coli* cells were routinely grown in Lysogeny broth (LB) broth at 37°C, with aeration. For  
295 induction of the *sciI* T6SS gene cluster, cells were grown in Sci1-inducing medium [SIM: M9  
296 minimal medium supplemented with glycerol 0.25 %, vitamin B1 200  $\mu\text{g.mL}^{-1}$ ,  
297 casaminoacids 40  $\mu\text{g.mL}^{-1}$ ,  $\text{MgCl}_2$  2 mM,  $\text{CaCl}_2$  0.1 mM, and LB (10% v/v)] [24]. Plasmids  
298 and chromosomal deletions and insertions were maintained by the addition of kanamycin (50  
299  $\mu\text{g.mL}^{-1}$ ), or ampicillin (100  $\mu\text{g.mL}^{-1}$ ). Gene expression from pTrc99A derivative plasmids  
300 was induced at  $A_{600 \text{ nm}} \approx 0.4$  by the addition of 2-10  $\mu\text{M}$  of isopropyl- $\beta$ -D-thio-  
301 galactopyranoside (IPTG, Sigma-Aldrich). The MreB antagonist S-(3,4-  
302 dichlorobenzyl)isothiourea hydrochloride (known as A22 [47], purchased from Sigma-  
303 Aldrich) has been added to the culture at the concentration of 10  $\mu\text{g.mL}^{-1}$  for 2 hours prior  
304 analyses. Membranes were stained with 10  $\mu\text{g.mL}^{-1}$  of the *N*-(3-triethylammoniumpropyl)-4-  
305 (6-(4-(diethylamino) phenyl) hexatrienyl) pyridinium dibromide dye (FM4-64, Molecular  
306 Probes, Life technologies).

307

308 **METHOD DETAILS**

309 **Plasmid construction.** All plasmids used in this study are listed in Table S2.  
310 Oligonucleotides used for plasmid construction are listed in Table S3. pTrc99A [48] and  
311 pKD4 [49] plasmid derivatives were engineered by ligation-free restriction-free cloning. PCR  
312 amplification were performed in a Biometra thermocycler using the Q5<sup>®</sup> DNA polymerase  
313 (New England Biolabs). Briefly, the fragment of interest was amplified and then used as  
314 oligonucleotides for a second PCR for amplification of the target plasmid. For construction of  
315 pTrc-B<sub>GFP</sub>-C<sub>6His</sub>, a fragment encoding *tssB-sfGFP* and *tssC-6×His* was amplified from EAEC  
316 17-2 TssB-sfGFP [46] genomic DNA using primers  
317 *GGATAACAATTCACACAGGAAACAGACCATGAGCAGTTCGTTTCAGAATGAAATCC*  
318 *C* and  
319 *CCCGGGTACCGAGCTCGAATTCTTAATGGTGATGGTGATGATGCGCTTTTGCCTTC*  
320 *GGCATCTGC* (6×His tag sequence underlined, sequence annealing on the target pTrc99A  
321 plasmid [48] italicized), and inserted into pTrc99A. The *hcp* gene was amplified from EAEC  
322 17-2 genomic DNA using primers  
323 *GCGCATCATCACCATCACCATTAAGAATTaggaggtattacaccATGGCAATTCAGTTTA*  
324 *TCTGTGGCTG* and  
325 *GGATCCCCGGGTACCGAGCTCGTTACTTGTCATCGTCATCTTTATAATCCGCGGTGG*  
326 *TACGCTCACTCC* (FLAG tag sequence italicized, sequence annealing on the target pTrc-  
327 B<sub>GFP</sub>-C<sub>6H</sub> plasmid underlined, Shine-Dalgarno ribosome-binding site in lower case), and  
328 inserted into pTrc-B<sub>GFP</sub>-C<sub>6His</sub> to yield pTrc-B<sub>GFP</sub>-C<sub>6H</sub>-Hcp<sub>F</sub>. For construction of plasmid  
329 pKD4-DivIVA-Nt allowing chromosomal insertion of *divIVA* at the 5'-end of genes, the  
330 *divIVA* gene was amplified from *Bacillus subtilis* str. 168 using primers  
331 *GGAACTTCGGAATAGGAACTAAGGAGGATATTCATATGCCATTAACGCCAAATG*  
332 *ATATTCACAACAAGAC* and

333 GCTGACATGGGAATTAGCCATGGTCCCCTCCGCCGGCCGCTGCTTCCTTTTCCTCA  
334 AATACAGCGTCGACTTC (3×Ala-3×Gly sequence linker italicized, sequence annealing on  
335 the target pKD4 plasmid underlined), and inserted into plasmid pKD4 [49]. For construction  
336 of plasmid pKD4-CFP-Ct allowing chromosomal insertion of *ecfp* at the 3'-end of genes, the  
337 *ecfp* gene was amplified from the pTrc99A-ecfp vector (gift from Leon Espinosa, LCB,  
338 Marseille, France) using primers  
339 GATTGCAGCATTACACGTCTTGAGCGATTGCAGCGGCCGGCGGAGGGGTGAGCAA  
340 GGGCGAGGAGC and  
341 GAACTTCGAAGCAGCTCCAGCCTACACTTACTTGTACAGCTCGTCCATGCCG  
342 (3×Ala-3×Gly sequence linker italicized, sequence annealing on the target pKD4 plasmid  
343 underlined), and inserted into plasmid pKD4 [49]. For construction of plasmid pKD4-YFP-Nt  
344 allowing chromosomal insertion of *eyfp* at the 5'-end of genes, the *eyfp* gene was amplified  
345 from the pCBP-EYFP vector (gift from Emmanuelle Bouveret, Institut Pasteur, Paris, France)  
346 using primers  
347 CGGAATAGGAACTAAGGAGGATATTCATATGGTGAGCAAGGGCGAGGAGC and  
348 CGGCTGACATGGGAATTAGCCATGGTCCCCTCCGCCGGCCGCTGCCTTGTACAGC  
349 TCGTCCATGCCGAGAG (3×Ala-3×Gly sequence linker italicized, sequence annealing on  
350 the target pKD4 plasmid underlined), and inserted into plasmid pKD4 [49]. All plasmids were  
351 verified by colony-PCR and DNA sequencing (Eurofins genomics).

352 **Strain construction.** Strains were engineered by  $\lambda$ -red recombination [49] using plasmid  
353 pKOBEG [50] and PCR products (oligonucleotides listed in Table S3). Briefly, a kanamycin  
354 cassette was amplified from plasmids pKD4, pKD4-DivIVA-Nt, pKD4-CFP-Ct, or pKD4-  
355 YFP-Nt, using oligonucleotides carrying 50-nucleotide extensions homologous to regions  
356 adjacent to the gene of interest. Cassette allowing deletion of the *hcp* gene was generated  
357 using the pKD4 vector template with primers

358 TCCCCTGCGCCGGAAGAGGGCGCATCAGAAAACATAACGGAGTAATTTTTTGTGT  
359 AGGCTGGAGCTGCTTCG and  
360 TGAAGAAAAAATAAAAAATGACGGACAGGATGCCCTGTCCGTCCGGCAGAACATA  
361 TGAATATCCTCCTTAGTTCC (50-bp sequence annealing on the 5' and 3' regions of the  
362 deleted gene underlined). For chromosomal insertion of DivIVA at the *tssM* locus, the  
363 DivIVA cassette was generated using the pKD4-DivIVA-Nt vector with primers  
364 TTTCATCCGGAGAAGAACATTTTATCAGTACTGTTACATCAGGAAACCAGAATG  
365 AATAACGATTGTGTAGGCTGGAGCTGCTTCGAAGTTCCTATAC and  
366 CACACCAATAAATACAATCCCCGGTCGCCCAAAGCGACCAGACAGACAGGCCAG  
367 TTTATTCCTCCGCCGGCCGCTGC (50-bp sequence annealing on the 5' and 3' regions of  
368 the *tssM* ATG start codon underlined). For chromosomal insertion of CFP at the *tssB* locus,  
369 the *cfp* cassette was generated using the pKD4-CFP-Ct vector with primers  
370 CCGGCACTGAGTCAGACGCTGCGTGATGAACTGCGTGCCTGGTGCCGGAAAAG  
371 GCGGCAGCGGCCGGCGGAGGG and  
372 GCAACGTTCTTTTCTTTCTGTACAGACATCAGCATTTTCTCTCGTAATCCGTTAAA  
373 CATATGAATATCCTCCTTAGTTCCTATTCCGAAGTTCC (50-bp sequence annealing on  
374 the 5' and 3' regions of the *tssB* TAA stop codon underlined). For chromosomal insertion of  
375 YFP at the *tagA* locus, the *yfp* cassette was generated using the pKD4-YFP-Nt vector with  
376 primers  
377 CTTTTCGTCCTGTTAATCATGATTTAATACAGCAACACCGAATCTGCCGCGATTG  
378 TGTAGGCTGGAGCTGCTTCGAAGTTCCTATAC and  
379 TCCGGTAATGACCGGGGGTCACCACCGGTTTTTCAGTTTCACTTCAGAAGTCCCTC  
380 CGCCGGCCGCTGC (50-bp sequence annealing on the 5' and 3' regions of the *tagA* ATG  
381 start codon underlined). Cassette amplicons were column-purified (NucleoSpin<sup>®</sup> Gel and PCR  
382 clean-up, Macherey Nagel), and 600 ng were electroporated into electrocompetent target cells

383 ( $\Delta tssBC$  for  $\Delta hcp$ ; 17-2, sfGFP-TssL and TssB-sfGFP for DivIVA; 17-2 for YFP-TagA; YFP-  
384 TagA for TssB-CFP), kanamycin-resistant clones were selected and verified by colony-PCR.  
385 When possible, kanamycin cassettes were excised by the FRT-specific FLP recombinase  
386 using vector pCP20 [49].

387 **SDS-PAGE, Western-blotting, imaging and quantification analyses.** Standard methods  
388 were used for sodium dodecyl-sulfate poly-acrylamide gel electrophoresis (SDS-PAGE) and  
389 protein transfer on nitrocellulose membranes. Membranes were probed with anti-GFP (clone  
390 7.1, Roche), anti-His (clone His1, Sigma), anti-FLAG (clone M2, Sigma), and anti-EF-Tu  
391 (clone mAb900, HyCult Biotech) monoclonal antibodies, and goat anti-mouse secondary  
392 antibodies coupled to AlexaFluor<sup>®</sup> 680 (Invitrogen). Images were recorded at  $\lambda=700$  nm using  
393 an Odyssey<sup>®</sup> infrared imaging system (LI-COR Biosciences). Image analyses were performed  
394 with the ImageJ processing program using the Fiji interface [51], as previously described [52].  
395 Briefly, the image was first converted to grayscale in .jpg format. The rectangle tool of  
396 ImageJ was used to select a rectangular area of the size corresponding to the lane width, in  
397 order to cover the minimal area to contain the whole of the largest band. The same frame was  
398 used to select each TssB, TssC, Hcp or EF-Tu band. For each selection, the number of pixels  
399 was calculated. A control region with no band was also selected to subtract the background.  
400 The number of pixels of each band, subtracted from the background, was then divided by the  
401 EF-Tu loading control intensity at the same IPTG concentration, to compensate for loading  
402 differences. The fold-change relative to the glucose sample was then calculated.

403 **Fluorescence microscopy and statistical analyses.** Cells were grown in SIM to a  $A_{600\text{ nm}} \approx$   
404 0.6–0.8, harvested and resuspended in fresh SIM to a  $A_{600\text{ nm}} \approx 10$ . For inhibition of MreB  
405 function, cells grown in SIM were treated at  $A_{600\text{ nm}} \approx 0.3$  for 2 hours with  $10\ \mu\text{g}\cdot\text{mL}^{-1}$  of A22  
406 prior to data acquisition, as previously published [53]. For membrane staining, cells were

407 labelled with FM4-64 ( $10 \mu\text{g.mL}^{-1}$ ) for 2 min prior to centrifugation. Concentrated cell  
408 mixtures were spotted on a thin pad of SIM supplemented with 2% agarose, or 2% agarose  
409 and A22 ( $10 \mu\text{g.mL}^{-1}$ ), covered with a cover slip, and incubated for 20-30 min at room  
410 temperature before microscopy acquisition. Fluorescence microscopy was performed on a  
411 Nikon Eclipse Ti microscope equipped with an Orcaflash 4.0 LT digital camera (Hamamatsu)  
412 and a perfect focus system (PFS) to automatically maintain focus so that the point of interest  
413 within a specimen is always kept in sharp focus at all times despite mechanical or thermal  
414 perturbations. All fluorescence images were acquired with a minimal exposure time to  
415 minimize bleaching and phototoxicity effects. Exposure times were typically 30 ms for phase  
416 contrast, 200 ms for TssB-sfGFP, 300 ms for TssB-CFP, 1 s for sfGFP-TssL, 1.5 s for YFP-  
417 TagA, and 50 ms for FM4-64. The experiments were performed at least in triplicate and a  
418 representative result is shown. Images were analyzed using ImageJ (<http://imagej.nih.gov/ij/>)  
419 and the MicrobeJ v5.11y plugin (<http://www.microbej.com/>) [54].

420

## 421 **QUANTIFICATION AND STATISTICAL ANALYSIS**

422 Statistical analyses of microscopy images were performed with several representative fields  
423 from at least three independent biological replicates, using Excel and the R software  
424 environment. The number of measured cells or events ( $n$ ) is indicated on each figure.  
425 Differences in sheath length between groups were examined by unpaired parametric Student  $t$   
426 test or nonparametric Wilcoxon  $t$  test. Relationship between sheath length and cell width was  
427 examined by Mann-Kendall test. Significance was defined by  $p < 0.001$  (\*\*\*) and  $p < 0.0001$   
428 (\*\*\*\*).

429

430 **DATA AND CODE AVAILABILITY**

431 This study did not generate datasets and codes.

432

433

434 **REFERENCES**

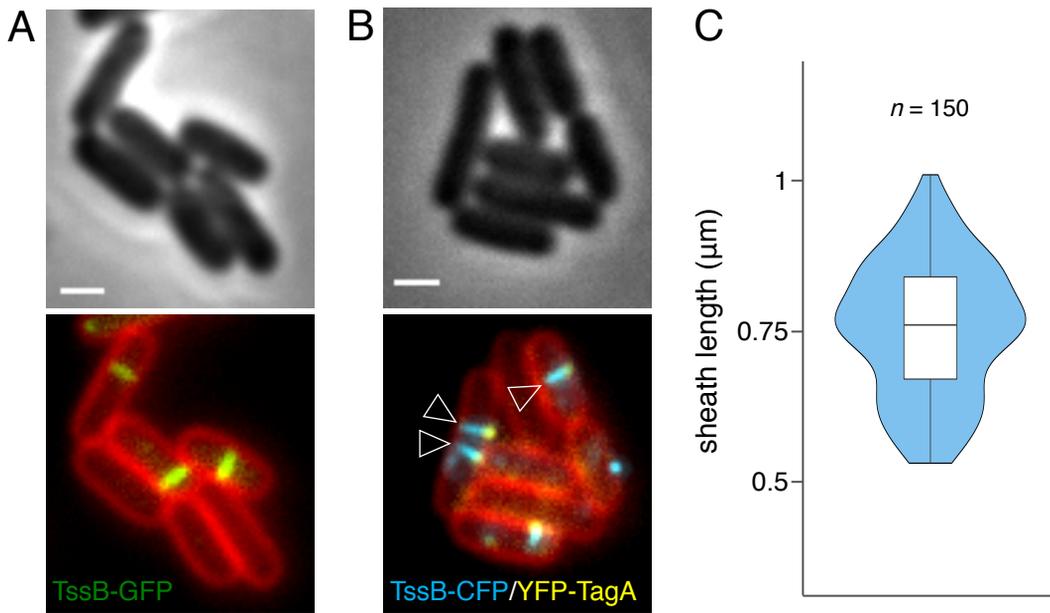
- 435 1. Cherrak, Y, Flaugnatti, N, Durand, E, Journet, L, and Cascales, E. (2019). Structure and  
436 activity of the type VI secretion system. *Microbiol. Spectrum* 7, PSIB-0031-2019.
- 437 2. Coulthurst, S. (2019). The Type VI secretion system: a versatile bacterial weapon.  
438 *Microbiol. 165*, 503–515.
- 439 3. Durand, E., Cambillau, C., Cascales, E., and Journet, L. (2014). VgrG, Tae, Tle, and  
440 beyond: the versatile arsenal of Type VI secretion effectors. *Trends Microbiol.* 22, 498–  
441 507.
- 442 4. Chassaing, B., and Cascales, E. (2018). Antibacterial weapons: targeted destruction in the  
443 microbiota. *Trends Microbiol.* 26, 329–338.
- 444 5. Sarris, P.F., Ladoukakis, E.D., Panopoulos, N.J., and Scoulica, E.V. (2014). A phage tail-  
445 derived element with wide distribution among both prokaryotic domains: a comparative  
446 genomic and phylogenetic study. *Genome Biol. Evol.* 6, 1739–1747.
- 447 6. Taylor, N.M.I., van Raaij, M.J., and Leiman, P.G. (2018). Contractile injection systems of  
448 bacteriophages and related systems. *Mol. Microbiol.* 108, 6–15.
- 449 7. Brunet, Y.R., Zoued, A., Boyer, F., Douzi, B., and Cascales, E. (2015). The type VI  
450 secretion TssEFGK-VgrG phage-like baseplate is recruited to the TssJLM membrane  
451 complex via multiple contacts and serves as assembly platform for tail tube/sheath  
452 polymerization. *PLoS Genet.* 11, e1005545.
- 453 8. Nazarov, S., Schneider, J.P., Brackmann, M., Goldie, K.N., Stahlberg, H., and Basler, M.  
454 (2018). Cryo-EM reconstruction of Type VI secretion system baseplate and sheath distal  
455 end. *EMBO J.* 37, e97103.
- 456 9. Cherrak, Y., Rapisarda, C., Pellarin, R., Bouvier, G., Bardiaux, B., Allain, F., Malosse,  
457 C., Rey, M., Chamot-Rooke, J., Cascales, E., *et al.* (2018). Biogenesis and structure of a  
458 type VI secretion baseplate. *Nat. Microbiol.* 3, 1404–1416.
- 459 10. Brunet, Y.R., Hénin, J., Celia, H., and Cascales, E. (2014). Type VI secretion and  
460 bacteriophage tail tubes share a common assembly pathway. *EMBO Rep.* 15, 315–321.
- 461 11. Leiman, P.G., Basler, M., Ramagopal, U.A., Bonanno, J.B., Sauder, J.M., Pukatzki, S.,  
462 Burley, S.K., Almo, S.C., and Mekalanos, J.J. (2009). Type VI secretion apparatus and

- 463 phage tail-associated protein complexes share a common evolutionary origin. *Proc. Natl.*  
464 *Acad. Sci. U. S. A.* *106*, 4154–4159.
- 465 12. Basler, M., Pilhofer, M., Henderson, G.P., Jensen, G.J., and Mekalanos, J.J. (2012). Type  
466 VI secretion requires a dynamic contractile phage tail-like structure. *Nature* *483*, 182–186.
- 467 13. Kudryashev, M., Wang, R.Y.-R., Brackmann, M., Scherer, S., Maier, T., Baker, D.,  
468 DiMaio, F., Stahlberg, H., Egelman, E.H., and Basler, M. (2015). Structure of the Type  
469 VI secretion system contractile sheath. *Cell* *160*, 952–962.
- 470 14. Aschtgen, M.-S., Gavioli, M., Dessen, A., Llobès, R., and Cascales, E. (2010). The SciZ  
471 protein anchors the enteroaggregative *Escherichia coli* Type VI secretion system to the  
472 cell wall. *Mol. Microbiol.* *75*, 886–899.
- 473 15. Durand, E., Nguyen, V.S., Zoued, A., Logger, L., Péhau-Arnaudet, G., Aschtgen, M.-S.,  
474 Spinelli, S., Desmyter, A., Bardiaux, B., Dujeancourt, A., *et al.* (2015). Biogenesis and  
475 structure of a type VI secretion membrane core complex. *Nature* *523*, 555–60.
- 476 16. Rapisarda, C., Cherrak, Y., Kooger, R., Schmidt, V., Pellarin, R., Logger, L., Cascales,  
477 E., Pilhofer, M., Durand, E., and Fronzes, R. (2019). In situ and high-resolution cryo-EM  
478 structure of a bacterial type VI secretion system membrane complex. *EMBO J.* *38*,  
479 e100886.
- 480 17. Katsura, I., and Hendrix, R.W. (1984). Length determination in bacteriophage lambda  
481 tails. *Cell* *39*, 691–698.
- 482 18. Katsura, I. (1990). Mechanism of length determination in bacteriophage lambda tails. *Adv.*  
483 *Biophys.* *26*, 1–18.
- 484 19. Abuladze, N.K., Gingery, M., Tsai, J., and Eiserling, F.A. (1994). Tail length  
485 determination in bacteriophage T4. *Virology* *199*, 301–310.
- 486 20. Belcaid, M., Bergeron, A., and Poisson, G. (2011). The evolution of the tape measure  
487 protein: units, duplications and losses. *BMC Bioinformatics* *12*, S10.
- 488 21. Rybakova, D., Schramm, P., Mitra, A.K., and Hurst, M.R.H. (2015). Afp14 is involved in  
489 regulating the length of anti-feeding prophage (Afp). *Mol. Microbiol.* *96*, 815–826.
- 490 22. Böck, D., Medeiros, J.M., Tsao, H.-F., Penz, T., Weiss, G.L., Aistleitner, K., Horn, M.,  
491 and Pilhofer, M. (2017). In situ architecture, function, and evolution of a contractile  
492 injection system. *Science* *357*, 713–717.
- 493 23. Vianelli, A., Wang, G.R., Gingery, M., Duda, R.L., Eiserling, F.A., and Goldberg, E.B.  
494 (2000). Bacteriophage T4 self-assembly: localization of gp3 and its role in determining  
495 tail length. *J. Bacteriol.* *182*, 680–688.
- 496 24. Brunet, Y.R., Bernard, C.S., Gavioli, M., Llobès, R., and Cascales, E. (2011). An  
497 epigenetic switch involving overlapping *fur* and DNA methylation optimizes expression  
498 of a type VI secretion gene cluster. *PLoS Genet.* *7*, e1002205.

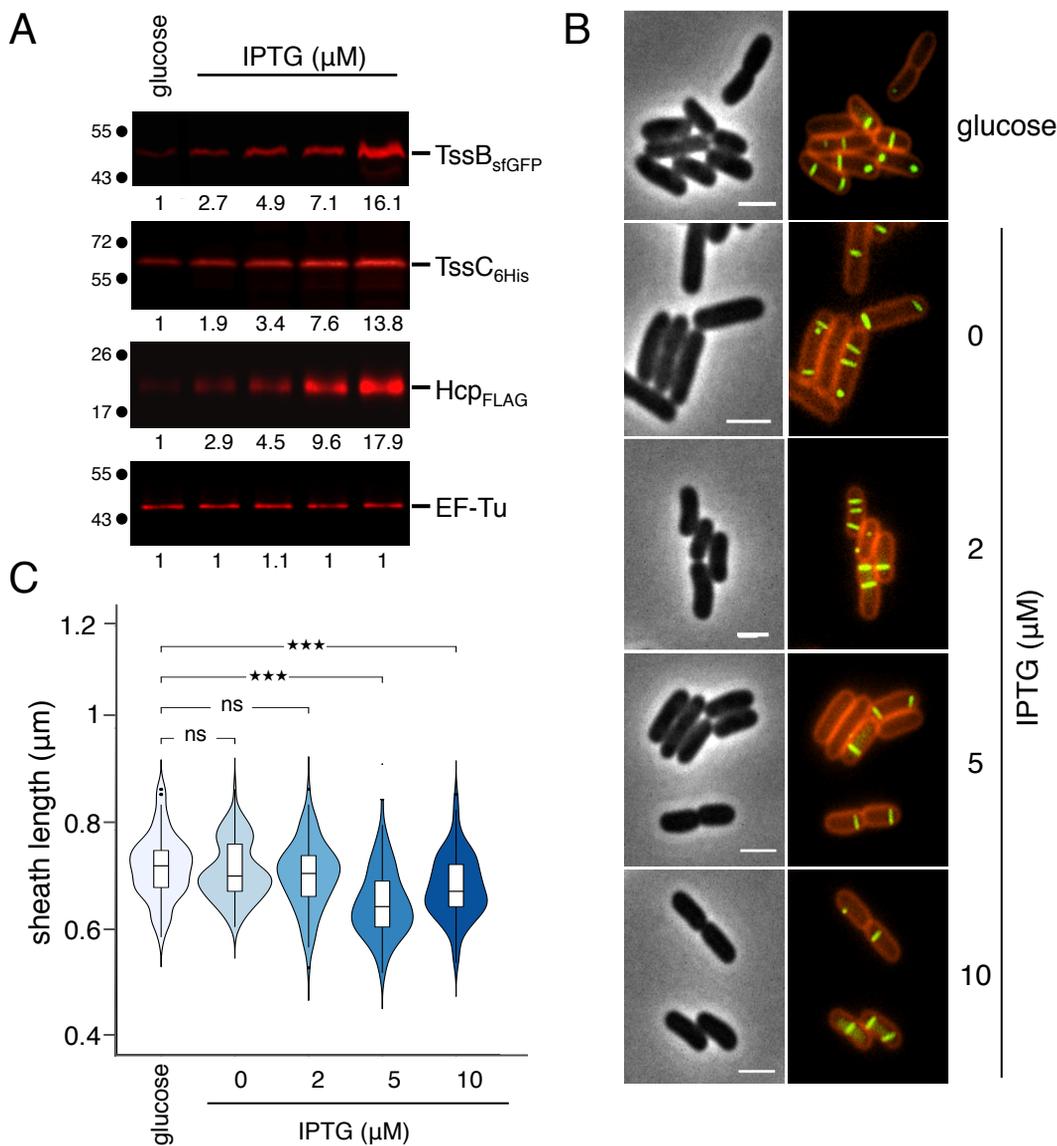
- 499 25. Santin, Y.G., Camy, C.E., Zoued, A., Doan, T., Aschtgen, M.-S., and Cascales, E. (2019).  
500 Role and recruitment of the TagL peptidoglycan-binding protein during Type VI secretion  
501 system biogenesis. *J. Bacteriol.* *201*, e00173-19.
- 502 26. Nivaskumar, M., and Francetic, O. (2014). Type II secretion system: a magic beanstalk or  
503 a protein escalator. *Biochim. Biophys. Acta* *1843*, 1568–1577.
- 504 27. Sauvonnet, N., Vignon, G., Pugsley, A.P., and Gounon, P. (2000). Pilus formation and  
505 protein secretion by the same machinery in *Escherichia coli*. *EMBO J.* *19*, 2221–2228.
- 506 28. Durand, E., Bernadac, A., Ball, G., Lazdunski, A., Sturgis, J.N., and Filloux, A. (2003).  
507 Type II protein secretion in *Pseudomonas aeruginosa*: the pseudopilus is a multifibrillar  
508 and adhesive structure. *J. Bacteriol.* *185*, 2749–2758.
- 509 29. Zoued, A., Durand, E., Brunet, Y.R., Spinelli, S., Douzi, B., Guzzo, M., Flaugnatti, N.,  
510 Legrand, P., Journet, L., Fronzes, R., *et al.* (2016). Priming and polymerization of a  
511 bacterial contractile tail structure. *Nature* *531*, 59–63.
- 512 30. Zoued, A., Durand, E., Santin, Y.G., Journet, L., Roussel, A., Cambillau, C., and  
513 Cascales, E. (2017). TssA: The cap protein of the Type VI secretion system tail.  
514 *Bioessays* *39*, 10.
- 515 31. Schneider, J.P., Nazarov, S., Adaixo, R., Liuzzo, M., Ringel, P.D., Stahlberg, H., and  
516 Basler, M. (2019). Diverse roles of TssA-like proteins in the assembly of bacterial type  
517 VI secretion systems. *EMBO J.* *12*, e100825.
- 518 32. Santin, Y.G., Doan, T., Lebrun, R., Espinosa, L., Journet, L., and Cascales, E. (2018). In  
519 vivo TssA proximity labelling during type VI secretion biogenesis reveals TagA as a  
520 protein that stops and holds the sheath. *Nat. Microbiol.* *3*, 1304–1313.
- 521 33. Katsura, I. (1987). Determination of bacteriophage lambda tail length by a protein ruler.  
522 *Nature* *327*, 73–75.
- 523 34. Boulanger, P., Jacquot, P., Plançon, L., Chami, M., Engel, A., Parquet, C., Herbeuval, C.,  
524 and Letellier, L. (2008). Phage T5 straight tail fiber is a multifunctional protein acting as a  
525 tape measure and carrying fusogenic and muralytic activities. *J. Biol. Chem.* *283*, 13556–  
526 13564.
- 527 35. Jiang, F., Li, N., Wang, X., Cheng, J., Huang, Y., Yang, Y., Yang, J., Cai, B., Wang, Y.-  
528 P., Jin, Q., *et al.* (2019). Cryo-EM structure and assembly of an extracellular contractile  
529 injection system. *Cell* *177*, 370-383.e15.
- 530 36. Journet, L., Agrain, C., Broz, P., and Cornelis, G.R. (2003). The needle length of bacterial  
531 injectisomes is determined by a molecular ruler. *Science* *302*, 1757–1760.
- 532 37. Cornelis, G.R., Agrain, C., and Sorg, I. (2006). Length control of extended protein  
533 structures in bacteria and bacteriophages. *Curr. Opin. Microbiol.* *9*, 201–206.
- 534 38. Hirano, T., Yamaguchi, S., Oosawa, K., and Aizawa, S. (1994). Roles of FliK and FlhB in  
535 determination of flagellar hook length in *Salmonella typhimurium*. *J. Bacteriol.* *176*,  
536 5439–5449.

- 537 39. Boyer, F., Fichant, G., Berthod, J., Vandenbrouck, Y., and Attree, I. (2009). Dissecting  
538 the bacterial type VI secretion system by a genome wide in silico analysis: what can be  
539 learned from available microbial genomic resources? *BMC Genomics* *10*, 104.
- 540 40. Vettiger, A., Winter, J., Lin, L., and Basler, M. (2017). The type VI secretion system  
541 sheath assembles at the end distal from the membrane anchor. *Nat. Commun.* *8*, 16088.
- 542 41. Atmakuri, K., Ding, Z., and Christie, P.J. (2003). VirE2, a type IV secretion substrate,  
543 interacts with the VirD4 transfer protein at cell poles of *Agrobacterium tumefaciens*. *Mol.*  
544 *Microbiol.* *49*, 1699–1713.
- 545 42. Lin, L., Lezan, E., Schmidt, A., and Basler, M. (2019). Abundance of bacterial Type VI  
546 secretion system components measured by targeted proteomics. *Nat Commun.* *10*, 2584.
- 547 43. Brunet, Y.R., Khodr, A., Logger, L., Aussel, L., Mignot, T., Rimsky, S., and Cascales, E.  
548 (2015). H-NS silencing of the *Salmonella* Pathogenicity Island 6-encoded type VI  
549 secretion system limits *Salmonella enterica* serovar Typhimurium interbacterial killing.  
550 *Infect Immun.* *83*, 2738–2750.
- 551 44. Brodmann, M., Dreier, R.F., Broz, P., and Basler, M. (2017). *Francisella* requires  
552 dynamic type VI secretion system and ClpB to deliver effectors for phagosomal escape.  
553 *Nat Commun.* *8*, 15853.
- 554 45. Liebl, D., Robert-Genthon, M., Job, V., Cogoni, V., and Attree, I. (2019). Baseplate  
555 Component TssK and spatio-temporal assembly of T6SS in *Pseudomonas aeruginosa*.  
556 *Front Microbiol.* *10*, 1615.
- 557 46. Zoued, A., Durand, E., Bebeacua, C., Brunet, Y.R., Douzi, B., Cambillau, C., Cascales,  
558 E., and Journet, L. (2013). TssK is a trimeric cytoplasmic protein interacting with  
559 components of both phage-like and membrane anchoring complexes of the type VI  
560 secretion system. *J. Biol. Chem.* *288*, 27031–27041.
- 561 47. Iwai, N., Ebata, T., Nagura, H., Kitazume, T., Nagai, K., and Wachi, M. (2004).  
562 Structure-activity relationship of S-benzylisothiourea derivatives to induce spherical cells  
563 in *Escherichia coli*. *Biosci. Biotechnol. Biochem.* *68*, 2265–2269.
- 564 48. Amann, E., Ochs, B., and Abel, K.J. (1988). Tightly regulated tac promoter vectors useful  
565 for the expression of unfused and fused proteins in *Escherichia coli*. *Gene* *69*, 301–315.
- 566 49. Datsenko, K.A., and Wanner, B.L. (2000). One-step inactivation of chromosomal genes in  
567 *Escherichia coli* K-12 using PCR products. *Proc. Natl. Acad. Sci. U. S. A.* *97*, 6640–6645.
- 568 50. Chaverroche, M.-K., Ghigo, J.-M., and d'Enfert, C. (2000). A rapid method for efficient  
569 gene replacement in the filamentous fungus *Aspergillus nidulans*. *Nucleic Acids Res.* *28*,  
570 e97.
- 571 51. Schindelin, J., Arganda-Carreras, I., Frise, E., Kaynig, V., Longair, M., Pietzsch, T.,  
572 Preibisch, S., Rueden, C., Saalfeld, S., Schmid, B., *et al.* (2012). Fiji: an open-source  
573 platform for biological-image analysis. *Nat. Methods* *9*, 676–682.

- 574 52. Zoued, A., Duneau, J.-P., Durand, E., España, A.P., Journet, L., Guerlesquin, F., and  
575 Cascales, E. (2018). Tryptophan-mediated dimerization of the TssL transmembrane  
576 anchor is required for type VI secretion system activity. *J. Mol. Biol.* *430*, 987–1003.
- 577 53. Kawazura, T., Matsumoto, K., Kojima, K., Kato, F., Kanai, T., Niki, H., and Shiomi, D.  
578 (2017). Exclusion of assembled MreB by anionic phospholipids at cell poles confers cell  
579 polarity for bidirectional growth. *Mol. Microbiol.* *104*, 472–486.
- 580 54. Ducret, A., Quardokus, E.M., and Brun, Y.V. (2016). MicrobeJ, a tool for high  
581 throughput bacterial cell detection and quantitative analysis. *Nat. Microbiol.* *1*, 16077.

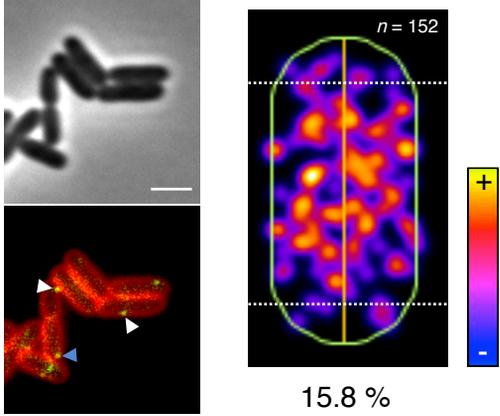


**Fig. 1. Statistical measure of the EAEC T6SS sheath length.** (A) Representative fluorescence micrograph of EAEC cells producing TssB-sfGFP and labelled with FM4-64 (upper panel, phase channel; lower panel, merge of GFP and FM4-64 channels). Scale bar, 1  $\mu\text{m}$ . (B) Representative fluorescence micrograph of EAEC cells producing TssB-CFP and YFP-TagA, and labeled with FM4-64 (upper panel, phase channel; lower panel, merge of CFP, YFP, and FM4-64 channels). The open arrowheads point T6SS extended sheaths in contact with the TagA stopper. Scale bar, 1  $\mu\text{m}$ . (C) Violin plot representation of the sheath length in wild-type cells. The distribution of the sheath lengths is represented by the outer shape. The bold horizontal bar represents the median value (median = 0.76  $\mu\text{m}$ ); the lower and upper boundaries of the internal box plot correspond to the 25th and 75th percentiles respectively; whiskers extend 1.5 times the interquartile range from the 25th and 75th percentiles. The number of measured sheaths ( $n=150$ ) is indicated above.

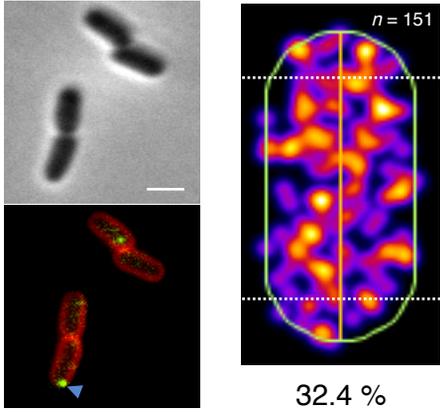


**Fig. 2. T6SS tail tube/sheath subunits levels do not determine T6SS sheath length.** (A) Western-blot analyses of tail tube/sheath component abundance.  $2 \times 10^8$  cells of  $\Delta tssBC\Delta hcp$  cells producing TssB-sfGFP (TssB<sub>sfGFP</sub>), 6 $\times$ His-tagged TssC (TssC<sub>6His</sub>) and FLAG-tagged Hcp (Hcp<sub>FLAG</sub>) from the pTrc-B<sub>GFP</sub>-C<sub>6H</sub>-Hcp<sub>F</sub> grown in presence of 0.4% of glucose or of the indicated concentration of IPTG were subjected to 12.5% acrylamide SDS-PAGE and immunodetected with anti-GFP, -His, -FLAG and -EF-Tu monoclonal primary antibodies and secondary antibodies coupled to AlexaFluor<sup>®</sup> 680. The EF-Tu cytoplasmic elongation factor is used as loading control. The increased fold values compared to the glucose condition, measured by densitometric quantification of the band signal intensities and relative to the loading control, are indicated below. Molecular weight markers (in kDa) are indicated on left. (B-C) Representative fluorescence microscopy recordings (B) and statistical analyses of sheath length measurements (C) of  $\Delta tssBC\Delta hcp$  cells producing Hcp<sub>FLAG</sub>, TssB-sfGFP and TssC<sub>6His</sub> in presence of 0.4% glucose or of the indicated concentration of IPTG, and labelled with FM4-64 (left panels, phase channel; right panels, merge of GFP and FM4-64 channels). Scale bar, 2  $\mu$ m. In the violin plot representation of the statistical analysis, the distribution of the sheath length is represented by the outer shape. The bold horizontal bar represents the median; the lower and upper boundaries of the internal box plot correspond to the 25th and 75th percentiles respectively; whiskers extend 1.5 times the interquartile range from the 25th and 75th percentiles. Outliers are shown as black dots. Statistical significance from three independent assays ( $n = 100$  for each conditions) relative to the glucose condition is indicated above the plots (ns, non-significant; \*\*\*,  $p < 0.001$ ; two-tailed Student's  $t$ -test). A comparison of tail tube/sheath subunits levels and sheath lengths is shown in Fig. S1.

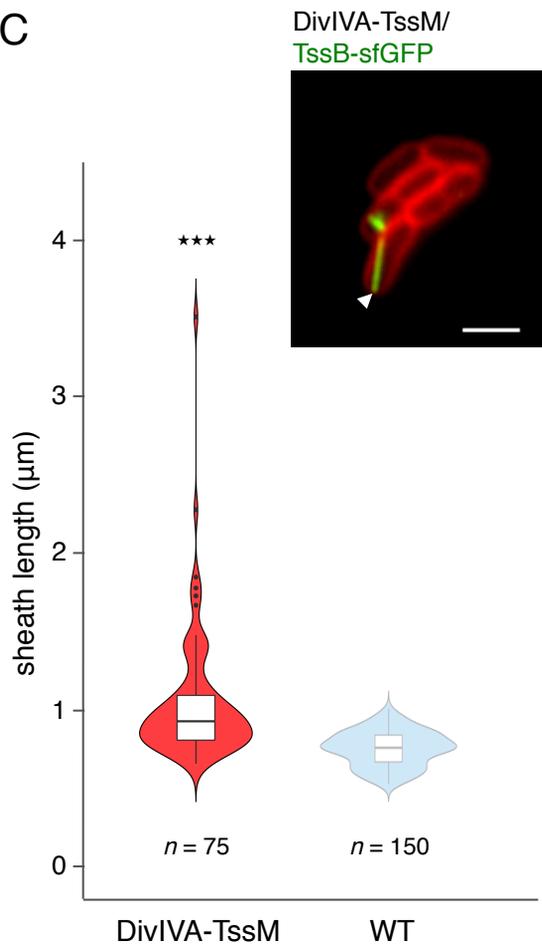
**A** WT/sfGFP-TssL



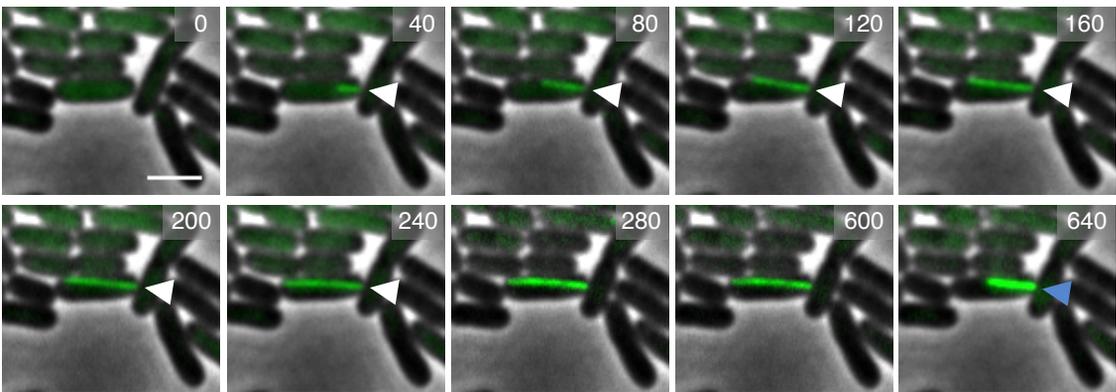
**B** DivIVA-TssM/sfGFP-TssL



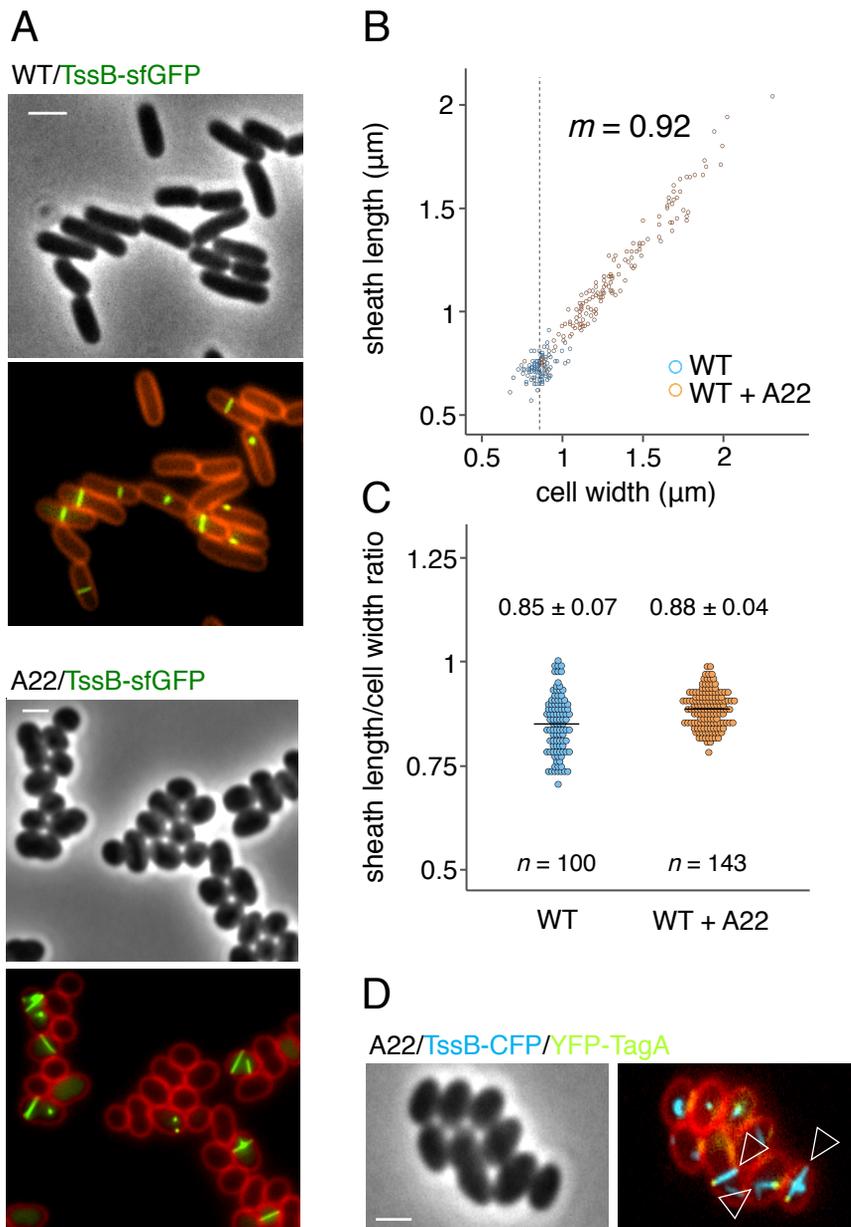
**C**



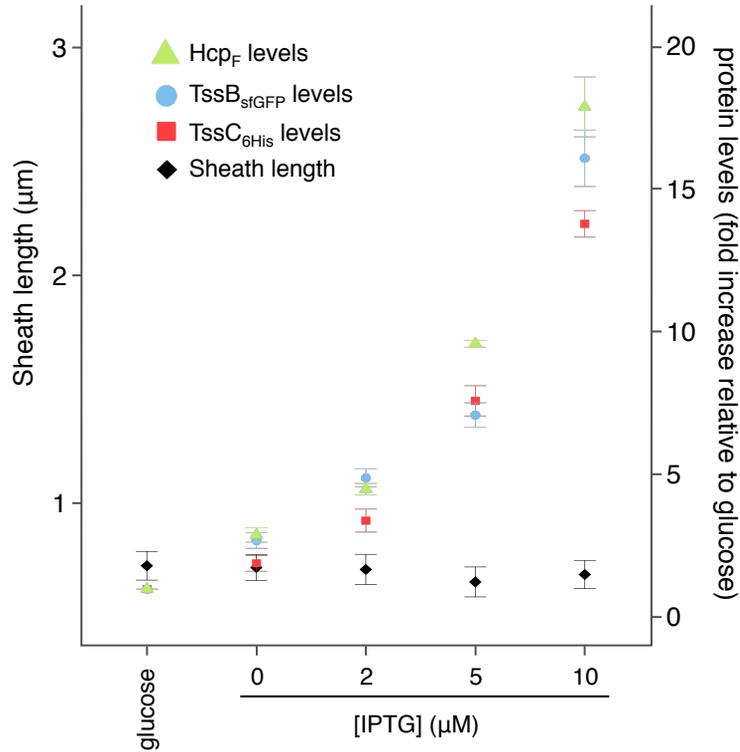
**D** DivIVA-TssM/TssB-sfGFP



**Fig. 3. Sheath length is not controlled by a tape measure protein.** Representative fluorescence microscopy recordings of EAEC cells producing sfGFP-TssL in WT (*A*) or DivIV-TssM (*B*) cells, and labelled with FM4-64 (upper panels, phase channel; lower panels, merge of GFP and FM4-64 channels). White and blue arrowheads indicate TssL foci with body or polar localizations, respectively. Scale bar, 2  $\mu\text{m}$ . The spatial repartition of sfGFP-TssL foci is shown on right, as a projection of foci from  $n=152$  and  $n=151$  WT and DivIVA-TssM cells, respectively, on a single cell (from blue to yellow, see heatmap color chart on right of panel *A*). The percentage of sfGFP-TssL foci with polar localization is indicated below. (*C*) Violin plot representation of sheath length measurements in DivIVA-TssM cells producing TssB-sfGFP (red). An example of a representative microscopy field is shown in the inset (scale bar, 2  $\mu\text{m}$ ). The distribution of sheath length in WT cells (shown in Fig. 1*B*) is reported in transparency for comparison (blue). The distribution of the sheath length is represented by the outer shape. The bold horizontal bar represents the median value (median = 0.93  $\mu\text{m}$  and 0.76  $\mu\text{m}$  for DivIVA-TssM and WT cells, respectively); the lower and upper boundaries of the internal box plot correspond to the 25th and 75th percentiles respectively; whiskers extend 1.5 times the interquartile range from the 25th and 75th percentiles. Outliers are shown as black dots. The number of measured sheaths ( $n=75$ ) is indicated below. Statistical significance relative to WT cells is indicated above the plots (\*\*\*,  $p < 0.001$ ; one-tailed Wilcoxon's  $t$ -test). (*D*) Fluorescence microscopy time-lapse recordings of DivIVA-TssM cells producing TssB-sfGFP highlighting polar T6SS sheath assembly (white arrowhead) and contraction (blue arrowhead). Scale bar, 2  $\mu\text{m}$ .



**Fig. 4. Cell width dictates T6SS sheath length.** (A) Representative fluorescence micrographs of EAEC cells producing TssB-sfGFP in absence (upper panel) or in presence of the MreB inhibitor A22 (lower panel), and labelled with FM4-64 (upper panel, phase channel; lower panel, merge of GFP and FM4-64 channels). Scale bar, 2  $\mu\text{m}$ . (B) Plot representation showing the relationship between sheath length and cell width in absence (blue) and presence of A22 (orange). The dashed line represents the mean of the WT cell width (mean = 0.87  $\mu\text{m}$ ). Value of the slope ( $m$ ) is indicated on right. Kendall's  $\tau = 0.82$ . (C) Dotplot of the ratios between sheath length and the width of the corresponding cell from cells grown in absence (blue) or presence of A22 (orange). Horizontal bars represent the mean in each condition. The values of the means and standard deviations are indicated above the plots. The number of analyzed cells ( $n$ ) is indicated below. (D) Representative fluorescence micrograph of EAEC cells producing TssB-CFP and YFP-TagA in presence of the MreB inhibitor A22, and labelled with FM4-64 (left panel, phase channel; right panel, merge of CFP, YFP, and FM4-64 channels). The open arrowheads point T6SS extended sheaths in contact with the TagA stopper. Scale bar, 2  $\mu\text{m}$ .



**Fig. S1. T6SS tail tube/sheath subunits levels do not determine T6SS sheath length.** Graph representation of the fold increase of Hcp<sub>FLAG</sub> (green triangles), TssB-sfGFP (blue circles), and TssC<sub>6His</sub> (red squares) cellular levels as a function of the IPTG concentration (relative to the glucose condition) from  $\Delta tssBC\Delta hcp$  cells bearing plasmid pTrc-B<sub>GFP</sub>-C<sub>6H</sub>-Hcp<sub>F</sub>. The corresponding sheath lengths are indicated with black diamonds. The mean and standard deviations from three independent experiments are shown.