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<td><strong>Original citation</strong></td>
<td>Gueguen E, Wills NM, Atkins JF, Cascales E (2014) Transcriptional Frameshifting Rescues Citrobacter rodentium Type VI Secretion by the Production of Two Length Variants from the Prematurely Interrupted tssM Gene. PLoS Genet 10(12): e1004869. doi:10.1371/journal.pgen.1004869</td>
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Transcriptional Frameshifting Rescues Citrobacter rodentium Type VI Secretion by the Production of Two Length Variants from the Prematurely Interrupted tssM Gene

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Abstract

The Type VI secretion system (T6SS) mediates toxin delivery into both eukaryotic and prokaryotic cells. It is composed of a cytoplasmic structure resembling the tail of contractile bacteriophages anchored to the cell envelope through a membrane complex composed of the TssL and TssM inner membrane proteins and of the TssJ outer membrane lipoprotein. The C-terminal domain of TssM is required for its interaction with TssJ, and for the function of the T6SS. In Citrobacter rodentium, the tssM1 gene does not encode the C-terminal domain. However, the stop codon is preceded by a run of 11 consecutive adenosines. In this study, we demonstrate that this poly-A tract is a transcriptional slippery site that induces the incorporation of additional adenosines, leading to frameshifting, and hence the production of two TssM1 variants, including a full-length canonical protein. We show that both forms of TssM1, and the ratio between these two forms, are required for the function of the T6SS in C. rodentium. Finally, we demonstrate that the tssM gene associated with the Yersinia pseudotuberculosis T6SS-3 gene cluster is also subjected to transcriptional frameshifting.

Introduction

The Type VI secretion system (T6SS) is a macromolecular machine widespread in proteobacteria that delivers protein toxins into either eukaryotic or bacterial cells [1–5]. The Vibrio cholerae T6SS has been shown to inject an effector domain carrying actin cross-linking activity into eukaryotic cells, preventing cytoskeleton rearrangements and allowing the bacteria to escape phagocytosis [6–8]. More recently, a number of T6SSs including those of Pseudomonas aeruginosa, V. cholerae, Serratia marcescens, enterohaemorrhagic Escherichia coli and Citrobacter rodentium have been shown to play antagonistic roles in interbacterial competition including competition occurring during host colonization [5,9–13]. Bacterial preys are killed through the actions of toxins that bear peptidoglycan hydrolase, phospholipase or DNase activities [13–15].

For toxin delivery, the T6SS is thought to use a dynamic mechanism resembling that of contractile tailed bacteriophages [3,4,16–18]. Recent cryo-electron microscopy experiments demonstrated that the T6SS is composed of a cytoplasmic tubular structure anchored to the cell envelope by a membrane complex [18]. The tubular structure is structurally and mechanistically similar to the tail of bacteriophages: the Hcp protein forms hexameric rings that stack on each other to assemble a tube resembling the internal tube of phages and tipped by a trimer of VgrG, which shares a fold similar to the trimeric bacteriophage gp27-gp5 hub – or cell-puncturing – complex [16,19–21]. This internal tube is wrapped into a structure composed of the TssB and TssC subunits [18,22]. This structure has been shown to be dynamic, as TssB proteins fused to the super-folder Green Fluorescent Protein (sfGFP) form long filaments that cycle between extended and contracted conformations, a mechanism reminiscent of bacteriophage sheaths [18,23–25]. The current model proposes that the mode of action of the T6SS is comparable to that of a crossbow [2–4]: the sheath assembles around the Hcp internal tube into an extended conformation. Upon contraction, the internal tube will be propelled towards the target cell allowing the VgrG protein to puncture the host cell and effector delivery. Indeed, recent studies have shown that contraction of the T6SS sheath-like structure coincides with killing of the target bacterial prey [23–25].

This “phage-related” complex is anchored to the cell envelope through interactions with membrane components. This membrane complex is composed of the TssL and TssM inner
membrane proteins and the TssJ outer membrane lipoprotein [3,4,26,27]. TssM is constituted of three trans-membrane helices with a large C-terminal domain of ~750 residues protruding into the periplasm [28,29]. TssM is a central component as it interacts with both TssL and TssJ [28,29]. The interaction with TssJ has been characterized and involves contacts between a specific loop of the lipoprotein and the 150 last residues of TssM [29]. This interaction is critical for T6SS function as disruption of the TssM-TssJ interaction abolishes Hcp release in the culture supernatant [29]. Although this C-terminal region of TssM is an essential determinant of T6SS function, the TssM protein encoded within the CTS1 T6SS gene cluster of C. rodentium, TssM1, is lacking this domain. However, this T6SS is functional as shown by its ability to release the Hcp1 protein in the culture supernatant and to mediate interbacterial killing [30]. Sequence analysis of the tssM1 gene showed that the stop codon is preceded by a polyadenosine sequence constituted of eleven consecutive adenosine residues [30,31]. Poly-A runs have been previously shown to be slippery sites for the RNA polymerase that cause frameshifting by incorporation of additional nucleotides in the mRNA and therefore restores the original framing. As a consequence, two different TssM variants are created by transcriptional frameshifting, including a full-length 130-kDa protein and an 88-kDa truncated variant. We further show that both forms, and the ratio between these two forms, are required for the function of the transport apparatus. Interestingly, a similar mechanism regulates the synthesis of two TssM variants in Yersinia pseudotuberculosis.

**Results**

**Sequence analysis of the C. rodentium CTS1 tssM1 gene**

Analysis of the Citrobacter rodentium tssM1 gene sequence (accession numbers: ROD_27701, Gene ID: 8713033) showed that the full-length gene is disrupted by the existence of a premature amber stop codon at position 2,421 (from the start codon) [31]. DNA sequencing of a cloned fragment encompassing this region showed that this amber codon is not a sequencing error. Premature arrest of tssM1 translation leads to the production of an 807-amino-acid (aa) TssM1 protein (TssM1[1–807]) (Fig. 1A and 1B). Transmembrane helix predictions and sequence alignment of TssM1[1–807] with TssS TssM proteins of known topology showed that TssM1[1–807] is constituted of the three N-terminal helices but lacks the C-terminal β-domain which has been previously shown to mediate the interaction with TssJ. Interestingly, a sequence corresponding to a β-domain similar to those of canonical TssM proteins is encoded on the +1 reading frame downstream the stop codon of tssM1[1–807]. Hence, a full-length 1129-aa TssM protein (TssM1-FL) will be produced if +1 frameshifting occurs before the stop codon of tssM1[1–807] (Fig. 1A and 1B). To test whether frameshifting occurs, we monitored TssM1 production by immunodetection. The 3829-bp sequence of tssM1-FL was cloned in an expression plasmid downstream the tet promoter. The cloning strategy included the insertion of (i) a FLAG epitope-encoding sequence immediately downstream the start codon and (ii) a 6×His-encoding sequence upstream the stop codon of tssM1-FL. Western-blot analyses of cell extracts of C. rodentium carrying this expression plasmid demonstrated the production of two proteins of ~85 and ~130 kDa, immunostained by the anti-FLAG antibody (Fig. 1C). The molecular weights of these two bands are similar to the expected sizes of TssM1[1–807] (88 kDa) and TssM1-FL (125 kDa). This result suggests that frameshifting occurs in the tssM1[1–807] sequence, yielding a full-length TssM1 protein. The production of TssM1-FL was confirmed as the ~130-kDa protein was detected by anti-5His immunostaining (Fig. 1C). Quantitative analyses showed that the intensity of the high molecular weight protein is ~1/3 of that of the low molecular weight protein, suggesting that +1 frameshifting occurs with a frequency of ~25%.

**C. rodentium tssM1 frameshifting involves a run of adenosines**

Sequence analysis showed that a stretch of 11 adenosines is localized 28 nucleotides upstream the tssM1[1–807] stop codon (Fig. 2A). It has been previously shown that poly-adenosine tracts might induce ribosome or RNA polymerase slippage [32–35]. To test whether this poly-A tract might be involved in the production of TssM1-FL, we used site-directed mutagenesis to engineer (i) a tssM1 variant in which the three AAA codons were substituted by three AAG codons (a construct hereof called tssM1-AAG) and (ii) a tssM1 variant with a disrupted poly-A and carrying a deletion of the last A to create an artificial +1 frameshift (called tssM1-AAGΔA) (Fig. 2A). Western-blot analyses showed that disruption of the poly-A tract prevents frameshifting as only the low molecular weight protein corresponding to TssM1[1–807] was detected by the anti-FLAG antibody. By contrast, only the TssM1-FL variant was detected with both anti-FLAG and anti-5His antibodies when the artificial frameshift construct was analyzed (Fig. 2B). To verify that frameshifting occurs, we used an alternate method by engineering translational fusion of TssM1 to the GFP. The GFP-encoding sequence was inserted 48-pb downstream the premature stop codon of TssM1[1–807] (TssM1-FL, Fig. 2C). This construct serves as negative control for fluorescence (Fig. 2D), as no GFP fusion can be produced (because of the in-frame stop codon). Additional GFP fusions were engineered. In the TssM1-FL construct, an additional nucleotide was inserted between the premature stop codon and the GFP-encoding sequence (Fig. 2C). This construct is a reporter of +1
frameshifting in the natural situation, as the fusion protein will be produced only if +1 frameshifting occurs. Indeed, a significant level of fluorescence compared to the WT sequence can be observed with this construct, demonstrating that frameshifting occurs (Fig. 2D). This frameshifting is dependent on the poly-A run as poly-A disruption by AAA to AAG substitutions in the TssM1+1/AAG construct (TssM1+1/AAG, Fig. 2C) decreases the fluorescence to TssM1-WT levels. Finally, a deletion of the 11th A nucleotide in the TssM1+1/AAG construct yields TssM1+1/AAGΔ (Fig. 2C). In this fusion, no frameshifting can occur but the frame is restored by the additional nucleotide placed after the initial stop codon. Hence, all the produced TssM1 proteins are fused to the GFP and the fluorescence levels reflect the fluorescence if +1 frameshifting occurred with an efficiency of 100%. Comparison of the TssM1-WT levels showed that the +1 frameshift frequency is ~20% (Fig. 2D), a value comparable to the frequency calculated from protein immunodetection (Fig. 1C). Taken together, the results from the Western-blot analyses and of the GFP fusions demonstrate that a frameshifting mechanism involving slippage onto a poly-A tract restores the reading-frame of the tssM1 gene of C. rodentium to produce two TssM1 variants: TssM1[1–807] and TssM1-FL.

C. rodentium tssM1 reading-frame restoration involves transcriptional slippage

The molecular mechanisms that yield frameshifting have been well described. Translational frameshift could occur during translation of mRNA by ribosomes at specific adenosine repeat, but this mechanism usually requires additional determinants within the mRNA such as Shine-Dalgarno-like sequences or specific mRNA secondary structures close to the stretch of adenosines [33,35,36]. However, none of these signals are found at proximity to the tssM1 frameshifting site. Long stretches of homopolymeric sequences are better known to induce transcriptional slippage, i.e., realignment of the growing RNA to its DNA template within the RNA polymerase. The incorporation of extra, nontemplated, A nucleotide[s] by the RNA polymerase during elongation results in the synthesis of a heterogeneous population of mRNA with different molecular masses [32,37]. To test whether
tssM1 frameshifting involves ribosome or RNA polymerase slippage, the molecular masses of tssM1 mRNA products were measured by electrospray ionization mass spectrometry (ESI/MS) as previously reported [37]. Total RNAs were collected from WT C. rodentium cells upon activation of the CTS1 T6SS gene cluster using the recombinant strain carrying inducible promoters [30] and tssM1 cDNA were synthesized and used as template for a PCR reaction. ESI/MS analyses of the PCR products show that products with masses corresponding to molecules bearing 10 to 15 As in the poly-A run were detected (Fig. 3A). The additional adenosines were not incorporated during reverse transcription and PCR amplification as only 11-A PCR products were observed by ESI/MS when a synthetic mRNA corresponding to the region of tssM1 mRNA subjected to reverse transcription was used as initial template (Fig. 3B). Hence, the presence of the stretch of adenosines induces reiterative transcription by the RNA polymerase and this transcriptional frameshifting restores the tssM1 reading-frame.

Both TssM1[1-807] and TssM1-FL are required for CTS1 T6SS function

At a functional level, the most frequent use of frameshifting is to allow the synthesis of a product additional to that of standard decoding. The products can have distinct functions and the ratio...
between the different products might be important. In other cases frameshifting serves a regulatory function [35]. To address the physiological relevance of the \textit{tssM1} frameshifting for T6SS function, a strain deleted of the \textit{tssM1-FL} gene was constructed. As we did not find conditions in which the CTS1 T6SS gene cluster is expressed, we used in this study recombinant strains in which the expression of the cluster is under the control of inducible promoters, as previously described [30]. CTS1 T6SS function was tested by monitoring Hcp1 release in the culture medium and CTS1-mediated interbacterial killing [30]. As shown previously, the CTS1 was non functional in absence of the \textit{tssM1} gene as shown by the absence of Hcp1 in culture supernatant and by the inability of CTS1 to confer a growth advantage to \textit{C. rodentium} in co-culture with \textit{E. coli} on solid medium (Fig. 4A; [30]). These phenotypes were complemented by the trans-expression of \textit{tssM1}, which produces both TssM1[1–807] and TssM1-FL. However, when TssM1[1–807] or TssM1-FL (from \textit{tssM1-AAG} or \textit{tssM1-AAGA4} respectively) were produced alone, the CTS1 T6SS was not functional: Hcp1 was not released and CTS1-mediated interbacterial killing was abolished (Fig. 4A). These data indicate that both variants of TssM1 are necessary for T6SS function. To further validate these results, we introduced the AAG and AAG \textit{D} substitutions on the chromosome to yield strains producing only one of the TssM1 variants. As shown in Fig. 4B, the CTS1 T6SS was not functional in these two strains; however, when the second variant was expressed in \textit{trans}, Hcp release and CTS1-mediated interbacterial competition were restored to levels comparable to the WT strain. Taken together, these results demonstrate that \textit{C. rodentium} CTS1 T6SS function requires both forms of TssM1, TssM1[1–807] and TssM1-FL, the latter being produced by transcriptional frameshifting.

Figure 3. Frameshifting is caused by transcriptional slippage. ESI/MS analyses. Mass spectra of PCR products encompassing the \textit{tssM1} poly-A tract generated by RT-PCR from \textit{C. rodentium} total RNA (mRNA; A) or from a synthetic mRNA (B). The two strands of the PCR products are observable. The molecular mass (in Da) is shown on the \textit{x} axis, and the relative intensity of the signal is indicated on the \textit{y} axis. The number of A or T residues in the homopolymeric run is shown above each peak. The measured and predicted masses (in Da) of each peak are shown in the inset for each panel. The difference between predicted and measured masses is expressed as the percentage error for each peak.

doi:10.1371/journal.pgen.1004869.g003

Altered ratio between the two TssM1 length variants impair T6SS function

As described above, Western-blot and fluorescence quantifications established that the TssM1[1–807]: TssM1-FL ratio was close to 3–4:1 (Figs. 1C, 2B and 2C). As both TssM1 variants were required for T6SS function, we asked whether the relative ratio between these two variants is critical. Each form was therefore independently cloned on compatible plasmids: pBAD18 (pBR322 origin) and pASK-IBA37+ (pUC origin). We first verified that producing the natural TssM1 variants in these two vectors (i.e., retaining the natural ratio between the two forms) did not impact the function of the CTS1 T6SS. Production of the two forms from pBAD18 (Fig. 4A) or from pASK-IBA37+ (Fig. 5A) complemented the T6SS-dependent Hcp1 secretion defect of \textit{D}tssM1 cells. As shown previously for the pBAD18 derivatives, Hcp1 was not released when each length variant was independently produced from pASK-IBA37+ (Fig. 5A). Fig. 5B shows that when TssM1[1–807] was produced at higher levels than TssM1-FL (i.e., the natural situation; Fig. 5B, lanes 7 and 8), Hcp1 release was abolished (Fig. 5B, lanes 3 and 4). These data therefore demonstrate that the CTS1 T6SS is functional only when the truncated form of TssM1 is produced in higher amount than the full-length TssM1 variant.

TssM transcriptional frameshifting is conserved in \textit{Yersinia pseudotuberculosis}

We wondered whether transcriptional frameshifting is a common character among \textit{tssM} genes. T6SS-associated \textit{tssM} gene nucleotide sequences collected from the National Center for
Biotechnology and Information (NCBI) were used to identify (i) \textit{tssM} genes with abnormal length and/or (ii) \textit{tssM} genes bearing A or T homopolymeric runs. Interestingly, we found that the \textit{tssM} gene encoded within the \textit{Yersinia pseudotuberculosis} T6SS-3 gene cluster, \textit{tssM3} (accession number: YpsIP31758_1373; gene ID 5385222), has a stretch of 9 As at position 2,394 relative to the start codon (Fig. 6A). The \textit{tssM3} gene encodes a 130-kDa protein. The \textit{tssM3} gene was cloned downstream a FLAG epitope-coding sequence. Western-blot analyses of cell extracts of \textit{Y. pseudotuber-
culosis} cells producing FLAG-TssM3 revealed a band at 80 kDa in addition to the full-length 130-kDa protein (Fig. 6B). This band results from frameshifting as (i) a stop codon is present downstream the poly-A tract in the +1 reading frame (Fig. 6A) and (ii) disruption of the poly-A tract by AAG substitutions of the AAA codons abolished synthesis of the 80-kDa protein (Fig. 6B). These data were confirmed by fluorescence levels of GFP fusion proteins: the putative slippery site was active as fusion of the GFP-encoding sequence in the +1 reading frame downstream the poly-A tract (\textit{TssM3}+1) led to GFP fluorescence (Fig. 6C and 6D). However, although the slippage mechanisms between the \textit{C. rodentium} \textit{tssM1} and \textit{Y. pseudotuberculosis} \textit{tssM3} genes are probably similar and allow the synthesis of two variants of different lengths, recoding in \textit{tssM1} leads to the synthesis of the longer variant, whereas recoding in \textit{tssM3} leads to the synthesis of the shorter variant. It is also important to note that the quantification of the anti-FLAG western-blots and the comparison between the fluorescence levels of the \textit{TssM3}-WT and \textit{TssM3}+1 GFP fusion constructs showed that the frequency of frameshifting is 15–25%, demonstrating that, in contrast to \textit{C. rodentium} \textit{TssM1}, the full-length protein is produced at higher levels compared to the truncated form.

**Discussion**

In this work, we showed that the sequence of one essential gene of the \textit{C. rodentium} CTS1 T6SS is disrupted by an early stop codon yielding a 88-kDa truncated protein, \textit{TssM1}[1–807], that lacks a large part of the C-terminal domain required for interaction with other components of the secretion machine; however, we demonstrated that the full-length 125-kDa \textit{TssM1} protein is produced during growth. We further demonstrated that transcriptional frameshifting occurs at a slippery site composed of 11 consecutive adenosine residues, located a few bases upstream the premature stop codon, that induces RNA polymerase infidelity and realignment. This mechanism, although unusual, is not unprecedented. Several examples of RNA editing have been described in viruses, eukaryotes and prokaryotes [33–35,38–41]. Frameshifting is particularly frequent in bacteriophages and bacterial insertion sequence (IS) elements [33–35]. Well-studied cases are the phage \textit{G} gene which encodes two tail proteins, gpG.
and gpGT, gpGT arising from translational frameshifting [42,43] and the dnaX gene, which encodes the ς and γ subunits of DNA polymerase III [37,44]. One striking example is the fusion between pgk and tim, two different genes that can be fused by translational frameshifting at the 3’ end of pgk, yielding a bifunctional chimera protein [38]. The overrepresentation of slippery sites in viruses and bacterial endosymbiots of insects, which have the smallest genomes, suggests that this mechanism helps to condense protein coding in compact genomes [35,40]. Interestingly, examples of translational frameshifting have been identified in other bacterial secretion systems such as the Shigella flexneri Type III secretion system (T3SS), a machinery that mediates entry of the bacterium into epithelial cells. Slippery sites that induce RNA polymerase infidelity have been identified and characterized in the mxiE gene that encodes a transcriptional activator of this system as well as in three genes encoding structural components of the T3SS, mxiA, spa13 and spa33 [45,46].

The efficiency of the tssM1 frameshifting was shown to be ~20–25% leading to a molecular ratio of 3–4:1 of TssM1[1–807] to TssM1-FL. A similar frequency was measured for Y. pseudotuberculosis tssM3. These frequencies are comparable to those measured for transcriptional slippage of the Shigella flexneri mxiA (15%), mxiE (20–30%), and spa33 (15%) genes and lower than those measured in the case of spa13 (55%) [45,46]. In this study, we have measured the slippage efficiencies during growth in rich medium (LB). It would be interesting to test whether the slippage frequency is impacted by the growth conditions or by regulatory elements, such as bacteriophage λ N protein, recently shown to influence transcriptional realignment by stabilizing the RNA/DNA hybrid in the RNA polymerase [47].

Figure 5. The ratio between the two TssM1 variants is critical for CTS1 T6SS function. Hcp release assays. C. rodentium ΔtssM1 cells expressing WT tssM1 (WT; producing both forms of TssM1: TssM1-FL and TssM1[1–807]) or TssM1 variants bearing mutations in the poly-A tract (AAG; producing only the TssM1[1–807] variant) or mutations in the poly-A tract and a deletion of the last nucleotide (AAGΔA; producing only the TssM1-FL variant) from the pASK-IBA37+ vector (A) or producing the indicated variants from the pBAD18 and pASK-IBA37+ vectors (B). Extracellular proteins were isolated by separating whole cells (C) and the supernatant fraction (S) from cultures induced with arabinose and anhydrotetracyclin. TssM1 variants were immunodetected using the anti-FLAG monoclonal antibody (upper panels). The relative intensities of the short and long TssM1 variants are indicated (as %). Total proteins were visualized by Coomassie blue staining (lower panels). Molecular mass markers are indicated on the left.

doi:10.1371/journal.pgen.1004869.g005
Using complementation assays, we further showed that both forms of TssM1 are required for T6SS function. Although further experiments are required to better understand what is the specific function of each of these two variants, this situation is reminiscent to that of the phage lambda G gene, in which both gpG and gpGT variants are required for efficient assembly of functional tails [48]. In this later case, it was shown that the ratio between gpG and gpGT is also important for formation of phage tails [48]. Similarly, we observed that the ratio between the two TssM1 variants is critical for maintaining a functional CTS1 T6SS. In the natural situation, the shorter variant (TssM1[1–807]) is 3-4 times more abundant than the full-length variant. Inversion of the ratio between the two forms abolishes the function of the CTS1 T6SS.

One additional intriguing result is the observation that a third TssM1 variant of ~40 kDa, truncated of the N-terminal region, is immunodetected by the C-terminal 6×His epitope (see * in Fig. 2B). This variant therefore corresponds to the C-terminal portion of the TssM1 80-kDa periplasmic domain that is likely retained into the cytoplasm. This variant might be produced from an internal start codon (although sequence analyses did not identify a potential ribosome binding site or an internal start codon) or might result from a proteolytic processing. Experiments are currently carried out to determine how this third variant is produced and to define whether it is necessary for proper assembly or function of the CTS1 T6SS.

Bioinformatic analyses of the T6SS-associated tssM genes showed that transcriptional slippery sites are not common as we only identified the tssM3 gene from Yersinia pseudotuberculosis with a poly-A run. Western-blot and fluorescence studies further demonstrated that this site is active as two TssM3 length variants are produced. Slippage occurs with a frequency comparable to that of the C. rodentium tssM1 situation. Although we have not

Figure 6. Transcriptional slippage is conserved in Y. pseudotuberculosis. (A) Representation of the nucleotide sequence of Y. pseudotuberculosis tssM3. The poly-A tract is shown in red. The codons and the amino-acids resulting from translation of the WT sequence, as well as those produced from +1 or +2 frameshifting are indicated with the size of the TssM3 variants. (B) Western-blot analyses of Y. pseudotuberculosis cells producing the TssM3 WT protein or a derivative mutated in the poly-A tract (AAG) bearing a FLAG-epitope tag at the N-terminus. Crude extracts from 10⁶ cells were subjected to 10%-acrylamide SDS-PAGE and immunodetection using the anti-FLAG monoclonal antibody. The positions of the TssM3-FL and [1–802] variants are indicated in the right using the schematic representation. The relative intensities of these two variants are indicated (as %). Molecular weight markers (in kDa) are indicated on the left. (C) Representation of the nucleotide sequence of Y. pseudotuberculosis tssM3 constructs used for fluorescence studies shown in panel (D). The poly-A tract is shown in red and additional nucleotides are shown in blue. (D) Fluorescence levels (in arbitrary units, A.U.) of cells producing the different TssM1 variants shown in panel (C).
tested whether these two variants are required for function of the apparatus, it is worthy to note that transcriptional frameshifting in *Y. pseudotuberculosis* *tssM3* leads to synthesis of a shorter protein whereas *C. rodentium* *tssM1* slippage leads to synthesis of the full-length protein. As a consequence, and in contrast to *C. rodentium* *tssM1*, the ratio in favor of the full-length variant. This is particularly intriguing as our data showed that the ratio between the two variants in *C. rodentium* is critical for the function of the apparatus, and it further suggests that the ratio between the two variants is tailored to fit specific needs during assembly and/or function of the T6SS in different bacteria. In the vast majority of T6SS-associated *tss* genes, no slippery site can be identified, suggesting that only the full-length protein is produced. However, stable TssM degradation products of ~83-kDa have been observed by Western-blot analyses of total extracts of WT cells producing TssM in *Agrobacterium tumefaciens* [28] and in enterohaemorrhagic *E. coli*. In these cases, two forms of TssM are therefore produced, the shorter being the result of a degradation mechanism. This observation is particularly fascinating and further experiments are required to understand whether this degradation is a controlled process, whether it is conserved in all TssM proteins, and whether the degradation product is important for the function of the T6SS machines in these bacteria.

**Materials and Methods**

**Bacterial strains and growth**

Strains used in this study are listed in S1 Table. *Citrobacter rodentium* strains used in this study are derivatives of DBS100 [ATCC51459] (kindly provided by Hervé LeMoual (McGill University, Montreal, Canada)); RLC2 (a spontaneous nalidixic acid resistant variant), RLC55 (a RLC2 derivative in which the promoter as been swapped with a divergent *plac*-para promoter) and RLC62 (a Δ*tsM1* derivative of RLC55) [30]. *Yersinia pseudotuberculosis* IP31738 [49] has been kindly provided by Anne Derbise and Elisabeth Carniel (Institut Pasteur, Paris). *Escherichia coli* DH5α, CC118pir have been used for cloning procedures. *E. coli* W3110 has been used for growth competition assays. MFDPir [50] has been used for mating assays with *C. rodentium*. Strains were routinely grown in Luria-Bertani (LB) broth, or on LB agar plates supplemented with kanamycin (50 μg/mL), chloramphenicol (30 μg/mL) or nalidixic acid (~20 μg/mL) when required. MFDPir cells were grown in medium supplemented with 0.3 mM dexamethasone. Induction of the CTS1 T6SS gene cluster expression was performed with IPTG and L-

**Plasmid construction**

Citrobacter constructs. Construction of the pBAD-18-kan plasmid carrying the full-length *tsM1* fragment, pRL39, has been previously described [30]. In this construct, the *tsM1* gene is fused to an N-terminal FLAG-coding sequence. Insertion of the 6-His coding sequence before the stop codon of the frameshifted *tsM1* gene was done by cloning a Eagl/BglII 448-bp fragment (corresponding to the 3′ end of *tsM1* fused to a 6×His tag sequence, obtained using oligonucleotide icmF-crod1-Cter-6xHis-BglII and icmF-Eagl-crod-fwd) into Eagl/BglII-linearized pRL39 to yield pRL46 (encoding *flag-tsM1*-his6 under the control of *areB* promoter). The vector producing the truncated form of *tsM1* followed by a 6×His tag (called AAG*6* was constructed by insertio~ of the 2424-bp of *tsM1* amplified from pRL39 using SacI-Nter-flag-Ndel-icmF-crod1-a d-icmF-tronq-crod1-Cter-6xHisXbal) into pBAD18-kan to yield pRL73 (encoding the *tsM1* truncated form fused to an N-terminal FLAG epitope and a C-terminal 6×His sequence).

A series of plasmids derived from pASK-IBA37 [IBA technology] was constructed to follow expression (under the control of the tet promoter) of *tsM1* and its derivatives. The pASK-IBA37+ vector was first modified t introduce the cat gene conferring chloramphenicol resistance. The cat gene was amplified from pBAD18-Cm using oligonucleotides pIBACm-up and pIBACm-down and inserted by restriction-free RF cloning [52] into the bla gene of pASK-IBA37+. To yield pRL81. flag-tssM1-his6 and *flag-tsM1-AAG*-his6 fragments were amplified from pRL46 and pRL73 respectively using oligo pairs NheI-flagfwd and XhoI-6xhiss-rev and introduced into NheI/Xhol-digested pRL81, yielding pRL102 and pRL109 respectively.

Plasmids carrying *C. rodentium* *tsM1*-GFP fusions were constructed into a pUA66 derivative [53] carrying the *gfp mutants* under the control of the constitutive ribosomal *rrnB* promoter (pUA66-*rrnB*). A 90-bp fragment corresponding to *tsM1* encompassing the poly-A run to the premature stop codon (molecules 2335-2425 of *tsM1*) was amplified and cloned downstream the ATG stop codon of *gfp mutants* by RF cloning using oligonucleotides pUA66-rrnB-tssM1-5 and pUA66-rrnB-tssM1-3 to yield pRL112 (TssM1-WT). A similar fragment carrying an additional base after the premature stop codon was amplified using pUA66-rrnB-tssM1-5 and pUA66-rrnB-tssM1-1 and cloned identically to yield pRL113 (TssM1+1).

Mutations AAG ([AAAAAAAAAA to AAGAAGAA]) and AAG/A ([AAAAAAAAAA to AAGAAGAA]) were introduced into pBAD-18-Cm, pASK-IBA37+ and pUA66-*rrnB* derivatives by quick-change mutagenesis using oligonucleotide pairs mutLys-icmF-crod1-fwd/mutLys-icmF-crod1-rev and mutLys-A-icmF-crod1-fwd/mutLys-A-icmF-crod1-rev respectively.

**Yersinia constructs.** The *Y. pseudotuberculosis* *tssM3* gene fused to FLAG and 6×His sequences was amplified using oligonucleotide pair SacI-Nter-FLAG-icmF_1373 and

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**Recombinant DNA methods**

PCR fragments used for strain and plasmid constructions were amplified with the Phusion high fidelity DNA polymerase (Thermo scientific). Colony PCR amplifications were performed with Taq DNA Polymerase with Standard Taq Buffer (New England BioLabs). Site-directed Quickchange mutagenesis amplifications were done using the Ph Turbo DNA polymerase (Agilent Technologies). Restriction enzymes were purchased from New England BioLabs. Custom oligonucleotides (listed in S2 Table) were synthesized by Sigma Aldrich.

**Strain construction**

The chromosomal poly-A sequence of *tsM1* was modified with the AAG and AAGΔA mutation by allelic exchange using the *sacB*-counter selectable suicide plasmid pSR47S. A *tsM1* fragments of ~600-bp surrounding the poly-A tract were amplified with oligo pair icmF-crod1-fwd-G/icmF-crod1-rev from mutated plasmids (see plasmid construction below) and cloned by TA cloning into pCR2.1 (Invitrogen). After DNA sequencing, BamH1/XbaI fragments from pCR2.1 were inserted into BamH1/SpeI-digested pSR47S, yielding plasmids pRL132 and pRL133. pSR47S derivatives were introduced into *C. rodentium* RLC55 by transformation using MFDPir as donor and the first recombination event was selected on kanamycin LB plates as previously described [51]. Insertion of pSR47S derivatives was verified by colony PCR. Successful counterselection was obtained as described [51] and insertion of the accurate mutation was verified by PCR on purified chromosomal DNA (DNeasy Blood & Tissue kit, Qiagen) and DNA sequencing.
XbaI-Cter-6xHis-icmF_1373 and cloned by TA cloning into pCR2.1. The flag-tsM3-his6 fragment was then amplified using oligonucleotide pair Nhel-flag-fwd and XhoI-6xhis-rev, digested by Nhel and XhoI, and cloned into pRL1b, to yield pRL103. Mutation of the tsM3 polyadenosine tract (AAAAAAA to AAAGAAGAAG) was introduced into pRL103 by quick-change mutagenesis using oligonucleotide pair icmF-1373-mulyis-fwd and icmF-1373-mulyis-rev, yielding pRL106.

Plasmids carrying *V. pseudotuberculosis* tsM3-GFP fusions were constructed by cloning into pUA66-rrnB. A 63-bp fragment corresponding to tsM3 encompassing the poly-A run was amplified using primers 2347–2409 of tsM3 was amplified and cloned downstream the ATG stop codon of gfpmut2 by RF cloning using oligonucleotides pUA66-rrnB-tssM3-5 and pUA66-rrnB-tssM3-3 to yield pRL120 (TsM3-WT). A similar fragment carrying an additional base after the poly-A run was amplified using pUA66-rrnB-tssM3-5 and pUA66-rrnB-tssM3+1-3 and cloned identically to yield pRL122 (TsM3+1).

All the plasmid constructs have been verified by restriction and DNA sequencing.

Preparation of *C. rodentium* total RNAs, cDNA synthesis and Electrospray Ion Mass Spectrometry (ESI/MS)

Total RNAs were extracted from exponentially-growing *C. rodentium* cells using the RNAeasy mini kit (Qiagen). RNA preparations were treated with TURBO DNase (Ambion) to avoid DNA contamination prior to Reverse Transcription (RT)-PCR. The absence of contaminating DNA in the Total RNA preparation was verified by PCR. tsM1-specific cDNA encompassing the poly-A run was synthesized from 500 ng of total RNA using oligonucleotide EC955 and the SuperScript II Reverse Transcriptase (Invitrogen). 56-nt PCR products were then amplified from 200 ng of cDNA using primers EC1267 and EC1267 and Phusion DNA polymerase, extracted using the ethanol precipitation procedure and analyzed by electrospray ion mass spectrometry as described previously [37]. As controls for reverse transcription and PCR, PCR products were generated by (i) from *C. rodentium* genomic DNA and (ii) from a 56-nt synthetic RNA (GCGGCUAUUAUGAGGCGUUUAAAAAAAAAAAA-UUGGGUCCGGGGCUGAUUGUUGUAG) (Eurogentec).

Hcp release and antibacterial competition assay

The Hcp1 release assay has been performed as previously described [30]. The antibacterial competition growth assay has been performed as previously described, using the *E. coli* K-12 strain W3110 bearing the pUA66-rrnB plasmid (KanR and strong and constitutive GFP fluorescence) as prey [30]. Briefly, *Citrobacter* and *E. coli* cells were mixed to a 4:1 ratio and the mixture was spotted onto prewarmed dry plates and incubated for 16 hours at 30°C. Fluorescent images were taken using a LI-COR Odyssey imager and the relative fluorescence was measured after resuspension of the bacterial cells using a TECAN Infinite M200 microplate reader.

**Fluorescence assay**

*C. rodentium* cells carrying the pUA66-rrnB plasmid derivatives were grown in LB at 37°C to an OD_{600} of ~1 and normalized to an OD_{600} of 0.5. Triplicates of 130 μl were transferred into wells of a black 96-well plate (Greiner) and the absorbance at 600 nm and fluorescence (excitation: 405 nm; emission: 530 nm) were measured with a TECAN infinite M200 microplate reader. The experiments were done in triplicate and the relative fluorescence was expressed as the intensity of fluorescence divided by the absorbance at 600 nm, after subtracting the values of a blank sample.

**Miscellaneous**

Gene expression from pBAD18 and pASK-IBA37(+) derivatives was induced in exponentially growing cultures (OD_{600} = 0.5) using arabinose (0.2%) for 1 hour and AHT (5 or 10 ng/ml) for 30 minutes respectively. For Western-blot analyses, cells were resuspended in Laemmli buffer (2 x 10^{15} cells/ml). Proteins were separated by SDS-PAGE analyses and transferred onto nitrocellulose membranes. Immunoblots were probed with anti-5HIs (Qiagen) or anti-FLAG (Sigma) antibodies, and anti-mouse secondary antibodies coupled to fluorophores. Immunodetection and band density analyses were performed using a LI-COR Odyssey imager.

**Supporting Information**

Table S1 Strains and plasmids used in this study. (DOCX)

Table S2 Oligonucleotides used in this study. (DOCX)

**Acknowledgments**

This work is dedicated to Guy Duval-Valentin. We thank Chad Nelson for mass spectrometry analyses, Emmanuella Bouveret for the pUA66-rrnB derivative and the use of the TECAN microplate reader, Hervé LeMoual (McGill University, Montreal, Canada) and Anne Derbie and Elisabeth Carrié (Institut Pasteur, Paris, France) for *C. rodentium* and *V. pseudotuberculosis* strains respectively, the members of the Cascales, Llobé`s, Bouveret and Mignot research groups for discussion, Isabelle Bringer, Annick Bruin and Olivier Uderzo for technical assistance, the four reviewers for their helpful comments and Thierry Chmonfis for encouragements.

**Author Contributions**

Conceived and designed the experiments: EG EC. Performed the experiments: EG NMW JFA EC. Wrote the paper: EC. Contributed reagents/materials/analysis tools: EG NMW JFA EC. Contributed reagents/materials/analysis tools: EG NMW JFA EC. Wrote the paper: EG.

**References**


