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ExoY, an actin-activated nucleotidyl cyclase toxin from *P. aeruginosa*: a minireview

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Abstract

ExoY is one of four well-characterised *Pseudomonas aeruginosa* type 3 secretion system (T3SS) effectors. It is a nucleotidyl cyclase toxin that is inactive inside the bacteria, but becomes potently activated once it is delivered into the eukaryotic target cells. Recently, filamentous actin was identified as the eukaryotic cofactor that stimulates specifically ExoY enzymatic activity by several orders of magnitude. In this review, we discuss recent advances in understanding the biochemistry of nucleotidyl cyclase activity of ExoY and its regulation by interaction with filamentous actin.

Keywords

Bacterial protein toxin; ExoY; *Pseudomonas aeruginosa*; T3SS, actin.

Highlights

ExoY is an effector of the opportunistic human pathogen *Pseudomonas aeruginosa*.

ExoY belongs to the subfamily of bacterial nucleotidyl cyclase toxins.

Activity of ExoY is strongly stimulated upon interaction with F-actin.

ExoY co-localises with F-actin in cells and alters F-actin turnover.

1. Introduction

Pseudomonas aeruginosa is a ubiquitous environmental bacterium and an opportunistic human pathogen. Equipped with different virulence factors and antibiotic resistance mechanisms, the bacteria colonise tissues and organs of both healthy and immunocompromised individuals and represent a major threat to patients with cystic fibrosis (for review (Engel and Balachandran, 2009; Hauser, 2009)). Because of its high viability in different environments or on various surfaces and its intrinsic resistance to many antibiotics, *P. aeruginosa* is a major cause of nosocomial infections, which are becoming a primary concern in hospitals all over the world (Fazeli et al., 2012).

During infection, clinical isolates of *P. aeruginosa* produce an extensive repertoire of virulence determinants including: (i) Exotoxin A, an ADP-ribosylating toxin secreted by the type 2 secretion system that enters eukaryotic cells by endocytosis where it inhibits elongation factor-2, thereby blocking polypeptide synthesis (for review (Michalska and Wolf, 2015)); (ii) Lipopolysaccharide, a major inflammatory molecule (Pier, 2007); (iii) Zinc metalloproteases such as ArpA, LasA and LasB that prevent flagellin-mediated immune recognition (Casilag et al., 2015); (iv) Phospholipases PlcH, PlcN, PldA, PldB that hydrolyse membrane components of the target cells (Barker et al., 2004; Jiang et al., 2014; Spencer and Brown, 2015); (v) ExlA, a recently characterised pore-forming toxin that causes host cell membrane disruption and is secreted by a two-partner secretion system by clinical *P. aeruginosa* isolates that lack a type 3 secretion system (T3SS) (Bouillot et al., 2017; Elsen et al., 2014); and (vi) several protein effectors, ExoS, ExoT,

ExoU and ExoY, that are delivered to the host cells by a functional T3SS. The ExoS and ExoT are toxins with an N-terminal GTPase-activating (GAP) domain and a C-terminal ADP-ribosyltransferase (ADPRT) domain (Iglewski et al., 1978; Riese et al., 2001). ExoS and ExoT are activated upon interaction with an eukaryotic factor (14-3-3 protein). Their N-terminal GAP-domains modulate the activity of small GTP-binding proteins of the Rho-family that control actin cytoskeleton organisation and rearrangements, while their C-terminal domains modify many proteins involved in vesicular trafficking, endocytosis, cell signaling or DNA synthesis regulation (Barbieri and Sun, 2004; Fu et al., 1993; Hauser, 2009). Therefore, ExoS and ExoT inhibit bacterial phagocytosis and facilitate *P. aeruginosa* movement across the epithelial monolayer (Goehring et al., 1999; Soong et al., 2008). Another T3SS effector, ExoU, belongs to the phospholipase A2 (PLA2) family (Sato et al., 2003; Sawa et al., 2014). This enzyme is activated upon interaction with ubiquitin or ubiquitinated proteins (Anderson et al., 2011; Tessmer et al., 2017) and hydrolyzes phospholipids and lysophospholipids (Sato et al., 2005; Tamura et al., 2004). The enzymatic activity of ExoU causes the disruption of cell membranes and cell death. As a result, this toxin is a major virulence factor responsible for acute lung injury in both animal models and patients with pneumonia caused by *P. aeruginosa* (Finck-Barbancon et al., 1997; Kurahashi et al., 1999).

The fourth described T3SS effector ExoY, a nucleotidyl cyclase toxin, was identified in 1998 (Yahr et al., 1998), by characterising *P. aeruginosa* transposon mutants defective in the T3SS apparatus. Several secreted proteins were absent in supernatant of these strains, including an unknown ≈ 42 -kDa polypeptide. Subsequent N-terminal sequencing of this polypeptide and bioinformatic analysis identified the corresponding open reading frame in the *P. aeruginosa* genome database. Analysis of the amino acid sequence of this unknown protein showed homology with catalytic regions of the well-known

calmodulin-activated adenylate cyclase toxins produced by *Bordetella pertussis* (CyaA or ACT) and *Bacillus anthracis* (edema factor, EF), the causative agents of whooping cough and anthrax, respectively (Carbonetti, 2010; Moayeri et al., 2015). Yahr et al. further cloned and expressed a recombinant ExoY and established that this toxin is endowed with an adenylate cyclase (AC) activity that was strongly stimulated by a heat-labile factor present in eukaryotic cell lysates. Yet, unlike CyaA and EF, the ExoY enzymatic activity was not stimulated by calmodulin (CaM) indicating that its activator was distinct from that of the other known AC bacterial toxins. The eukaryotic ExoY cofactor remained elusive until our group recently identified filamentous actin (F-actin) as the activator of ExoY (Belyy et al., 2016). Upon binding to F-actin ExoY undergoes structural rearrangements that increase its catalytic turnover rate to generate supraphysiological amounts of cyclic nucleotides, which in cell cultures disrupt cell signalling, inducing cytoskeleton disorganisation and eventually cell death (Sayner et al., 2004). Very recently, two groups independently demonstrated that ExoY activity can also lead to the inhibition of the host immune responses by suppressing the activation of TAK1 and decreasing the production of IL-1 β (He et al., 2017; Jeon et al., 2017). The contribution of ExoY to *P. aeruginosa* virulence during acute and/or chronic infections were recently reviewed by T. Stevens and colleagues (Morrow et al., 2017). This mini-review summarizes some recent biochemical studies on ExoY and its regulation by actin.

2. ExoY expression and secretion

The *exoY* gene is present in almost 90% of clinical isolates (Feltman et al., 2001). In the reference PAO1 strain, the gene is not clustered with the ExoS and ExoT genes, and surrounded by two hypothetical genes of unknown function and not associated with an operon. A general T3SS transcriptional activator ExsA binds specifically to a -35 RNA

polymerase binding site and an A-rich sequence upstream to the ExoY gene (Brutinel et al., 2008). Translation of the corresponding mRNA results in a protein of 378 amino acids and 41.7 kDa. Whether ExoY undergoes additional post-translational modifications or associates with other proteins inside the bacteria remains unknown. Yet, by analogy with other T3SS toxins, ExoY may need to interact with a presently unidentified chaperone that could maintain the protein in a partially unfolded state until it is delivered to the secretion apparatus (for review on T3SS chaperones (Burkinshaw and Strynadka, 2014)).

3. ExoY as a member of the family of bacterial nucleotidyl cyclase toxins

Bacterial adenylate cyclases toxins are pathogenic factors able to invade eukaryotic cells where they are stimulated by endogenous cofactors to produce large amounts of 3'5'-cyclic nucleoside monophosphates (cNMP). This results in disruption of cell signalling and alteration of cell physiology, eventually leading to cell death. Indeed, the well-characterized CyaA toxin from *B. pertussis* and edema factor, EF, from *B. anthracis* are key virulence factors of these organisms. They target mainly the immune cells to disable the immune response and thus facilitate bacterial colonization of their hosts (for review (Carbonetti, 2010; Moayeri et al., 2015)).

These two toxins are rather selective adenylate cyclase enzymes that only marginally produce other cNMPs (Beckert et al., 2014). In contrast, *P. aeruginosa* ExoY is a promiscuous nucleotidyl cyclase, which synthesizes cGMP, cAMP, cUMP and cCMP (Bahre et al., 2015; Beckert et al., 2014).

The family of bacterial cyclase toxins can be divided into two subgroups based on the nature of the activator. As discussed previously, while EF and CyaA are activated by calmodulin, ExoY defines a novel sub-family of nucleotidyl cyclase toxins activated by

actin: this latter also includes various ExoY-like (ExoY-L) modules identified in several members of multifunctional autoprocessing RTX (MARTX) toxins that are produced by various Gram negative pathogens (see below) (Belyy et al., 2016; Ziolo et al., 2014). The overall amino acid sequence conservation between ExoY and EF or CyaA is rather low (44.3% and 40.9% sequence similarity, respectively) (Belyy et al., 2016), but three regions of these proteins display high similarity (up to 66%). Site directed mutagenesis and structural studies demonstrated that, in EF and CyaA, these three regions are directly involved in substrate binding and catalysis (Drum et al., 2002; Glaser et al., 1989, 1991). The corresponding conserved amino acid sequences in ExoY are thus predicted to be part of the catalytic site. Indeed, Yahr et al. originally showed that the residues K81 and K88, in catalytic region 1 (CR1) of ExoY are essential for catalysis. By analogy with EF and CyaA, these residues are likely to hold the α -phosphate of the bound nucleotide substrate. Residues D212 and D214 of the catalytic region 2 might play a role in stabilising the β - and γ -phosphates of the bound nucleotide via Mg^{2+} . Residues H291, D294 and N297 of the CR3 are conserved in CyaA and EF and were shown to be involved in contacting the base moiety of the nucleotide (Drum et al., 2002; Guo et al., 2005). By analogy with other T3SS substrates, the N-terminal residues of ExoY are hypothesised to harbour a T3SS secretion signal and a potential chaperone-binding domain (Maresso et al., 2006). The schematic structures of the toxins and partial sequence alignments are presented in fig. 1.

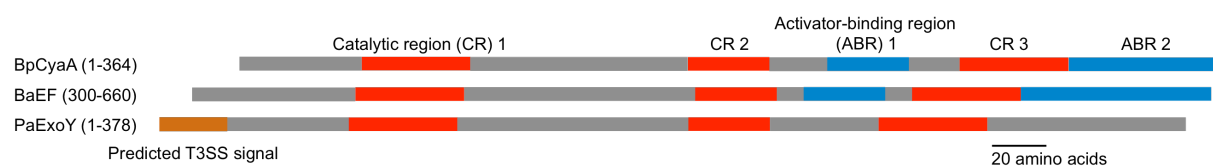


Figure 1 in JPG format

150 Part of CR 1

151 PaExoY 70-VTTLIEEGFPT**K**GFSVKG**K**SSNWGPQAGFICVDQHLSKREDR-111
 152 BpCyaA 46-STSLIAEGVAT**K**GLGVHA**K**SSDWGLQAGYIPVNPNSKLFGR-88
 153 BaEF 335-ATNLIKSGVAT**K**GLNVH**G**KSSDWGPVAGYIPFDQDL SKKHGQ-376
 154 Cons * . * * . * . . * * : . * : . * * * . :
 155

156 CR 2

157 PaExoY 194-SEAVQVLASPACGL--AMTAD**Y**DLFLVAPSIE-223
 158 BpCyaA 171-FEAVKVIGNAA-GI--PLTAD**I**DMFAIMPHLS-199
 159 BaEF 471-WRNIEVMAKNVEGV LKPLTAD**Y**DLFALAPSLT-502
 160 Cons . : : * : . . * : . : * * * * : * : * :
 161

162 CR 3

163 PaExoY 259-DMARGNITPRTRQLVDALNDCLGRGEH--REMFH**H**SD**D**AG**N**PGSHMGDN--305
 164 BpCyaA 266-DMNIGVITDFELEVRNALNRRHAVGA--QDVVQ**H**GTE**Q**NNP-FPEADEK-312
 165 BaEF 543-DSTKGTLSNWQKQMLDRLNEAVKYTG YTG GDVVN**H**GTE**Q**D**N**EEFPEKDNE-592
 166 Cons * * : : : : * * : : : * . : . * *
 167

168 Figure 1. A. Schematic domain organisation of the catalytic domains of *B. pertussis* CyaA
 169 (BpCyaA), *B. anthracis* EF (BaEF) and *P. aeruginosa* ExoY (PaExoY). The catalytic regions
 170 CR1, CR2 and CR3 that display high sequence similarity are indicated by red boxes while
 171 the CaM Binding Regions CBR of CyaA and EF are indicated by blue boxes. The Activator
 172 Binding Region(s), ABR, of ExoY is/are still unknown. The predicted N-terminal T3SS
 173 signal of *P. aeruginosa* ExoY (PaExoY) is indicated by an orange box.

174 B. Alignments of the catalytic regions CR1, CR2 and CR3. **Bold** amino acids are directly
 175 involved in the catalytic process. The alignment was performed by the T-coffee
 176 algorithm (Notredame et al., 2000).

178 **4. ExoY activation by filamentous actin**

179 Cyclic nucleotides are important messengers in intracellular signal transduction in
 180 eukaryotes and bacteria. To avoid the detrimental influence of toxin activity in their
 181 bacterial hosts, the nucleotidyl cyclase toxins possess a low basal activity in the

prokaryotic environment and become active only after delivery to the eukaryotic cells where they are activated upon interaction with a specific activator. The activator of CyaA and EF has been known for a long time to be the highly conserved calcium-mediator calmodulin. In contrast, the activator of ExoY remained elusive until its recent identification as actin in our laboratory (Belyy et al., 2016), as briefly summerized below.

ExoY is toxic for numerous cell types, including mammalian and yeast cells (Arnoldo et al., 2008). This indicated that its activator should be evolutionary conserved in all eukaryotic cells. To identify the ExoY activator, a TAP-tagged inactivated variant of ExoY (to avoid cytotoxicity), ExoY-K81M, was expressed in yeast and affinity purified. The proteins that co-purified with the ExoY bait were analyzed by mass spectrometry. A label-free quantification score estimation of the data revealed that actin was the most abundant protein in the samples (apart the ExoY bait). This result suggested a specific interaction between ExoY and actin in yeast, and it was further confirmed, by co-sedimentation and pull-down experiments, that *in vitro* the recombinant ExoY indeed associates with the polymeric form of mammalian actin. ExoY was further shown to bind along the lateral side of actin filaments. This lateral side binding inhibits the filament's disassembly and disturbs the binding and regulation of other lateral side binding proteins such as the Actin-depolymerizing factor (ADF). The lateral side binding of ExoY was thus shown to decrease the intrinsic or regulated turnover of actin filaments *in vitro*. In line with these findings, we showed that, in transfected cells, ExoY is recruited to actin filaments and increases the content of F-actin by stabilizing filaments and disturbing the balance of their assembly and disassembly by eukaryotic actin-binding proteins. Moreover, *in vitro* assays indicated that actin potently stimulates ExoY

207 nucleotidyl cyclase activities in a dose-dependent manner with a half maximal activation
208 at about 0.2 μM of ATP-Mg²⁺-loaded actin (Belyy et al., 2016), which correlates with the
209 critical concentration above which ATP-actin spontaneously polymerizes (i.e. 0.1 μM
210 (Pollard et al., 2000))

211 Interestingly, certain toxins from the Multifunctional-Autoprocessing Repeats-in-ToXin
212 (MARTX) family produced by various pathogenic proteobacterial species, contain among
213 various effector domains an ExoY-like module. Ziolo et al. (Ziolo et al., 2014), indeed
214 demonstrated that the ExoY-like domain from the *Vibrio vulnificus* Biotype 3 MARTX
215 toxin is endowed with adenylate cyclase activity and is essential for virulence in mice.
216 We then showed that actin stimulates in a dose-dependent manner, a recombinant
217 ExoY-like module, VnExoY-L, derived from the MARTX toxin from *Vibrio*
218 *nigripulchritudo*, a marine pathogen infecting shrimps (Belyy et al., 2016). This suggests
219 that ExoY and the other ExoY-like modules present in MARTX toxins belong to a specific
220 subfamily of actin-activated nucleotidyl cyclase toxins. However, at variance with *P.*
221 *aeruginosa* ExoY, the ExoY-like modules from the *V. vulnificus* (Ziolo et al., 2014) or *V.*
222 *nigripulchritudo* (Belyy et al., 2016) MARTX toxins only synthesize cAMP. Hence, the
223 subfamily of actin-activated nucleotidyl cyclase toxins displays different substrate
224 selectivity, and may thus differ significantly in the range of cellular pathways they affect
225 in host cells.

226 By analogy with CyaA and EF, one can hypothesise, that upon interaction with the
227 activator, the catalytic regions CR1, 2, and 3 of ExoY are stabilised in an active
228 configuration, resulting in high catalytic activity. Indeed, the key step of the activation of
229 EF by CaM, is the stabilisation of a catalytic loop called switch B, corresponding to amino
230 acids H577-E592 of EF (Drum et al., 2002) and H298-K312 in CyaA (Guo et al., 2005).
231 The similar region CR3 in ExoY -residues H291-N305 - contains, an asparagine residue,

N297, homologous to EF N583 or CyaA N304, which were shown to be important for holding the ATP ribose in place upon substrate binding and hence the catalytic activity of those enzymes.

5. Actin as a target and an activator of toxins

Actin is a 42-kDa multifunctional protein, present either in a monomeric G-form (G-actin) or as a part of a filamentous linear polymer (F-actin). Actin is a highly conserved and essential component of every eukaryotic cell. As a matter of fact, the actin cytoskeleton is the target of a wide variety of toxins produced by various organisms including many microbial pathogens (Colonne et al., 2016; Rappuoli and Montecucco, 1997). Several fungi and sponges produce nonproteinaceous toxins, such as latrunculin, cytochalasin, jasplakinolide, that target the actin cytoskeleton by modulating the G to F-actin equilibrium in cells. Bacterial toxins are affecting the actin cytoskeleton either by targeting specific actin-regulatory proteins or through direct modification of actin (for review (Aktories et al., 2017)). For example, *Clostridium difficile* C2-toxin, *C. perfringens* iota toxin and *C. spiroforme* toxin attack actin cytoskeleton by ADP-ribosylation of Arg177 of actin. The modified actin acts as a capping protein and prevents further actin elongation, poisoning actin polymerisation and leading to actin depolymerization in cells (Perieteanu et al., 2010; Wegner and Aktories, 1988). By contrast, modification of actin Thr148 by *Photobacterium luminescens* TCC3 toxin leads to polymerisation and aggregation of F-actin (Lang et al., 2017). Several MARTX toxins from *Vibrio* species and other pathogens contain enzymatic domains that display an actin-crosslinking activity that results in the formation of deleterious non-polymerisable actin oligomers that both poison actin polymerisation and trap key regulatory proteins of the actin cytoskeleton

dynamics such as formins in non-functional complexes (Fullner and Mekalanos, 2000; Kudryashov et al., 2008).

Interestingly, apart from ExoY and ExoY-like toxins, another toxin has been reported to be activated by actin. This toxin, YpkA (also known as YopO) is a protein kinase produced by various *Yersinia* species and delivered to target cells by a T3SS (Juris et al., 2000; Trasak et al., 2007). The YpkA/YopO kinase is activated upon binding to monomeric actin and subsequent autophosphorylation. Recent structural and functional studies revealed that YpkA binds to the subdomain 4 of actin (figure 2), and uses actin as a bait to recruit actin-binding proteins (eg VASP, WASP, formin, and gelsolin) and phosphorylate them (Lee et al., 2015). Phosphorylation of actin regulatory proteins by YpkA/YopO appears as a novel regulatory mechanism by which pathogenic bacteria can potentially manipulate actin dynamics, and thus impair phagocytosis (Ono, 2017; Singaravelu et al., 2017).

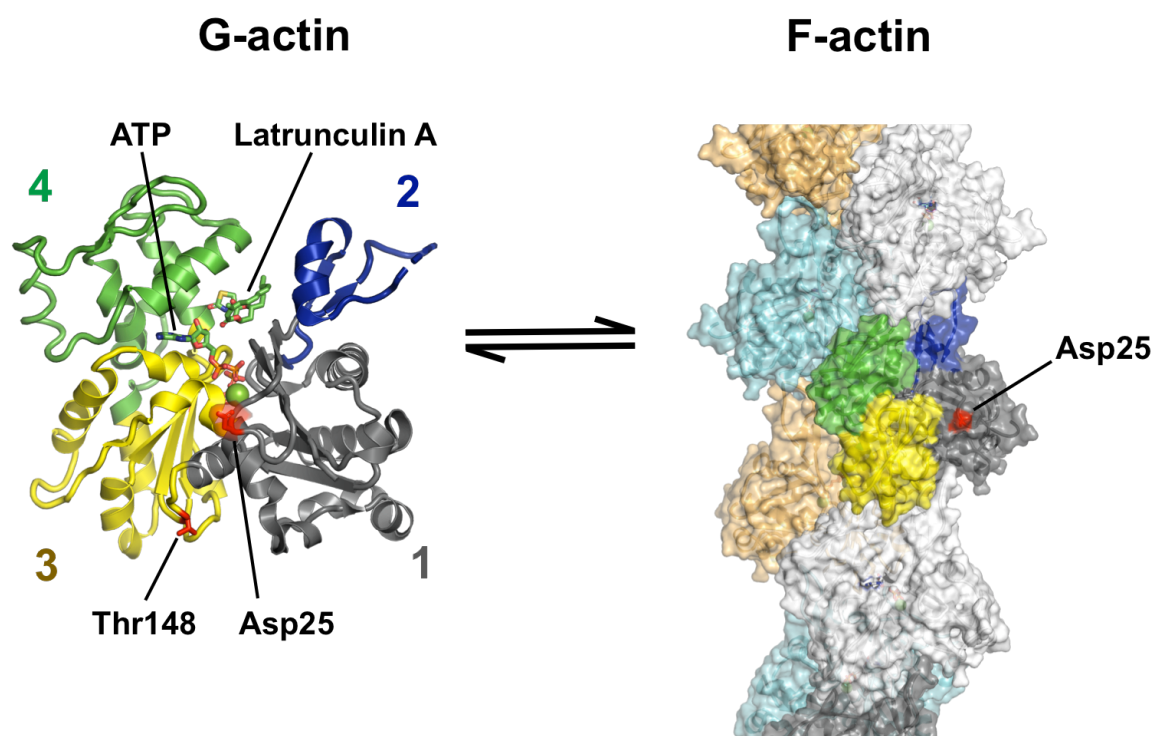


Figure 2 in JPG format

Figure 2. Structures of G-actin bound to Latrunculin A (PDB 1IJJ), a toxin extracted from the red sea sponge *Latrunculia magnifica* and inhibiting actin polymerization, and F-actin (PDB 2ZWH). The 4 subdomains of G-actin are shown in different colours and labeled from 1 to 4. Actin subunits in F-actin are represented by their surface in different colours, with one subunit shown with the same colour codes as G-actin. The side chains of actin Thr148, which is modified by *Photorhabdus luminescens* TCC3 toxin, and actin Asp25, whose mutation D25N abolishes the activation of ExoY by actin filaments and its cytotoxicity in yeast, are shown in red ball-and-stick presentation.

6. Molecular characterisation of actin-ExoY interaction: identification of actin variants that do not activate ExoY

To further characterise the molecular determinants of the ExoY-actin interaction, we attempted to identify mutations in actin that prevent binding and activation of ExoY. For this, we performed a random mutagenesis of actin using as a model organism the yeast *S. cerevisiae* that contains a single actin-encoding gene *ACT1* (figure 3). The actin gene was mutagenized *in vitro* by error-prone PCR (1) and cloned in a low-copy yeast plasmid (carrying a His3 marker) (2, 3). The resulting library was then transformed into an engineered yeast strain (4), in which the chromosomal actin gene was inactivated while a functional wild-type copy of *ACT1* gene was provided in trans by a plasmid bearing an uracil marker, URA3 (Belyy et al., 2015).

After transformation of the library, all transformed cells were pooled and replicated on a medium containing 5-fluoroorotic acid (5-FOA) to eliminate the plasmid carrying the uracil marker and the WT actin (5). The resulting cells thus relied only on the mutagenized actin gene (on the His3-bearing plasmid) for growth and as actin is an essential protein, only cells harbouring functional variants of actin could survive this selection. The surviving yeast cells (*i.e.* containing mutagenized yet functional actins)

were finally transformed with an ExoY-expressing plasmid and plated on a galactose-containing medium in order to trigger ExoY expression (6). In these conditions only yeast carrying actin variants unable to activate ExoY could survive. Few surviving clones were isolated and sequencing of their actin genes revealed two different alleles, both with mutations of Asp25. Further experiments confirmed that this amino acid is indeed crucial for ExoY activation: the single mutation D25N in actin was sufficient to render yeast resistant to ExoY *in vivo*, and a corresponding yeast lysate was unable to activate ExoY in *in vitro* assays. The D25 residue is well conserved among all isoforms of eukaryotic actin. The acidic N-terminus of actin as well as the D24 and D25-residues were shown to be an interaction site with myosin (Bertrand et al., 1988; von der Ecken et al., 2016). This indicated that D25 is fully accessible at the surface of the actin filament and could therefore establish direct contacts with ExoY. Our results also suggest that ExoY might compete with myosin for binding to actin filaments, but such possible competition and *in vivo* effects remain to be established.

In addition, the fact that the D25N mutation in actin is sufficient to confer resistance to ExoY toxicity in yeast demonstrated that actin is the **only** activator of this toxin in this organism. This observation was indeed crucial to ascertain that actin activates ExoY through direct contacts and not indirectly *via* actin-binding proteins and/or actin post-translational modifications (eg ubiquitinylation, (Terman and Kashina, 2013)).

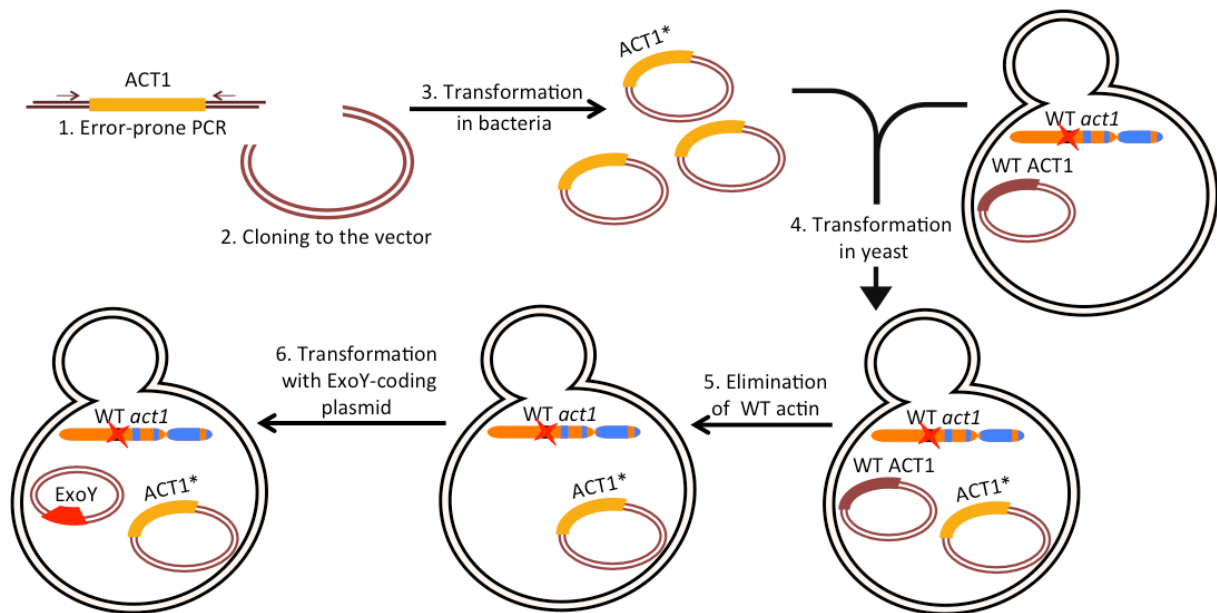


Figure 3 in JPG format

Figure 3. Strategy for actin mutagenesis and selection of ExoY-resistant actin variants in yeast. The key steps (1 to 6) are described in the main text.

7. Structural basis of ExoY discrimination between eukaryotic and homologous proteins of prokaryotic origin

The identification of actin as the ExoY activator also raises interesting questions from an evolutionary point of view. Indeed, bacteria possess several actin homologs (for review (Shaevitz and Gitai, 2010)), such as MreB, FtsA or ParM. These proteins display structural similarities to eukaryotic actin and are capable of ATP-dependent polymerization into linear filaments. However as mentioned earlier, it is crucial that ExoY (like other cyclase toxins) is kept inactive in its bacterial host to prevent any toxicity. Therefore, this implies that the ExoY toxin must possess a high selectivity of recognition of eukaryotic actins but not the endogenous *P. aeruginosa* actin-like proteins. It is particularly noteworthy that the polypeptide region around the key Asp25 residue is organised in eukaryotic actins in a loop with a net negative charge, while it

forms a turn with no net charge or a net positive charge between two beta-strands in prokaryotic actin-like proteins (Figure 4). This structural difference may be a key feature allowing ExoY to specifically discriminate between the eukaryotic actins and the prokaryotic actin homologs.

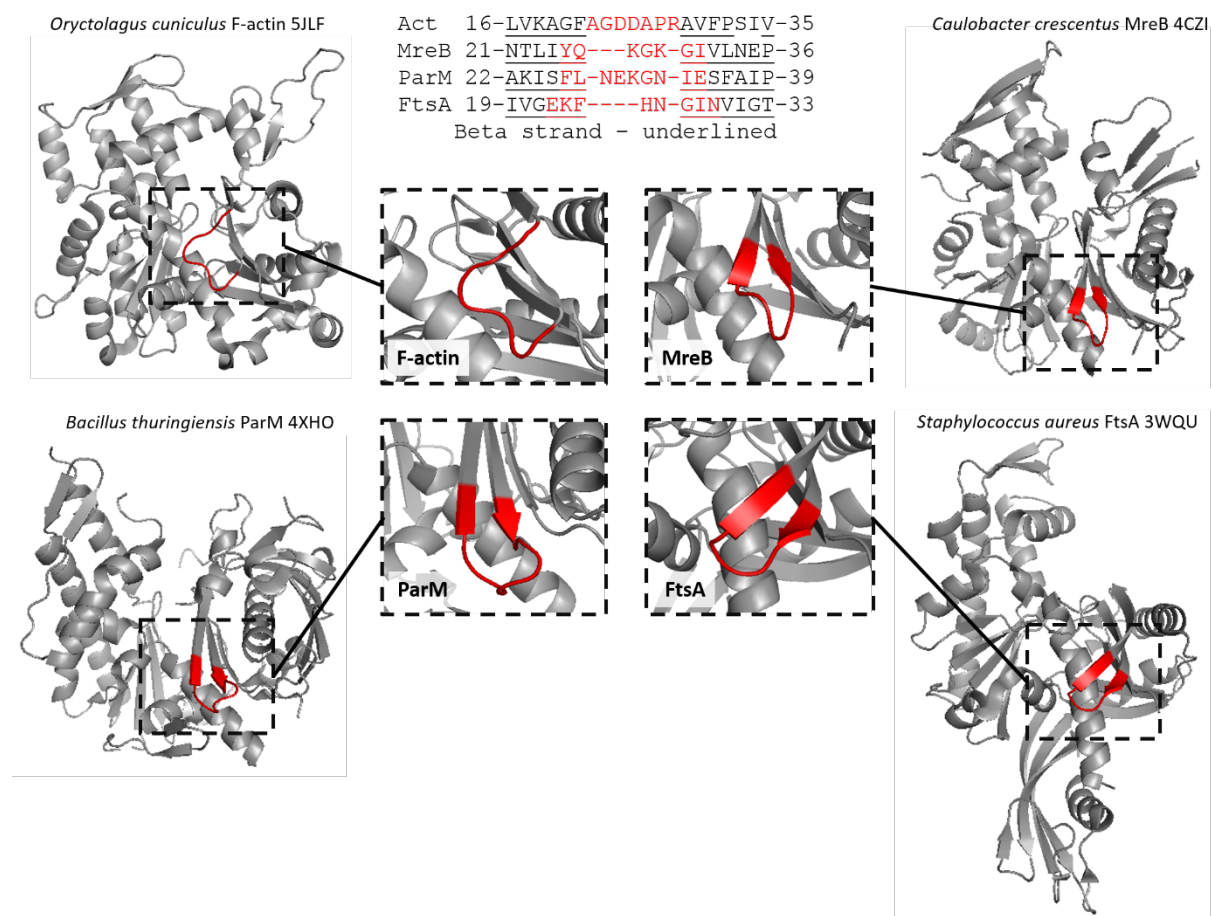


Figure 4 in JPG format

Figure 4. Comparison of the structural models of an actin monomer from rabbit muscle (5JLF, (von der Ecken et al., 2016)), *Caulobacter crescentus* MreB (4CZI, (van den Ent et al., 2014)), *Bacillus thuringiensis* ParM (4XHO, Jiang et al., unpublished) and *Staphylococcus aureus* FtsA (3WQU, (Fujita et al., 2014)). The D25 surrounding region in mammalian F-actin and the corresponding regions in bacterial actin homologs are

highlighted in red. In the sequence alignment panel above, the amino acids belonging to the flanking beta-strands are underlined.

8. Conclusions

Bacterial nucleotidyl cyclase toxins are potent virulence factors that hijack cell cNMP signalling in eukaryotic cells. These toxins are inactive inside their bacterial host and need to interact with specific eukaryotic cofactors in eukaryotic target cells to convey their high catalytic activity. The recent discovery of actin as the activator of ExoY and ExoY-like modules present in MARTX toxins suggests that the family of bacterial nucleotidyl cyclase toxins is composed of two distinct branches distinguished by the nature of their activator, calmodulin vs actin. It is noteworthy that both activators are abundant proteins and highly conserved in the entire eukaryotic kingdom. The recent advances in understanding of the mechanism of ExoY activation are now paving the way for further exploration of the biological function of this virulence factor that still remains the least characterized protein among the four T3SS effectors of *P. aeruginosa*. Among key issues that are currently of prime interest are (i) the structural basis for ExoY activation by F-actin and its broad nucleotide specificity; (ii) the potential influence of the *P. aeruginosa* exotoxins ExoS/ExoT, that modulate the actin cytoskeleton dynamics, on ExoY activation *in vivo*; (iii) the characterisation of putative ExoY chaperones in the bacterial host and (iv) the characterisation of the functional and enzymatic specificities of ExoY-like toxins from other gram-negative pathogens.

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