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REVIEW

Yersinia type III effectors perturb host innate immune responses

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Abstract

The innate immune system is the first line of defense

against invading pathogens. Innate immune cells recognize molecular patterns from the pathogen and mount a response to resolve the infection. The production of proinflammatory cytokines and reactive oxygen species, phagocytosis, and induced programmed cell death are processes initiated by innate immune cells in order to combat invading pathogens. However, pathogens have evolved various virulence mechanisms to subvert these responses. One strategy utilized by Gram-negative bacterial pathogens is the deployment of a complex machine termed the type III secretion system (T3SS). The T3SS is composed of a syringe-like needle structure and the effector proteins that are injected directly into a target host cell to disrupt a cellular response. The three human pathogenic Yersinia spp. (Y. pestis, Y. enterocolitica, and Y. pseudotuberculosis) are Gramnegative bacteria that share in common a 70 kb virulence plasmid which encodes the T3SS. Translocation of the Yersinia effector proteins (YopE, YopH, YopT, YopM, YpkA/YopO, and YopP/J) into the target host cell results in disruption of the actin cytoskeleton to inhibit phagocytosis, downregulation of proinflammatory cytokine/chemokine production, and induction of cellular apoptosis of the target cell. Over the past 25 years, studies on the Yersinia effector proteins have unveiled tremendous knowledge of how the effectors enhance Yersinia virulence. Recently, the long awaited crystal structure of YpkA has been solved providing further insights into the activation of the YpkA kinase domain. Multisite autophosphorylation by YpkA to activate its kinase domain was also shown and postulated to serve as a mechanism to bypass regulation by host phosphatases. In addition, novel Yersinia effector protein targets, such as caspase-1, and signaling pathways including activation of the inflammasome were identified. In this review, we summarize the recent discoveries made on Yersinia effector proteins and their contribution to Yersinia pathogenesis.

Key words: Type III secretion; *Yersinia*; Effectors; Innate; Virulence



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Core tip: The study of *Yersinia* type III secretion system effector proteins has provided critical insights into bacterial pathogenic strategies and host innate immune responses. Identification of the crystal structure of YpkA revealed how a bacterial effector can counteract phagocytosis at multiple levels including inhibition of actin polymerization by sequestering actin, inhibition of actin signaling molecules *via* both its kinase and dissociation-like inhibitor domains, and inhibition of actin-cytoskeletal components *via* phosphorylation. YpkA/YopO multisite autophosphorylation may allow YpkA/YopO to bypass regulation by host phosphatases and thus prolong its ability to interfere with phagocytosis. Additionally, an emerging theme is the role of caspases in anti-*Yersinia* host defenses.

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INTRODUCTION

The Yersinia genus consists of Gram-negative coccobacilli or rod-shaped bacteria in which three are pathogenic to humans: Y. pestis, the causative agent of the plague, and the two enteric pathogens, Y. enterocolitica, and Y. pseudotuberculosis^[1]. Infected fleas serve as a vector for the transmission of Y. pestis to humans. Alternatively, the pneumonic form of the plague can be transmitted from an infected individual to another person via aerosolized droplets. Y. enterocolitica and Y. pseudotuberculosis are transmitted through ingestion of contaminated food or water. Upon transmission, Y. pestis migrates to regional lymph nodes where it utilizes the type III secretion system (T3SS; see below) to evade host immune cells. In doing so, Y. pestis is capable of replicating extracellularly and causes bubonic plague. If the infection becomes systemic it can result in the septicemic and pneumonic forms of plague. Y. enterocolitica and Y. pseudotuberculosis also have a trophism for lymphoid tissue whereupon ingestion the pathogens cross the specialized epithelial M cells found in the ileal tract of the small intestine. Once across the epithelial tissue of the small intestine Y. enterocolitica and Y. pseudotuberculosis infect the underlying lymphoid tissue such as the Peyer's patches and mesenteric lymph nodes resulting in gastrointestinal diseases^[2]. Systemic infections by the two enteric Yersinia pathogens are rare in humans, but mouse infection models show colonization of other tissues such as the spleen and liver.

The T3SS is a virulence mechanism found in a wide array of Gram-negative bacteria that are pathogenic to mammals or plants, as well as in symbiotic bacteria of plants and insects^[3]. The T3SS is composed of a needlelike syringe termed the injectisome and the effector proteins that are injected directly into a target host cell from the bacterium's cytosol to disrupt, hijack, or mimic host signaling proteins. Although the T3SS may be used for different functions depending on the life cycle and infection process of the pathogenic bacteria, it is primarily used to subvert the host response to favor survival of the pathogen. Bacterial pathogens lacking the T3SS, expressing a translocation-defective T3SS, or expressing an effectorless T3SS are attenuated *in vivo*, and thus underscore the essential role of the T3SS to bacterial virulence.

All three pathogenic Yersinia species share in common a 70 kb virulence plasmid that encodes proteins of the T3SS^[4]. Expression of the proteins is observed at 37 °C under low Ca²⁺ concentration in vitro whereas in vivo it is also dependent on cellular contact of the Yersinia bacterium with the target host cell. Adhesion of the Yersinia bacterium to a target host cell is mediated through the binding of adhesion proteins such as invasin (Inv) and YadA to host cell surface proteins^[5]. Once attached, the injectisome forms a pore at the plasma membrane of the host cell and subsequently translocates the effector proteins termed Yersinia outer proteins (Yops). There are 6 known Yop effector proteins that are translocated through the injectisome by pathogenic Yersinia species to disrupt the host response: YopE, YopH, YopT, YpkA (YopO in Y. enterocolitica), YopJ (YopP in Y. enterocolitica), and YopM (Table 1). Once in the target host cell these effector proteins function in concert to thwart the host response by altering the actin cytoskeletal structures to inhibit phagocytosis, as well as induce cell death and downregulate proinflammatory responses (Figure 1)^[6].

Both the innate and adaptive immune systems mount a response to combat against invading pathogens with the former being the first line of defense^{1/3}. Macrophages, neutrophils, dendritic cells, and natural killer (NK) cells are innate immune cells that respond to resolving the infection. Upon ligand binding by receptors such as pattern recognition receptors innate immune cells engage in phagocytosis, production of reactive oxygen species (ROS), and induction of inflammation and cell death to combat the pathogen. All three Yersinia species are capable of downregulating innate immune responses to promote survival of the Yersinia pathogens. Cells of the innate immune system are also involved in activating the adaptive immune response, and thus highlight the significance of why pathogens evolved effective mechanisms to disarm the innate immune system.

Recent studies are unveiling new target substrates and signaling pathways that are inhibited by the *Yersinia* effector proteins. The discovery of the crystal structure of YpkA, the identification of multisite YpkA autophosphorylation to activate its kinase domain, and the establishment that YpkA phosphorylates actinbinding proteins are shedding light on YpkA and its

| Table 1 The resulta effector proteins, then nost substrates, and centular effects | | | |
|---|------------------------------|---|--|
| Yop effectors | Enzymatic function | Target substrates | Cellular effects |
| YpkA/YopO | Serine/threonine kinase | Gαq, EVL, VASP, WASP, WIP, gelsolin, | Disruption of the actin cytoskeleton to contribute to inhibition |
| | | mDia1, INF2, and cofilin | of phagocytosis; additional effects are unknown |
| | Guanine nucleotide | RhoA, Rac1, and Rac2 | Disruption of the actin cytoskeleton to contribute to inhibition |
| | dissociation-like inhibitor | | of phagocytosis |
| YopE | GTPase activating protein | RhoA, Cdc42, Rac2, and RhoG | Disruption of the actin cytoskeleton to contribute to inhibition |
| | | | of phagocytosis; inhibition of caspase-1 activation and |
| | | | maturation of IL-18 and IL-1β |
| YopH | Protein tyrosine phosphatase | FAK, p130 ^{Cas} , paxillin, Fyb, SKAP-HOM, | Disruption of focal adhesion complexes and actin stress |
| | | PRAM-1, SLP-76, Vav, PLCγ2, p85, | fibers to inhibit phagocytosis; inhibition of proinflammatory |
| | | Gab1, Gab2, Lck, and LAT | cytokine and MCP-1 production; inhibition of early calcium |
| | | | response and ROS production; inhibition of the PI3K/Akt |
| | | | pathway |
| YopP/J | Acetyltransferase/cysteine | TRAF2, TRAF6, ΙκΒα, MAPKKKs, | Inhibition of adhesion molecules, proinflammatory cytokine |
| | protease/deubiquintase | MAPKKs, IKK β , RICK, and eIF2 α | and chemokine production; activation of caspase-1 and |
| | | | maturation of IL-18 and IL-1β; induction of apoptosis |
| YopT | Cysteine protease | RhoA, Rac1, Cdc42, and RhoG | Disruption of the actin cytoskeleton to contribute to inhibition |
| | | | of phagocytosis; inhibition of NFκB |
| YopM | Leucine-rich repeat protein | RSK and PRK isoforms, caspase-1, and | Inhibition of proinflammatory cytokine production; inhibition |
| | | IQGAP1 | of caspase-1 activation; induction of apoptosis; induction of |
| | | | anti-inflammatory cytokine production |

IL: Interleukin; FAK: Focal adhesion kinase; PLC- γ 2: Phospholipase C- γ 2; MAPK: Mitogen-activated protein kinase; MAPKK: MAPK kinase; MAPKKK: MAPK kinase; Akt: Protein kinase; NF_KB: Nuclear factor kappa b; IKK β : Inhibitor of kappa B kinase beta; I_KB α : Inhibitor of kappa B alpha; IQGAP1: IQ motif containing GTPase activating protein 1; Lck: Lymphocyte-specific protein tyrosine kinase; LAT: Linker for activation of T cell; eIF2 α : Eukaryotic initiation factor 2; PRK: Protein kinase C-related kinase; RSK: Ribosomal S6 protein kinase; VASP: Vasodilator-stimulated phosphoprotein; WASP: Wiskott-Aldrich syndrome protein; WIP: WASP-interacting protein; p130_{Cas}: Crk associated tyrosine kinase substrate; Fyb: Fyn-binding protein; SKAP-HOM: Src kinase-associated phosphoprotein 55 homologue; PRAM-1: PML-retinoic acid receptor alpha regulated adaptor molecule 1; SLP-76: SH2 domain containing leukocyte protein of 76 kDa; EVL: Ena/VASP-like; INF2: Inverted formin 2; TRAF: TNF-receptor associated factor; RICK: Rip-like interacting caspase-like apoptosis-regulatory protein kinase; MCP-1: Monocyte chemotactic protein 1; ROS: Reactive oxygen species; PI3K: Phosphatidylinositol 3-kinase; mDia1: Mammalian diaphanous 1; Gab: Grb-associated-binder.

molecular function within the host cell. Additionally recent findings emphasize the central role of caspases in anti-*Yersinia* host defenses. *Yersinia* effector proteins and their effects on the host innate immune response are the focus of this review. Although we will be focusing our discussions on findings within the past 5 years, we will also draw upon relevant studies performed in the prior years.

YERSINIA OUTER PROTEINS

YopH inhibits early response of innate immune cells to enhance Yersinia virulence

YopH is a 50 kDa protein tyrosine phosphatase (PTPase) containing an N-terminal substrate binding domain and a C-terminal PTPase domain^[8,9]. Mouse infection studies showed that YopH is essential to enhance Yersinia virulence, especially at the early stages of an infection to evade innate immune cells^[10-13]. Studies on YopH and its PTPase activity demonstrate that it inhibits phagocytosis by epithelial cells, macrophages, neutrophils, and dendritic cells when working in concert with other Yops^[10,14-19]. Translocation of YopH into these immune cells results in inhibition of the early calcium signaling and ROS production, as well as the production of some proinflammatory cytokines [tumor necrosis factor- α , interleukin (IL)-10, and IL-1 β] and the chemokine, monocyte chemotactic protein $1^{[18,20-22]}$. YopH was recently implicated to function in concert with YopE to inhibit integrin β 1-mediated inflammasome activation in epithelial cells; however whether YopH also inhibits inflammasome activation in immune cells still remains to be determined^[23].

YopH targets kinases and/or adapter proteins of innate immune cells

To date, it has been reported that YopH binds to and dephosphorylates the focal adhesion kinase (FAK), Crk associated tyrosine kinase substrate (p130^{Cas}), and paxillin in epithelial cells whereas p130^{Cas}, Fynbinding protein, and SKAP-HOM are targeted in macrophages^[17,24-26]. Although not discussed here, YopH also affects the adaptive immune system where it targets lymphocyte-specific protein tyrosine kinase, linker for activation of T cell, as well as SLP-76 in T-cells^[27,28]. Interestingly, YopH only targets a subset of these proteins in a cell specific manner. Recently, the translocation of YopH was shown to directly or indirectly affect phosphorylation of the PRAM-1/SKAP-HOM and the SLP-76/Vav/phospholipase C-y2 (PLC-y2) signaling cascades in polymorphonuclear neutrophils (PMNs)^[21]. Moreover, the Grb-associated binder 1 and 2 (Gab1 and Gab2) adapter proteins, the phosphatidylinositol 3-kinase (PI3K) subunit, p85, and the Vav adapter protein were shown to associate with recombinant YopH in a pulldown experiment. The dephosphorylation of the p85 subunit of PI3K by YopH accounts for the previously reported YopHmediated dephosphorylation of PI3K to perturb PI3K-



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Figure 1 Modulation of host signaling pathways by the Yersinia effector proteins. Pathogenic Yersinia utilizes the T3SS to subvert the host innate immune response. During an infection, the Yersinia bacterium adheres onto the target host cell by using adhesion proteins such as YadA and invasin to bind onto host β1 integrin. This enables the injectisome of the T3SS to form a pore at the host plasma membrane and the subsequent translocation of the Yersinia effector proteins directly into the cytoplasm. The Yersinia effector proteins localize to distinct subcellular locations where they mimic host proteins/functions to disrupt host signaling pathways. The Ser/Thr kinase YpkA binds actin monomers resulting in YpkA autophosphorylation and kinase activation. Upon GPCR activation of the host G protein Gaq, YpkA binds to and phosphorylates Gaq to inhibit Gaq-mediated activation of the Rho GTPases and subsequent actin stress fiber formation. YpkA also uses actin as bait for actin binding proteins (i.e., VASP, cofilin, and WASP) whereby YpkA then phosphorylates these proteins. In addition, YpkA binds onto the Rho GTPases, RhoA and Rac1, to inhibit the exchange of GDP for GTP. YopE is a GAP protein that facilitates the intrinsic GTPase activity of the Rho proteins resulting in their inactivation. The cysteine protease, YopT, disrupts the actin cytoskeleton by cleaving post-translationally modified Rho GTPases. Cleavage of the Rho proteins results in the mislocalization and inactivation of the Rho proteins. YopH, a PTPase, dephosphorylates focal adhesion components such as FAK, p130^{Cas}, paxillin, Fyb, SKAP-HOM, PRAM-1, and SLP-76 to disrupt focal adhesion complexes, β1 integrin signaling, and activation of the Rho protein, Rac1. Together, the enzymatic activity of YpkA, YopE, YopT, and YopH affects organization of the actin cytoskeleton to inhibit phagocytosis. YopP/J is an acetyltransferase with deubiquitinase activity and a putative cysteine protease function. YopP/J targets signaling components of the MAPK and NF kB signaling pathways following activation of Toll-like receptor 4 to inhibit production of proinflammatory cytokines. In addition to inhibiting the MAPK and NFkB signaling pathways, YopP/J activates the inflammasome complex resulting in the maturation of caspase-1, the production of IL-1β and IL-18, and the cell death process termed pyroptosis. YopE and YopT were implicated in inhibiting inflammasome and caspase-1 activation by targeting Rac1. YopM is a protein with leucine-rich repeats that localizes to the cytoplasm and the nucleus of the cell. The translocation of YopM results in the inhibition of proinflammatory cytokine production. Cytoplasmically-localized YopM inhibits caspase-1 activity by binding to the upstream component, IQGAP1, to pro-caspase-1, or to mature caspase-1. YopM also binds onto the PRK and RSK isoforms and inhibits phosphatase-mediated deposphorylation of these two host kinases. The underlying function of targeting these two kinases by YopM is still unclear, but is linked to the production of the antiinflammatory cytokine, IL-10. T3SS: Type III secretion system; GPCR: G protein-coupled receptor; IL: Interleukin; FAK: Focal adhesion kinase; MAPK: Mitogenactivated protein kinase; NFxB: Nuclear factor kappa b; IQGAP1: IQ motif containing GTPase activating protein 1; PRK: Protein kinase C-related kinase; RSK: Ribosomal S6 protein kinase; GAP: GTPase activating protein; VASP: Vasodilator-stimulated phosphoprotein; WASP: Wiskott-Aldrich syndrome protein; p130^{Cas}: Crk associated tyrosine kinase substrate; Fyb: Fyn-binding protein; SKAP-HOM: Src kinase-associated phosphoprotein 55 homologue; PRAM-1: PML-retinoic acid receptor alpha regulated adaptor molecule 1; SLP-76: SH2 domain containing leukocyte protein of 76 kDa.

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dependent chemokine production^[22,29]. Interestingly, the p85 subunit of the PI3K protein complex (p85/p110) binds onto the Gab proteins enabling signal transduction through the PI3K signaling pathway following activation of the cell surface receptor^[30]. Thus, YopH may exploit the Gab1, Gab2, and Vav adapter proteins in order to gain access to signaling molecules.

YopE facilitates GTPase activity of the Rho family of GTPases

YopE is a 23 kDa GTPase activating protein (GAP) that is translocated by Yersinia into the target host cell where it exerts its GAP activity on the Rho family of GTPases (for a review refer to^[31]). YopE is essential to Yersinia virulence in vivo due to its effective ability to inhibit phagocytosis by innate immune cells^[32]. Earlier findings showed that YopE stimulates the GTPase activity of RhoA, Rac1, and Cdc42 in vitro; however the selective targeting of the Rho proteins in cellulo or in vivo depends on the cellular localization of YopE and the Rho proteins^[31,33-36]. In addition to the well studied Rho GTPases, YopE also targets RhoG and Rac2^[33,35,37]. Intriguingly, activation of a Rho GTPase can mediate the activation of another Rho protein, and thus YopE may be targeting multiple Rho GTPases at once to enhance Yersinia virulence.

YopE-mediated inhibition of the Rho GTPases also perturbs inflammasome activation and ROS production

The GAP activity of YopE on Rho proteins causes disruption of the actin cytoskeleton and inhibits phagocytosis; however, inactivating the Rho proteins also has other effects^[38]. Thinwa *et al*^[23] demonstrated that infection of epithelial cells with the YopE-deficient *Y. enterocolitica* mutant in part induces the maturation of caspase-1 and IL-18; a hallmark of inflammasome activation^[39]. The discovery that YopE inhibits inflammasome activation is not new, but does corroborate the previously reported finding that YopE inhibits maturation of caspase-1 and caspase-1-mediated responses in macrophages^[40].

Once in the lymphoid tissue Yersinia utilizes the T3SS to evade the host immune response. Infection of mice with a Y. pseudotuberculosis mutant strain deficient in expressing YopE showed higher association of Yersinia with PMNs one day post infection. Furthermore, the mutant can colonize and disseminate better in PMNdepleted mice^[13]. The translocation of YopE into neutrophils enables Yersinia to thwart the neutrophil response. The inhibition of ROS production along with phagocytosis by YopE is crucial for Yersinia colonization of the spleen of infected mice^[37]. Since Rac2 is primarily expressed in hematopoetic cells it is likely that YopE targets Rac2 in immune cells such as neutrophils to perturb the killing of Yersinia during an infection. Additionally, the YopE-mediated inhibition of RhoG was speculated to affect proper neutrophil functions since RhoG^{-/-} murine neutrophils are deficient in proper ROS production when stimulated with different agonists^[35,41]. Although the reported Rac2-dependent ROS production

is independent of RhoG, the activation of Rac2 at the early time points upon agonist stimulation was affected in RhoG knockout neutrophils^[37,41]. Thus, it appears that YopE may be targeting multiple signaling pathways in immune cells that mediate the production of ROS.

YopT targets the Rho family of GTPases

The cysteine protease, YopT, is a 35.5 kDa protein that is translocated into the target host cell by pathogenic Yersinia to target the Rho family of GTPases^[42-44]. YopT is a member of the "CA" clan of cysteine proteases containing the conserved Cys, His, and Asp amino acids required for the catalytic activity of cysteine proteases^[43]. The catalytic action of YopT was observed to act upon the post-translationally modified Rho GTPases where YopT cleaves upstream of the isoprenylated cysteine residue resulting in the mislocalization of the membrane-bound Rho protein, and the disruption of the actin cytoskeleton^[45]. Unlike the other Yops, YopT is not found in all pathogenic Yersinia species namely in some serotypes of Y. pseudotuberculosis due to an internal deletion of the yopT gene. Thus, the molecular role of YopT is complemented by the other translocated Yops such as YopE in the yopT-deficient Yersinia strain as demonstrated in mouse infection studies^[42,46]. Moreover, the inhibition of Rac1 by YopT and YopE inactivates caspase-1 suggesting an overlap of function between YopT and some of the other Yop effector(s) $^{[40]}$.

YopT has been demonstrated to play a role in inhibiting phagocytosis by macrophages and neutrophils, but not by dendritic cells^[47]. The Rho GTPases are key signaling molecules involved in remodeling the actin cytoskeleton to mediate phagocytosis^[48,49]. YopT has been shown to cleave the post-translationally modified RhoA, Rac1, and Cdc42 in vitro^[50]. However, the enzymatic activity of YopT appears to be more selective in targeting different Rho protein(s) depending on the cell type and subcellular localization of the Rho proteins^[35,51]. In addition to targeting the well studied Rho proteins, YopT also cleaves membrane bound RhoG to inhibit RhoG-mediated uptake of Yersinia; however, since RhoG is also required for proper neutrophil functions, it remains to be tested whether YopT also affects other response mediated by RhoG in immune cells^[35,41].

YopT induces expression of host's KLF2 and GILZ to inhibit NFkB signaling

The translocation of YopT results in decreased IL-8 production suggesting that the catalytic activity of YopT on Rho proteins not only results in the disruption of the actin cytoskeleton, but also modifies the host transcriptional profile^[22,46,52,53]. YopT was shown to mediate expression of the zinc-finger transcription factor, Kruppel-like factor 2 (KLF2), and the leucine zipper, glucocorticoid induced-leucine zipper (GILZ), in macrophages and/or epithelial cells upon infection with *Yersinia*^[54,55]. In host cells both KLF2 and GILZ inhibit the NF_KB signaling pathway to downregulate

 $NF_{\rm K}B$ -mediated proinflammatory responses^[56,57]. Thus, YopT usurps a normal host regulatory mechanism to counteract anti-*Yersinia* immune responses. However, it is still unclear at what stage(s) of *Yersinia* infection KLF2 and GILZ expression are required to promote *Yersinia* pathogenesis.

The multi-domains of YpkA/YopO

Yersinia protein kinase A (YpkA; YopO in Y. enterocolitica) is an 80 kDa serine/threonine (Ser/Thr) kinase that when translocated into the target cell causes disruption of the actin cytoskeleton^[58]. Interestingly, YpkA is a multifaceted effector protein with regards to the functional eukaryotic-like enzymatic domains that include a Ser/Thr kinase domain and a guanine nucleotide dissociation-like inhibitor (GDI) domain^[59,60]. YpkA is the only Yersinia effector protein with two enzymatic domains. Activities of both domains affect the actin cytoskeleton by targeting the activation state of the Rho GTPases, RhoA and Rac1. Rho GTPases cycle between an active GTP-bound and an inactive GDPbound state where the former is catalyzed by guanine nucleotide exchange factors (GEFs) to exchange GDP for GTP. Active Rho proteins activate downstream effectors to remodel the actin cytoskeleton to regulate cellular processes such as phagocytosis^[49]. The intrinsic Rho GTPase activity is facilitated by GAP that hydrolyze GTP resulting in the inactivation of the Rho proteins. Inactive Rho proteins are bound to GDI and are kept in an inactivate state. Similar to host GDI, the GDI domain of YpkA binds directly to the Rho GTPases to inhibit GTP loading whereas the kinase domain targets the alpha subunit of the heterotrimeric G protein complex, Gq, to inhibit activation of downstream Rho proteins by the LARG RhoGEF^[60,61]. However, the YpkA GDI domain alone can mediate the disrupted actin cytoskeleton phenotype, and thus underscores the prediction that the kinase activity of YpkA also targets additional host signaling pathways (see below). Although mouse infection studies with Yersinia mutant strains expressing either a kinase inactive YpkA mutant or only the GDI domain controversially argue one domain being more essential than the other, these studies taken together suggest that both domains of YpkA contribute to Yersinia virulence^[30,59,62,63]

The secretion/translocation domain of YpkA (Sec/ Trans; amino acids 1-77) located at its N-terminus mediates translocation of YpkA into the host cell^[64]. Intriguingly though, multiple regulatory domains also overlap with the Sec/Trans domain of YpkA. To date, the chaperone binding domain (amino acids 20-77), the membrane localization domain (MLD; amino acids 20-90), and the substrate-binding domain (SBD; amino acids 40-49) all overlap with the Sec/Trans domain^[65,66]. Salomon *et al*^[67] also showed that residues located within amino acids 1-125 of YpkA mediate binding to phosphoinositides to perhaps localize YpkA to the plasma membrane after being translocated. Altogether, the MLD, SBD, and phosphoinositide-binding residues may regulate an aspect of YpkA activity such as the phosphorylation of $G\alpha q$ and/or the selective inhibition of Rho proteins. Downstream of these domains is the kinase domain (amino acids 150-400), the GDI domain (amino acids 431-612), and the actin binding domain (ABD; amino acids 709-729).

Kinase activation of YpkA and the targeting of actin regulating proteins

YpkA is expressed as an inactive kinase in the Yersinia bacterium^[59]. The kinase activity of YpkA is activated by binding onto globular actin via the ABD upon translocation into the target cell^[68]. The crystal structure of the Y. enterocolitica YopO-actin complex showed that actin binding allosterically positions the catalytic and activation loops of YpkA in an active conformation^[69]. Actin binding induces YpkA autophosphorylation on Ser90 and Ser95 in vitro^[59,66,68]. Interestingly, mutation of Ser90 and Ser95 to alanine on YpkA does not affect its kinase activity in cellulo whereas mutation of all serine residues on YpkA resulted in a catalytically inactive kinase^[66]. Further analysis showed that mutation of all serine residues to alanine within amino acids 436-710 to alanine does not affect YpkA kinase activity in vitro or in cellulo. Moreover, mutation of serine residues to alanine within amino acids 1-150 or 150-400 results in decreased YpkA autophosphorylation in vitro, but has no effect on its kinase activity in cellulo; however, mutation of all serine residues to alanine within amino acids 1-400 results in an inactive YpkA kinase mutant^[66]. Together, the results suggest that once translocated YpkA autophosphorylates on multiple serine residues within its N-terminus to activate its kinase domain. Additionally, due to the fact that YpkA is translocated at a lower level relative to other Yersinia effectors, it appears that the YpkA kinase activity has been fine tuned to where it can function efficiently within the target host cell by autophosphorylation on multiple serine residues^[58]. It is predicted that this multisite autophosphorylation mechanism by YpkA enables it to bypass the regulatory control imposed by host proteins such as phosphatases.

YpkA-mediated phosphorylation of $G\alpha q$ results in the inhibition of the $G_{\alpha}q$ signaling cascade^[61]. Activation of $G\alpha q$ and its effector, phospholipase C, regulates an array of cellular responses such as neuronal signaling, platelet aggregation, cell growth and proliferation, and development^[70]. However, further study is still needed to establish the molecular contribution of YpkA-mediated inhibition of $G_{\alpha}q$ to Yersinia pathogenesis. Although it remains to be explored, YpkA may be targeting $G_{\alpha}q$ mediated NF_{κ}B activation through the scaffolding protein, CARMA3. CARMA family members form a complex with Bcl10, MALT1, and TRAF6 to activate NF_{κ}B resulting in the induction of a proinflammatory response^[71]. Alternatively, YpkA may be targeting $G\alpha q$ to inhibit activation of the dual oxidase-dependent production of ROS^[71,72]. The production of ROS is involved in mediating killing of pathogens by directly damaging the pathogen cellular components (i.e.,

DNA damage and amino acid modification), as well as indirectly by regulating responses such as phagosomal protease activity and immune signaling^[73]. In addition to binding directly to $G\alpha q$ to mediate phosphorylation, YpkA utilizes actin as bait to recruit the actin filament elongators (EVL and VASP), the formin proteins (mDia1 and INF2), the nucleation-promoting factors (WASP and WIP), the actin filament severing protein (gelsolin), and the actin depoylmerizing protein (cofilin) for phosphorylation in vitro^[69]. Since all of these proteins are involved in regulating actin assembly and disassembly, these proteins are likely targeted by YpkA to inhibit some aspect of phagocytosis as reported for VASP^[74]. An alternative mechanism of phagocytosis (also known as bacterial uptake) is activated by binding of the Yersinia adhesion proteins, Inv and YadA, to host $\beta 1$ integrin. Subsequently, focal adhesion proteins and Rac1 signal downstream molecules to remodel the actin cytoskeleton resulting in uptake of Yersinia^[1]. Uptake of E. coli expressing the YadA protein by human umbilical vein endothelial cells was inhibited by the kinase activity of YpkA^[68]. Phosphorylation of proteins regulating actin polymerization by YpkA may be responsible for the inhibition of bacterial uptake via the YadA-B1 integrin signaling pathway.

YpkA inhibits the Rac GTPases

Early studies on YpkA identified the Rho GTPases as target substrates of the YpkA GDI domain where binding of YpkA to RhoA and Rac1 inhibits their activation^[60,75,76]. Moreover, phagocytosis of opsonized sheep red blood cells (IgG-sRBC) by COS-7 cells expressing the $Fc\gamma$ receptor showed that YpkA localizes to phagocytic cups and inhibits phagocytosis^[77]. This is achieved through the selective inhibition of Rac1 by the GDI domain of YpkA suggesting that once translocated into innate immune cells YpkA inhibits Fcy receptor-mediated phagocytosis. Interestingly, the Rac2 isoform was also identified as an interacting partner of YpkA^[69,77]. Rac2 is primarily expressed in hematopoietic cells at varying levels depending on the immune cell type and is involved in activation of the NADPH oxidase to produce ROS, as well as phagocytosis^[78]. Thus, it is tempting to suggest that aside from targeting Rac1 for inhibition YpkA also inhibits Rac2 activity in immune cells. Additionally, the Rac1- and Rac2-regulated protein, PLC- γ 2 isoform, was identified as an interacting partner with the YopO-actin complex^[69,79]. This further supports the speculation that YpkA also targets Rac2 signaling in immune cells.

The many target substrates of YopP/J

YopJ (YopP in *Y. enterocolitica*) is a 34 kDa acetyltransferase with a deubiquitinating and putative cysteine protease function which was previously shown to inhibit production of proinflammatory molecules. YopP/J suppresses a proinflammatory response by interfering with the mitogen-activated protein kinase (MAPK) and NF_KB signaling pathways^[80-84]. More recently, YopJ was reported to acetylate the MAPKK kinase family member, TAK1, and the Ser/Thr kinase, RICK, to inhibit their activity^[85,86]. Production of chemoattractants (KC, MIP-2, and G-CSF) and adhesion molecules are also effected by YopP/J presumably to inhibit the early recruitment of neutrophils to the site of infection; however, inhibition of chemoattractant expression levels in vivo may involve the function of other Yop effectors^[87-89]. Moreover, the YopJ homolog, YopP, of Y. enterocolitica inhibits phosphorylation of the Tyk2 kinase and STAT4 of the Jak-STAT signaling pathway through a yet-to-be identified mechanism^[90]. Of all the effectors that *Yersinia* translocates, it should be noted that YopP/J translocates at various amounts depending on the Yersinia strain which reflects its associated cytotoxicity^[87,91,92]. This was further seen in studies conducted with different concentrations of recombinant YopJ^[93-95].

YopP/J induces apoptosis through caspase-8

Similar to what was observed with extracellular Yersinia, translocation of YopJ by intracellular Yersinia induces apoptosis of macrophages^[96]. Apoptosis is a process initiated by an extracellular "death" signal (extrinsic pathway) or an intracellular signal (intrinsic pathway) that converges on the mitochondria and the release of cytochrome C. The extrinsic and intrinsic pathway involve the activation of caspase-8 or caspase-9, respectively, and the subsequent processing of the effector caspases (e.g. caspase-3) to induce apoptosis^[97]. YopP/ J-mediated inhibition of the MAPK and NF_{κ}B signaling pathways, along with Toll-like receptor 4 signaling, induces apoptosis of macrophages and dendritic cells^[98-102]. This reported YopJ-induced cellular apoptosis was shown to be a result of signal transduction via the receptor-interacting Ser/Thr kinase 1 (RIPK1), Fas-associated death domain and caspase-8 signaling cascade to induce apoptosis^[103,104]. Additionally, activated caspase-8 mediates the maturation of the inflammasomeassociated caspase-1^[103,104]. Although inflammasome activation triggers the cell death process termed pyroptosis, YopJ-induced cell death is primarily through caspase-8-induced apoptosis^[105,106]. However, in contrast to the experimental findings reported, YopJ-mediated activation of caspase-1 was observed in cells undergoing necrosis^[107]. Since activated RIPK3 is downstream of RIPK1, and is the signaling molecule that triggers programmed necrosis termed necroptosis, it is likely the candidate for the observed necrosis^[107,108]. In support of this is the evidence that YopJ-mediated activation of caspase-8 suppresses RIPK3 induced necrosis^[103,104]. Thus, there appears to be an intimate crosstalk between caspase-8 and RIPK3 in determining the fate of a Yersinia infected cell containing YopP/J.

YopP/J utilizes host signaling pathways to promote Yersinia virulence

YopP/J activity affects macrophages, dendritic cells, NK cells, and to varying degrees neutrophils^[90,98,109-111]. However, activity of YopP/J *in vivo* varies depending on the *Yersinia* strain, YopP/J variant, experimental para-



meters, and infection model^[62,92,112-115]. Nevertheless, translocation of YopP/J results in the inhibition of key signaling pathways that mediate a proinflammatory response, and also induces production of specific cytokines^[83,89,116-118]. In particular is the well established observation that YopJ activity on the MAPK and $\mathsf{NF}_{\mathsf{K}}\mathsf{B}$ signaling pathways mediates the maturation of caspase-1^[98,103-105]. Activated caspase-1 cleaves pro-IL-18 and pro-IL-1 β to produce active IL-18 and IL-1 $\beta^{[39]}$. Studies using RIPK3/caspase-8 knockout mice showed reduced cytokine production in response to Yersinia infection, and thus, underscores the crucial role of caspase-8 and caspase-1 in mediating a host response to Yersinia when the MAPK and NF_{κ}B signaling pathways are inhibited^[103,104]. Why would Yersinia utilize YopJ to induce the activation of caspase-8 and caspase-1? Is it a mechanism evolved by the host to counteract a Yersinia infection when the MAPK and NF_{κ}B signaling pathways are inhibited, or is it a virulence strategy employed by Yersinia? Recent studies are alluding to both situations being the case and are dependent on the association of caspase-1 with inflammasome components, NLRP12, NLRP3/ASC or NOD2^[85,106,111]. Thus, although the functions of IL-18 and IL-1 β induce an anti-Yersinia response, Yersinia may also exploit the normal functions of these cytokines at certain stages of infection to promote Yersinia virulence. YopJ was also linked to the inhibition of the host alpha subunit of the eukaryotic initiation factor 2 (eIF2 α). Although the underlying mechanism and biological relevance is still unclear, modulating $eIF2\alpha$ activity by YopJ results in an increased cellular invasion of MEF cells by Yersinia and decreased cytokine production^[119].

YopM is indispensable to Yersinia virulence

YopM is a leucine-rich repeat (LRR) protein that localizes to both the cytoplasm and the nucleus of the target host cell upon translocation^[120,121]. The molecular contribution of YopM to Yersinia pathogenesis is still unclear; however, it has been shown to target immune cells to effect different immune cell populations of the spleen and liver of infected mice, downregulate proinflammatory responses, and upregulate the antiinflammatory cytokine, IL-10^[122-125]. IL-10 downregulates the production of proinflammatory cytokines by multiple innate immune cells, as well as regulates T cell function and proliferation^[126]. The production of IL-10 was proposed to counteract the PMN response against Yersinia; however whether YopM is solely responsible for inducing production of IL-10 remains to be further explored^[124]. YopM was also shown to inhibit platelet aggregation^[127]. Although YopM is required to enhance Yersinia virulence in mouse infection models, varying results suggest that the route of infection and mouse strain used affects the reported contribution of YopM to Yersinia pathogenesis^[122]. Moreover, this could also be attributed to the LRR motifs of the YopM variants, as well as the natural route of infection of the pathogenic Yersinia species.

YopM targets extra- and intracellular host proteins

Of the six effectors that are translocated by the T3SS of the pathogenic Yersinia species into the target host cell, YopM has been shown to also be secreted into the extracellular matrix where it binds α -thrombin and α 1antitrypsin^[128-130]. Extracellular YopM can also penetrate culture cells^[131]. Whether YopM enters the target host cells by crossing the lipid bilayer or via the T3SS it targets the ribosomal S6 protein kinase (RSK) and the protein kinase C-related kinase (PRK) isoforms^[132,133]. Dephosphorylation of the RSK isoforms by phosphatase was inhibited by YopM in cellulo and in vitro^[134]. The YopM mutant variant of Y. pseudotuberculosis 32777 that is defective in binding RSK1 and PRK2 was unable to induce IL-10 production^[133]. More recently, YopM has been shown to inhibit the activity of mature caspase-1. This is achieved by the binding of YopM to the substratebinding site of caspase-1, inhibition of recruitment of pro-caspase-1 to the inflammasome complex, and/or by targeting the scaffold protein, IQ motif containing GAP 1 (IQGAP1), which is known to activate caspase- $1^{[135,136]}$. Moreover, YopM has also been shown to activate caspase-3 to presumably induce apoptosis of PMNs and/ or macrophages in the liver of infected mice, and thus promote Yersinia virulence^[137].

CONCLUSION

A major theme emerging from studies of the Yersinia effector proteins is the important role caspases play in host anti-Yersinia defenses. In particular are the effects of the Yersinia effector proteins on caspase-1 activity. Upon the detection of a pathogen by innate immune cells, the inflammasome complex is activated by the oligomerization of nucleotide-binding domain and LRR- containing (NLR) family of proteins. The caspase activation and recruitment domain found on NLRs or an associated adaptor protein such as ASC then recruits pro-caspase-1. Subsequently, autoproteolytic cleavage of pro-caspase-1 is induced to produce the mature caspase-1 form. Mature caspase-1 then mediates the maturation of IL-1 β and IL-18, as well as induces pyroptosis. The targeting of Rac1 by YopE and YopT inhibits maturation of caspase-1 whereas the binding of IQGAP1, pro-caspase-1, and caspase-1 by YopM inhibits inflammasome activation, or the enzymatic function of caspase-1. Moreover, the dephosphorylation of FAK by YopH inhibits caspase-1 activation in epithelial cells which suggests that YopH also inhibits caspase-1 activity when translocated into innate immune cells. Alternatively, YopP/J was shown to activate caspase-1 through inflammasome activation, as well as the extrinsic cell death pathway. Whether this is beneficial or detrimental to Yersinia pathogenesis depends on the stage of infection; however, the kinetics of caspase-1 activation in the presence of multiple Yersinia effector proteins requires further exploration. An additional translocated Yop protein, YopK, which is involved in regulating translocation of the Yersinia effector proteins also inhibits inflammasome activation (for a review on YopK refer to^[138]. Lastly, although YpkA has not been shown to affect caspase-1 activation or its activity, a study has shown that YpkA induces cellular apoptosis of murine macrophages through the intrinsic pathway which activates caspase-3^[139]. Altogether, the *Yersinia* effector proteins effectively enable pathogenic *Yersinia* spp. to thwart the host innate immune response by regulating some aspect of programmed cell death, as well as inhibit the induction of proinflammatory cytokine production and phagocytosis. Future studies may lead to the identification of novel targets for the *Yersinia* effector proteins and thus additional targets for therapeutic interventions.

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