

Editorial

Pathogen Hijacking of Crk Adaptor Proteins and Crk-Regulated Signal Transduction Pathways

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Received: March 03 2014; Accepted: March 05 2014;

Published: March 07 2014

Microbial pathogens have evolved a variety of strategies to promote their own survival and utilize different tactics to divert host immune responses. Many types of pathogenic bacteria employ unique secretion systems through which they deliver novel 'weapons', or virulence factors into eukaryotic cells, which promote bacterial invasion and/or perturb diverse host cell functions to facilitate bacterial colonization.

Among the cellular host proteins that are targeted by invading pathogens, Crk adaptor proteins, which link different surface receptors to their corresponding signaling pathways, appear to be preferred targets. Crk was discovered in the late 1980s as a chicken retroviral oncogene product that consists of SH2 and SH3 domains [1,2]. It was later found to have three mammalian homologs: CrkI and CrkII, which are alternative spliced forms of a single gene, and CrkL, which is encoded by a separate gene [3,4]. The Crk proteins are involved in the regulation of many different cellular activities, including gene expression, cell adhesion, migration, proliferation and differentiation, as well as cell transformation and apoptosis [5]. Furthermore, Crk proteins integrate signals that are critical for immune cell functions [6,7], and are therefore potential drug targets in maladies caused by cancer, autoimmunity and infection diseases [8,9].

Recent studies suggested that Crk adaptor proteins contribute to bacterial and perhaps also viral pathogenesis by promoting pathogen entry into cells and by serving as targets for virulence factors that subvert the cellular machinery to create a microenvironment which is beneficial for the pathogen.

Involvement of Crk adaptor proteins in bacterial entry into mammalian cells was first noted in *Yersinia pseudotuberculosis* infection of human epithelial cells [10,11]. *Yersinia* is a Gram-negative bacterium with a type-III secretion system (T3SS), and its intracellular invasion involves an interaction between the bacterial protein, invasin, and the host cell $\beta 1$ integrin receptor, which triggers the cellular machinery that supports *Yersinia* uptake. Invasin binding

to the $\beta 1$ integrin initiates a host response leading to activation of FAK (focal adhesion kinase)- and/or Src protein tyrosine kinases [12,13]. and phosphorylation of p130Cas (Crk-associated substrate, 130kDa). A subsequent interaction between phospho-p130Cas and Crk is required for further activation of the GTP-binding protein, Rac1, which promotes actin rearrangement and bacterial internalization. Cell transfection with CrkII point mutants in the SH2 (R38V) or SH3N(W169L) domains, which are unable to interact with p130Cas or DOCK180(dedicator of cytokinesis, 180kDa; an upstream regulator of Rac1), respectively, resulted in decreased bacterial uptake, demonstrating the critical role of CrkII and its SH2- and SH3N-domain-binding partners in the bacterial internalization process.

Crk proteins are also required for cell infection by *Shigella flexneri*, another intracellular Gram-negative bacterium with a T3SS [14]. Entry of *S. flexneri* into mammalian cells is made possible by binding of the IpaA and IpaB bacterial proteins to the host cell integrin $\alpha 5\beta 1$ and CD44 surface receptors, respectively, which establish the initial contact [15,16]. A key event in the early phase of the infection is the induction of actin polymerization and cytoskeletal reorganization at the bacteria-host cell contact area, which promotes bacterial internalization. This step involves Abl/Arg-mediated tyrosine phosphorylation of CrkII, which in turn activates the Rho family GTPases, Cdc42 and Rac, leading to actin polymerization and rearrangement of the cytoskeleton [17]. Phosphorylation of CrkII at tyrosine 221 (Y221) is an essential event during cell infection by *S. flexneri*, and is essential for bacterial invasion. Overexpression of a phosphorylation-deficient mutant of CrkII, in which tyrosine 221 is replaced by phenylalanine (Crk Y221F), inhibits bacterial entry into the cells [14].

Additional Crk-regulated host cell proteins that are involved in non-phagocytic cell invasion by *S. flexneri* are cortactin and Unc119 [18,19]. Cortactin is involved in *S. flexneri* entry into epithelial cells through its binding to and cooperation with the Crk protein, thus promoting actin polymerization and cytoskeletal rearrangement [18]. Unc119 acts as an upstream negative regulator of Abl, therefore inhibits Abl-mediated CrkII phosphorylation at tyrosine 221, and consequently, reduces *S. flexneri* uptake by cells. In agreement, knockdown of Unc119 enhanced bacterial invasion, while cell treatment with a cell permeable Unc119 protein led to a partial inhibition of bacterial internalization [19].

While *Pseudomonas aeruginosa* [20,21], and *Salmonella enteric* [22], possess distinct T3SSs and utilize different arrays of virulence factors to promote cell invasion, they subvert common host signaling pathways to support their uptake. This two-pathogen entry into nonphagocytic cells by utilizing the Abl-dependent Crk-mediated signaling pathways that manipulate the host cell actin assembly and promote cytoskeleton rearrangement. Furthermore, the *P. aeruginosa*

virulence factor, ExoT, can disrupt host cell signaling pathways by ADP-ribosylating CrkI and CrkII at Arg20 within the SH2 domain, thereby interfering with Crk binding to p130Cas and modulating p130Cas-dependent signaling events.

A somewhat different mechanism for cell invasion has been proposed for the intracellular Gram-positive bacteria, *Listeria monocytogenes*, [23,24]. This bacterium possesses a surface protein, termed INIB, which interacts with a host cell surface receptor tyrosine kinase, termed Met. Binding of INIB activates the Met catalytic domain, which stimulates a CrkII and Gab1 adaptor protein-regulated signal transduction pathway. Consequently, phosphoinositide 3-kinase (PI-3K) undergoes activation and promotes additional events that support bacterial entry into the cells. Recently it was shown that the SH3C domain of CrkII is required for activation of PI-3K. This activation promotes changes in actin polymerization necessary for bacterial entry. The finding that the Crk-SH3C domain is essential for bacterial uptake is surprising, since in contrast to the Crk-SH2 and SH3N domain, Crk-SH3C has no known binding partners, and is assumed to function as an integral regulatory region.

A different and novel strategy of interaction with host cells has been adopted by the Gram-negative bacteria *Helicobacter pylori* [25,26], which colonize the gastric epithelia. *H. pylori* mediates persistent infection by inhibiting cell apoptosis, thereby preventing the rapid epithelial cell turnover that facilitates bacterial clearance. This mechanism is made possible by the *H. pylori* virulence protein, CagA, which is delivered into the host cells where it upregulates survival mechanisms and induces anti-apoptotic pathways. The molecular basis of this process involves binding of CagA to CrkI, CrkII and CrkL adaptor proteins, leading to induction of signaling events that activate pro-survival effector molecules, including the MEK/ERK cascade and the anti-apoptotic protein MCL1 (myeloid cell leukemia sequence 1).

It is interesting to note that the Gram-negative bacteria, *Escherichia coli*, also utilize a T3SS to deliver virulence factors that ultimately modify the Crk signaling pathway. While CrkII was found to be selectively recruited to the pedestal of the *enteropathogenic E. coli* (EPEC) and not to that of the *enterohemorrhagic E. coli* (EHEC) [27], recent studies revealed that EHEC infection coincides with intracellular delivery of a virulence protein NleH1, which physically interacts with CrkL [28]. Binding of CrkL to IKK β and interaction with NleH1 promotes NleH1 association with the ribosomal protein S3 (RPS3), which leads to modulation of the RPS3/NF κ B signaling pathway? While the exact effect of NleH1 in the host cell is not fully clear, it is assumed to promote bacterial survival by inhibiting innate immune responses.

A recent study demonstrated that *Chlamydia trachomatis*, a Gram-negative obligate intracellular bacteria and the causative agent of trachoma and sexually transmitted diseases, also engage CrkI and CrkII to promote bacterial recruitment to nascent inclusions, and thereby altering innate anti-*Chlamydia* immune mechanisms [29]. This activity is carried out by TepP (translocated early phosphoprotein), which is translocated into the host cells during the early phase of cell entry. TepP undergoes phosphorylation by a host cell kinase and acts as a bacterial linker that associates with host cell

CrkI/CrkII to alter the regulation of innate immune response genes.

Viruses also utilize a variety of strategies to evade host cells and/or neutralize anti-viral responses. The 1918 Spanish influenza virus and the avian influenza. A virus was found to utilize Crk-regulated signaling pathways to promote intracellular viral replication [30-32]. These viruses utilize their NS1 (nonstructural protein 1) virulence factor, which possesses a proline-rich SH3-binding motif, to bind CrkI/II and CrkL proteins with high affinity, in order to downregulate JNK-ATF2 signaling. The JNK-ATF2 pathway suppresses apoptosis, which is detrimental to viral proliferation, and is therefore inhibited by the virus. Knock-down of the host cell CrkI/II and CrkL proteins have shown to significantly impair viral propagation, indicating that NS1-Crk interaction is critical for viral replication [30].

Altogether, the studies described here demonstrate that Crk adaptor proteins are essential for cell infection and propagation of a variety of pathogens. Exogenous manipulation of Crk protein expression or function might therefore serve as potential strategies for inhibition of pathogen replication and survival. Furthermore, better understanding of the mechanisms by which different virulence factors hijack cellular effector molecules and signaling pathways may provide crucial information for the design of drugs that ban pathogen propagation by diverting different cellular machineries.

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