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Host and bacterial factors that regulate LC3 recruitment to *Listeria monocytogenes* during the early stages of macrophage infection

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Keywords: autophagy, diacylglycerol, innate immunity, LC3, LC3-associated phagocytosis, *Listeria monocytogenes*, reactive oxygen species, ubiquitin

Abbreviations: LAP, LC3-associated phagocytosis; ROS, reactive oxygen species; SLAPs, spacious *Listeria*-containing phagosomes; LLO, Listeriolysin O; PLC, phospholipase C; CBD, cell wall binding domain; SQSTM1, sequestosome-1; DPI, diphensylidenonium; Cm, chloramphenicol; DAG, diacylglycerol; PLD, phospholipase D; PPAP2A, phosphatidic acid phosphatase; DGK, DAG kinase

*Listeria monocytogenes* is a bacterial pathogen that can escape the phagosome and replicate in the cytosol of host cells during infection. We previously observed that a population (up to 35%) of *L. monocytogenes* strain 10403s colocalize with the macroautophagy marker LC3 at 1 h postinfection. This is thought to give rise to spacious *Listeria*-containing phagosomes (SLAPs), a membrane-bound compartment harboring slow-growing bacteria that is associated with persistent infection. Here, we examined the host and bacterial factors that mediate LC3 recruitment to bacteria at 1 h postinfection. At this early time point, LC3+ bacteria were present within single-membrane phagosomes that are LAMP1+. Protein ubiquitination is known to play a role in targeting cytosolic *Listeria monocytogenes* to macroautophagy. However, we found that neither protein ubiquitination nor the ubiquitin-binding adaptor SQSTM1/p62 are associated with LC3+ bacteria at 1 h postinfection. Reactive oxygen species (ROS) production by the CYBB/NOX2 NADPH oxidase was also required for LC3 recruitment to bacteria at 1 h postinfection and for subsequent SLAP formation. Diacylglycerol is an upstream activator of the CYBB/NOX2 NADPH oxidase, and its production by both bacterial and host phospholipases was required for LC3 recruitment to bacteria. Our data suggest that the LC3-associated phagocytosis (LAP) pathway, which is distinct from macroautophagy, targets *Listeria monocytogenes* during the early stage of infection within host macrophages and allows establishment of an intracellular niche (SLAPs) associated with persistent infection.

Introduction

Macroautophagy (hereafter referred to as autophagy) is a key component of host innate immune defense against many pathogenic microorganisms,1 limiting bacterial escape from the phagosome2-4 as well as targeting cytosolic bacteria to the lysosomes for clearance.5,6 Furthermore, components of the autophagy pathway can also contribute to immunity by mechanisms independent of the formation of autophagosomes7,8 (recently reviewed by Cemma et al.)9. One notable example is LC3-associated phagocytosis (LAP), a pathway that is involved in promoting phagosome maturation, killing of microbes (e.g., *S. cerevisiae*), as well as suppressing proinflammatory signals.9,10,11 LAP requires some essential components of the autophagy pathway (ATG5 ATG7, BECN1) but not others (ULK1).11 While the mechanisms regulating LAP are not clear, reactive oxygen species production by the CYBB/NOX2 NADPH oxidase is required.10 LC3 recruitment to phagosomes containing the BopA mutant of *Burkholderia pseudomallei* is suggested to promote killing of bacteria trapped in phagosomes.12 Whether LAP targets other bacteria during infection, and whether this pathway can be subverted/exploited by intracellular pathogens, is not known.

*Listeria monocytogenes* (*L. monocytogenes*) is the causative agent of listeriosis, a gastroenteritis that is self-limiting in healthy individuals but may become life-threatening for neonates or young children, elderly and immunocompromised individuals.13 *L. monocytogenes* can colonize host cells, including macrophages, during infection.14 Upon invasion, a population of bacteria is able to escape from the phagosome and colonize the nutrient-rich cytosol where they replicate rapidly. Phagosomal escape is mediated by the bacterial pore forming toxin Listeriolysin O (LLO) and two phospholipase C enzymes (PLCs). PLCs are thought to not only degrade the phagosome to promote escape but can also activate signal transduction cascades within the
host cell as a result of their catalytic activity. Upon entry to
the cytosol, the bacteria use a cell surface protein, ActA, to drive
actin-based motility in the host cytosol, and eventual cell-to-cell
transfer.

Previous studies have shown that *L. monocytogenes* strain
10403S colocalizes with LC3 at 1 h postinfection (p.i.). This
colocalization is thought to give rise to spacious *Listeria-
containing phagosomes* (SLAPs), a membrane-bound compart-
ment harboring slow-growing bacteria that is associated with
persistent *L. monocytogenes* infection. A number of questions
remain regarding the mechanism of LC3 recruitment to bacteria
at 1 h p.i. Given the recent findings that LC3 can be involved in
other degradative pathways that are independent of autophagy,
it is unclear which pathway is activated upon *L. monocytogenes*
infection. Furthermore, since *L. monocytogenes* can escape from
the phagosome, it is unclear whether bacteria are targeted by LC3
within phagosomes or in the cytosol at the peak of LC3 colocal-
ization. Finally, it is also unknown which host and/or bacterial
factor(s) mediate LC3 colocalization with *L. monocytogenes*. We
have previously demonstrated that a nonmotile (ActAΔ) mutant
of *L. monocytogenes* colocalizes with ubiquitinated proteins in
the cytosol. Recent work by Sasakawa and colleagues suggests
that this protein ubiquitination event mediates recruitment of
adaptor proteins such as SQSTM1/p62 that leads to autophagic
targeting of the ActA virulence factor. Thus, we first confirmed the ability of
the CBD-YFP probe to detect cytosolic *L. monocytogenes* by quanti-
tifying the number of CBD-YFP− bacteria that were also posi-
tive for polymerized actin at 4 h p.i. when bacteria are known
to be localized in the cytosol. As expected, the majority (60%) of
CBD-YFP+ *L. monocytogenes* were also actin+, confirming that
the CBD-YFP can detect cytosolic *L. monocytogenes* after their
escape from phagosomes (Fig. 1E and F). In contrast, we did not observe any accumulation of CBD-YFP to the LC3+ popula-
tion of *L. monocytogenes* at 1 h p.i. (Fig. 1G and H). Together,
these data demonstrate that LC3 is recruited to *L. monocytogenes*
within phagosomes at early stages of infection.

Next, we examined LC3+ *L. monocytogenes* using correlative
light and electron microscopy. We observed that LC3+ bacte-
ria at 1 h p.i. were present in phagosomes that have a single
membrane (Fig. II), consistent with our previous analysis of
*L. monocytogenes* infected cells analyzed at 1 h p.i. by con-
ventional transmission electron microscopy. This is in con-
trast to double-membrane autophagosomes observed during
autophagy of nonmotile (ActAΔ) bacteria from the cytosol,
that were observed by Webster and colleagues. We also did
not observe multilamellar (3 to 4 membranes) structures
observed when bacteria in disrupted phagosomes are targeted by
autophagy.

**Results**

LC3 colocalizes with wild-type *L. monocytogenes* in single-
membrane phagosomes. Consistent with previous work, we
found that LC3 recruitment to *L. monocytogenes* peaks at 1 h p.i.
in an LLO-dependent manner (Fig. 1A and B). However, based
on published reports of *L. monocytogenes* phagosome-escape
kinetics, it is unclear whether *L. monocytogenes* is in the phago-
some or cytosol during the peak of LC3 targeting. To determine
whether *L. monocytogenes* is present inside phagosomes or the
cytosol at 1 h p.i., we first quantified the percentage of *L. monocyt-
genese* that were both LC3+ and LAMP1+ associated. Previously,
we have reported that roughly 70% to 80% of LC3+-associated
*L. monocytogenes* are also LAMP1+ associated. Here, we found
that the majority (78%) of LAMP1+ bacteria were also LC3+ (Fig. 1C and D). Together, these observations suggest that LC3
is targeted to *L. monocytogenes* within an intracellular com-
partment and not the cytosol. Furthermore, our data suggest
that LC3 recruitment is a common fate for bacteria trapped in
phagosomes.

To further examine LC3 recruitment to *L. monocytogenes*, we
employed a recently described probe constructed from the cell
wall binding domain (CBD) of a *Listeria* bacteriophage
protein. A yellow fluorescent protein fusion to CBD (CBD-YFP)
was developed by Swanson and colleagues to track phagosome
escape by *L. monocytogenes*. CBD-YFP expressed within host
cells binds to cytosolic bacteria, resulting in an accumulation of
YFP fluorescence around the bacteria. Upon escape from the
phagosome, *L. monocytogenes* also polymerizes actin via the
ActA virulence factor. Thus, we first confirmed the ability of
the CBD-YFP probe to detect cytosolic *L. monocytogenes* by quanti-
tifying the number of CBD-YFP+ bacteria that were also posi-
tive for polymerized actin at 4 h p.i. when bacteria are known
to be localized in the cytosol. As expected, the majority (60%) of
CBD-YFP+ *L. monocytogenes* were also actin+, confirming that
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tion of *L. monocytogenes* at 1 h p.i. (Fig. 1G and H). Together,
these data demonstrate that LC3 is recruited to *L. monocytogenes*
within phagosomes at early stages of infection.

**Protein ubiquitination is not a signal for recruitment of
LC3 to *L. monocytogenes* at 1 h.p.i.** Previous studies suggest
that protein ubiquitination mediates autophagic targeting of
*L. monocytogenes* in the cytosol via the ubiquitin-binding adap-
tor SQSTM1. Autophagy of damaged phagosomes containing
*Salmonella enterica* serovar Typhimurium and *S. flexneri* has also
been shown to involve protein ubiquitination and ubiquitin-bind-
ing adaptors. These observations suggest the possibility that
protein ubiquitination may also play a role in LC3 recruitment
to *L. monocytogenes* within phagosomes. However, we observed
that the majority (98%) of the LC3+ population of *L. monocyt-
genese* did not colocalize with ubiquitinated proteins at 1 h p.i.
(Fig. 2A and B). Consistent with this finding, expression of the
ubiquitin-binding adaptor SQSTM1 was not required for LC3
recruitment to *L. monocytogenes* at 1 h p.i. as siRNA-mediated
**Figure 1.** LC3 is recruited to wild-type *L. monocytogenes* strain 10403S in macrophage phagosomes during early stages of infection. (A) Confocal images of RAW 264.7 macrophages transfected with GFP-LC3 and infected for 1 h with wild-type *L. monocytogenes*. (B) Quantification of LC3 colocalization with intracellular wild-type or LLOΔ bacteria over time. (C) Confocal images of RAW 264.7 macrophages transfected with GFP-LC3 and infected for 1 h with wild-type *L. monocytogenes*. Cells were then stained for LAMP1. (D) Quantification of the percentage of LAMP1+ bacteria that are LC3+ or percentage of LAMP1- bacteria that are LC3+. (E) Confocal images of RAW 264.7 macrophages transfected with CBD-YFP and infected for 1 h with wild-type *L. monocytogenes*. Cells were then stained with phallolidin to label F-actin. (F) Quantification of the percentage of CBD-YFP+ bacteria that are actin+. (G) Confocal images of RAW 264.7 macrophages expressing RFP-LC3 and CBD-YFP and infected for 1 h with wild-type *L. monocytogenes*. (H) Quantification of the percentage of LC3+ *L. monocytogenes* that are CBD-YFP+. The inner panels represent a higher magnification of the boxed areas. Size bars: 5 μm. The brightness and contrast for the image (but not the inset) was enhanced to allow visualization of fluorescence inside the cell. (I) Correlative imaging of RAW 264.7 macrophage expressing GFP-LC3 infected with NHS-647 labeled wild-type *L. monocytogenes*. Images of the same cell were captured using either electron microscopy (upper row) or fluorescence microscopy (lower row). Size bars as indicated. Arrowheads indicate single membrane while arrows indicate double membrane. The asterix indicates a multivesicular body.
silencing of \textit{Sqstm1} did not alter LC3 colocalization with bacteria (Fig. 2C). However, siRNA-mediated silencing of \textit{Atg12} showed an expected drop in LC3 recruitment.

Since LC3\textsuperscript{+} \textit{L. monocytogenes} localized to single-membrane compartments that were formed independently of protein ubiquitination and SQSTM1 targeting, autophagy is not likely to be responsible for LC3 localization to the bacteria. Instead, our data imply that LC3 recruitment to \textit{L. monocytogenes} is likely to be mediated via the LAP pathway. Our data are consistent with a model whereby a population of bacteria become trapped in LC3\textsuperscript{+} phagosomes that do not undergo normal maturation steps (e.g., fusion with lysosomes) but rather become SLAPs through continued low level expression of LLO. In support of this model, we previously showed that bacteria in SLAPs do not colocalize with ubiquitinated proteins, indicating they were not exposed to the cytosol.\textsuperscript{20} Furthermore, we showed that monomeric red fluorescent protein expressed in the cytosol was not delivered to the lumen of SLAPs.\textsuperscript{20} Together, these findings suggested that targeting of \textit{L. monocytogenes} by the LAP pathway at 1 h p.i. gives rise to the formation of SLAPs. Our model predicted that host factors promoting LAP targeting of bacteria at 1 h p.i. would also impact on the formation of SLAPs at subsequent stages of infection.

ROS production by the CYBB/NOX2 NADPH oxidase is required for recruitment of LC3 to \textit{L. monocytogenes} at early stages of infection. We previously showed that reactive oxygen species (ROS) production by the CYBB/NOX2 NADPH oxidase is required for the LAP pathway when macrophages are fed IgG-coated latex beads or zymosan particles.\textsuperscript{10} Therefore, we examined the role of ROS in LC3 recruitment to \textit{L. monocytogenes}. We inhibited ROS production via the addition of the NADPH oxidase inhibitor, diphenyliodonium (DPI), which at 1 h p.i. significantly reduced LC3 colocalization with \textit{L. monocytogenes}. LC3 colocalization was also reduced when antioxidants, resveratrol and \( \alpha \)-tocopherol, were added (Fig. 3A). These findings are consistent with a role for ROS in regulating LAP of \textit{L. monocytogenes}.

Next, we examined LC3 recruitment to \textit{L. monocytogenes} in bone-marrow macrophages deficient in CYBB/NOX2 NADPH oxidase activity (\textit{cybb}\textsuperscript{−/−}) (Fig. 3B and C). We found that \textit{cybb}\textsuperscript{−/−} macrophages displayed a significant reduction in LC3 colocalization with wild-type \textit{L. monocytogenes} (Fig. 3B and C). Furthermore, consistent with previous studies,\textsuperscript{16-18} LC3 recruitment to bacteria was dependent on LLO expression. Colocalization of LC3 with LLO\textsubscript{Δ} mutant bacteria was restored upon LLO complementation (Fig. 3C). LLO\textsubscript{Δ} mutant with or without LLO expression did not colocalize with LC3 in \textit{cybb}\textsuperscript{−/−} macrophages.

Previous studies by Webster and colleagues showed that ActA deficient \textit{L. monocytogenes} (ActA\textsubscript{Δ}) are targeted by autophagy in the cytosol after the addition of chloramphenicol (Cm), an agent that blocks bacterial protein synthesis.\textsuperscript{6} Cells were infected with ActA\textsubscript{Δ} mutant bacteria for 3 h, followed by a 5 h treatment with Cm, after which autophagy of bacteria was detected by electron microscopy.\textsuperscript{6} Following a similar protocol of infection and Cm treatment, we observed significant colocalization of LC3 with the ActA\textsubscript{Δ} \textit{L. monocytogenes}, consistent with autophagy of bacteria (Fig. 3D). However, this LC3 colocalization was unaltered when cells were treated with DPI and Cm concomitantly. Thus, ROS production by the CYBB/NOX2 NADPH oxidase plays a key role in LC3 recruitment to \textit{L. monocytogenes} at early stages of infection (1 h p.i.) presumably via LAP, but not in autophagy of ActA\textsubscript{Δ} \textit{L. monocytogenes} in the cytosol at later stages of infection.

ROS production by the CYBB/NOX2 NADPH oxidase is required for spacious \textit{Listeria}-containing phagosomes (SLAPs) formation. Previously, we showed that LC3 recruitment to \textit{L. monocytogenes} at 1 h p.i. is associated with the formation of SLAPs, \textit{L. monocytogenes}-containing compartments that are spacious, neutral pH, nondegradative, LAMP1\textsuperscript{−} and LC3\textsuperscript{+}, and appearing after 4 h p.i.\textsuperscript{20} Formation of SLAPs was found to require bacterial expression of low levels of LLO, insufficient to allow bacterial

Figure 2. Protein ubiquitination and the ubiquitin-adaptor protein p62/SQSTM1 do not mediate LC3 recruitment to \textit{L. monocytogenes} at 1 h p.i. (A) Confocal images of RAW 264.7 macrophages transfected with GFP-LC3 and infected for 1 h with wild-type \textit{L. monocytogenes}. Cells were then stained for ubiquitinated proteins (Ub\textsuperscript{+}). (B) Quantification of the percentage of LC3\textsuperscript{+} \textit{L. monocytogenes} that are Ub\textsuperscript{+} The inner panels represent a higher magnification of the boxed areas. Size bars: 5 \( \mu \)m. (C) Quantification of LC3 colocalization to wild-type \textit{L. monocytogenes} in RAW 264.7 macrophages with siRNA silencing of \textit{Sqstm1} or \textit{Atg12} (positive control). Knockdown was confirmed using sodium dodecyl sulfate polyacrylamide gel electrophoresis (SDS-PAGE).
escape into the cytosol. We proposed that SLAPs represent a “stalemate” between the host and bacteria, allowing slow bacterial replication in SLAPs that may allow persistent L. monocytogenes infection in a host. Indeed, compartments resembling SLAPs have been observed in a mouse model of L. monocytogenes persistent infection. Consistent with the notion that early LC3 recruitment to bacteria leads to SLAP formation, we observed that DPI treatment reduced the formation of SLAPs (Fig. 4A and B). SLAP formation was also decreased in cybb−/− bone marrow-derived macrophages compared with wild-type macrophages (Fig. 4C and D). These findings suggest that ROS-dependent LC3 recruitment to L. monocytogenes may be required for the later formation of SLAPs. Thus, signals that mediate early LC3 recruitment to L. monocytogenes may also be important in determining events that lead to establishment of persistent infection in a host.

Host and bacterial factors promote DAG accumulation on phagosomes containing L. monocytogenes. Next, we examined the signals that are upstream of ROS production by the CYBB/NOX2 NADPH oxidase. Previous studies have shown that L. monocytogenes infection induces diacylglycerol (DAG) production in a manner dependent on the activity of LLO, bacterial PLCs, and host phospholipases. Generation of DAG is upstream of ROS production via the CYBB/NOX2 NADPH oxidase (reviewed by Lam et al.). Therefore, it is conceivable that DAG production on the phagosome may play a role in mediating LAP of L. monocytogenes.

To visualize DAG during L. monocytogenes infection, we employed a fluorescent probe constructed from the DAG binding C1 domain of PKCδ (PRKCD) fused to green fluorescent protein (PRKCD-C1-GFP). The majority (90%) of LC3+ L. monocytogenes were observed to be DAG+ (Fig. 5A). DAG colocalization with L. monocytogenes was observed prior to the peak of LC3 recruitment (Fig. 5B and C), suggesting it may serve as an upstream signal for LAP.

The kinetics of DAG colocalization with L. monocytogenes lacking both PLCs (PI-PLCΔ PC-PLCΔ) was also examined. As shown in Figure 5C, the percentage of DAG+ PI-PLCΔ PC-PLCΔ bacteria was approximately 50% less than wild-type bacteria at 30 min and 45 min p.i. This suggests that bacterial PLCs contribute to DAG production on phagosomes containing L. monocytogenes. However, the decrease in DAG localization to PI-PLCΔ PC-PLCΔ bacteria was not complete, raising the possibility that host factors may also contribute to DAG production. Indeed, host phospholipases were previously shown to contribute to DAG production during L. monocytogenes infection.
DAG production is required for LC3 recruitment to *L. monocytogenes* at early stages of infection. To investigate whether DAG plays a role in mediating LC3 recruitment to *L. monocytogenes*, we examined LC3 recruitment to both wild-type and PI-PLCΔPC-PLCΔ mutants upon treatment with PLD and PPAP2A inhibitors (Fig. 6A). Similar to what we observed with DAG localization in Figure 5D, LC3 recruitment to wild-type *L. monocytogenes* did not change upon PLD or PPAP2A inhibition. In contrast, LC3 recruitment to the PI-PLCΔ PC-PLCΔ mutant was significantly inhibited upon treatment with either the PLD inhibitor (90% decrease) or the PPAP2A inhibitor (73% decrease). This suggests that DAG is important for LC3 recruitment to *L. monocytogenes*. Consistent with these findings, inhibition of DAG turnover via inhibition of DAG kinase (DGK) results in increased DAG and LC3 colocalization to *L. monocytogenes* confirming that the presence of DAG on *L. monocytogenes* containing phagosomes is correlated with LC3 recruitment (Fig. 6B).

To confirm the contribution of PLD-mediated generation of DAG to LC3 targeting, dominant negative constructs for

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**Figure 4.** ROS production and LC3-associated phagocytosis is required for SLAP formation during later stages of infection. ROS production by the CYBB/NOX2 NADPH oxidase is required for the generation of SLAPs. (A) Confocal images of RAW 264.7 macrophages infected for 4 h with wild-type *L. monocytogenes*, with or without DPI. Cells were stained with LAMP1 antibodies. Size bar: 5 μm. White arrowheads indicate spacious *Listeria* phagosomes (SLAPs) while the white arrow indicates LAMP1 colocalization with bacteria that are not in SLAPs. (B) Quantification at 4 h p.i. of the percentage of infected macrophages that form SLAPs in the presence or absence of DPI, resveratrol or α-tocopherol, as indicated. (C) Confocal images of wild-type or *cybb*−/− bone marrow-derived macrophages infected for 8 h with wild-type *L. monocytogenes*. Cells were stained with LAMP1 antibodies. Size bar: 5 μm. White arrowheads indicate SLAPs while the white arrows indicate LAMP1 colocalization and not SLAPs. (D) Quantification at 8 h p.i. of the percentage of infected wild-type or *cybb*−/− bone marrow-derived macrophages that form SLAPs from (C).
both isoforms of PLD (PLD1 and PLD2) were employed (Fig. S1). Similar to the pharmacological evidence, dominant negative forms of PLD reduced DAG recruitment (40 to 62% decrease) as well as LC3 recruitment (60% to 61% decrease) to PI-PLCΔ PC-PLCΔ mutants (Fig. 6C). Taken together, both bacterial and host mediated production of DAG can contribute to LC3 recruitment to L. monocytogenes.

Discussion
In this study, we examined LC3 recruitment to L. monocytogenes during the early stages of infection (1 h p.i.) and how this affects later stages of infection. Our data suggest that LC3 colocalizes with bacteria not as a result of autophagy as previously thought,16,18 but rather by the LAP pathway. This conclusion is supported by the following evidence: (1) the LC3+ population of L. monocytogenes at 1 h p.i. was confined to single-membrane, LAMP1+ phagosomes; (2) LC3+ bacteria were not exposed to the cytosol as judged by a lack of colocalization with F-actin or the cytosolic probe CBD-YFP; (3) ubiquitinated proteins did not colocalize with LC3+ bacteria, as was previously observed for other bacteria targeted by autophagy;2 (4) the ubiquitin-binding autophagy adaptor SQSTM1 was not required for LC3 recruitment to L. monocytogenes though it is required for autophagy of these bacteria within the cytosol;22 (5) ROS production by the CYBB/NOX2 NADPH oxidase was required for LC3 recruitment to bacteria, consistent with previous studies of LAP using model phagosomes containing latex beads or zymosan particles.10 Our study provides a strong argument for LAP as the main pathway for LC3 recruitment to L. monocytogenes at 1 h p.i., although we do not discount the possibility that autophagy may also contribute to LC3 colocalization with bacteria at this early time of infection.

Our data suggests that L. monocytogenes can be targeted by two potentially degradative pathways involving components of the autophagy pathway during infection (see model in Fig. 7), thus serving as a reminder that LC3 must be used carefully as a marker for studies of autophagy. We propose that in the phagosome, bacteria are targeted by the LAP pathway via localized DAG enrichment and downstream ROS production via the CYBB/NOX2 NADPH oxidase (Fig. 7, left-hand pathway). In contrast, cytosolic ActAΔ L. monocytogenes strain 10403S treated with Cm is targeted by autophagy via protein ubiquitination and the recruitment of autophagy adaptors such as SQSTM1 (Fig. 7B, right-hand pathway). This model is consistent with other studies that indicate mammalian cells have evolved multiple pathways that utilize autophagy components to contribute to host immunity (reviewed by Cemma et al.).9 While our study focused on L. monocytogenes infection in macrophages, we expect that both LAP and autophagy will be capable of targeting other bacteria during infection in other cell types. Nonphagocytic cells can also produce ROS but via expression of other members of the NOX/DUOX family (reviewed by Nauseef26) and thus, LAP may be relevant in bacterial infections of all cell types.

Previous studies showed that LAP targets B. pseudomallei mutants lacking its type III secretion system or the type III secreted effector BopA.12 In this case, LC3 recruitment to LAMP1+ phagosomes correlated with enhanced killing of bacteria. In the case of L. monocytogenes, LC3 recruitment to wild-type bacteria strain 10403S correlates with slow growth of bacteria with SLAPs. Our studies imply that bacteria may exploit the LAP pathway and SLAPs to cause persistent infection,20 a model supported by the observation of structures resembling SLAPs in the

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**Figure 5.** Host and bacterial factors promote DAG accumulation on phagosomes containing L. monocytogenes. (A) Confocal images of RAW 264.7 macrophages co-transfected with RFP-LC3 and PRKCD-C1-GFP and infected for 1 h with wild-type L. monocytogenes. PRKCD-C1-GFP is a specific probe for DAG. Size bar: 5 μm. Quantification at 1 h p.i. of the percentage of LC3+ L. monocytogenes that are PRKCD-C1-GFP+. (B) Confocal images of RAW 264.7 macrophages transfected with PRKCD-C1-GFP and infected for 1 h with wild-type, LLOΔ or PI-PLCΔ PC-PLCΔ bacteria. Size bar: 5 μm. (C) Quantification of the percentage of intracellular wild-type, LLOΔ or PI-PLCΔ PC-PLCΔ L. monocytogenes that are DAG+ over time. (D) Quantification at 45 min p.i. of intracellular wild-type or PI-PLCΔ PC-PLCΔ L. monocytogenes that are PRKCD-C1-GFP+ upon treatment with DMSO, 1-butanol, propranolol or tert-butanol.
liver of SCID mice after 28 d of infection. The finding that the CYBB/NOX2 NADPH oxidase contributes to early LC3 recruitment to bacteria and the subsequent formation of SLAPs is intriguing, pointing to a role for this enzyme (and possible other NADPH oxidases) in the establishment and/or maintenance of persistent infections. It is noteworthy that Swanson and colleagues suggest a role for the CYBB/NOX2 NADPH oxidase in restricting phagosome escape by *L. monocytogenes*, possibly by limiting LLO activity. Therefore, ROS production by the CYBB/NOX2 NADPH oxidase may serve a dual function in limiting the activity of bacterial virulence factors and also promoting phagosome maturation. Whether other pathogens exploit the LAP pathway to cause persistent infection is an important question for future studies.

Materials and Methods

Reagents and antibodies. The following drugs were used as indicated: 0.3% v/v 1-butanol (Sigma, B7906), 0.3% v/v tert-butanol (Sigma, 360538), 250 μM propranolol hydrochloride (Biomol International, AR107-0100), 10 μM DGK inhibitor I (Sigma, R59022) and 10 μM DPI (Sigma, D2926). Rabbit polyclonal antibodies against *L. monocytogenes* were a gift from Dr. Pascale Cossart (Institut Pasteur), mouse monoclonal antibodies against GFP were from Invitrogen (A-11120); rat monoclonal antibodies against LAMP1 (clone ID4B) was from Developmental Studies Hybridoma Bank (University of Iowa); and antibodies against mono- and poly-ubiquitinated protein were from Biomol International (FK2; BML-PW8810-0500). All fluorescent secondary antibodies—goat anti-rabbit 405, goat anti-rat Cy3, goat anti-mouse 568, goat anti-mouse 488—were AlexaFluor conjugates from Molecular Probes (Invitrogen, A31556, A10522, A11004, A11029).

Bacterial strains and tissue culture. Bacterial strains used in this study were as follows: wild-type *L. monocytogenes* 10403S38 and isogenic mutants lacking hly (LLOΔ; DP-L2161),39 and plcA, plcB (PI-PLCΔ PC-PLCΔ; DP-L1936). The LLO complementation mutant, LLOΔ + LLO (DP-L4818) was also used.40 RAW 264.7 macrophages were from American Type Culture Collection (TIB-71). RAW 264.7 cells were maintained in DMEM (HyClone, SH30271.01) supplemented with 10% FBS (Wisent, 090-510) at 37°C in 5% CO2 without antibiotics. Macrophages were seeded at 1.25 × 10^5 cells/well 48 h prior to infection. Bone marrow-derived macrophage generation and culture conditions. All experimental protocols involving mice were approved by the Animal Care Committee of The Hospital for Sick Children. Mice were euthanized by cervical dislocation. The femur and tibia were removed, cleansed of muscle fibers and cut distally. The bone marrow was then removed via a 10 sec pulse of centrifugation at 2000 rpm. The resulting cells were centrifuged at 1500 rpm for 5 min, washed with growth media and plated on 10 cm tissue culture dishes. Media was replaced with fresh RPMI growth media (see below) every 3 d. 10^6 bone marrow-derived macrophages (BMDM) were typically recovered after 7 d. Murine macrophages were maintained in RPMI-1640 medium (Wisent, SH3002701) supplemented...
with 10% FBS (Wisent, 090-510), 5% sodium pyruvate (Invitrogen, 11360-070), 5% antibiotics (Invitrogen, 15140122), 5% nonessential amino acids (Invitrogen, 1140050) and 0.5 μM β-mercaptoethanol (Invitrogen, 21985023). BMDMs were differentiated in 30% L929 conditioned media. L929 conditioned medium was generated by growing L929 cells (CCL-1; ATCC) in 150-cm² flasks at an initial density of 1 × 10⁸ cells per flask in growth media as described above. After 3 d, confluence was reached and the growth media was substituted with DMEM alone. After 7 to 10 d, culture supernatant was collected and centrifuged at 1,500 rpm for 5 min, aliquotted and stored at -20°C.

Plasmids, transfections and siRNA silencing. Transfections were performed 24 h prior to infection. Transfection reagents FuGene 6 and FuGene 6 HD (Roche Applied Sciences, 11 815 091 001; 04 709 691 001) were used according to the manufacturer’s instructions. BMDM were transfected using the Amaxa Primary Murine Macrophage Transfection kit according to the manufacturer’s instructions (Amaxa, VPA-1009). Constructs used were GFP-LC3 (provided by Tamotsu Yoshimori, Osaka University, Japan),41 RFP-LC3 (provided by Walter Beron, Universidad Nacional de Cuyo, Argentina), PRKCD-C1-GFP (provided by Sergio Grinstein, Hospital for Sick Children, Canada)42 and HA-PLD1 K898R and HA-PLD2 K758R (provided by Michael Frohman, SUNY, USA).43 siGenome SMARTpool siRNA reagents (Dharmacon) were used for targeting murine Atg12 (GUG GGC AGU AGA GCG AAC A) and Sqstm1 (Dharmacon, D-010230-02) as well as scrambled control siRNA (Dharmacon, M-011020-01).

Bacterial infection conditions. Bacteria were grown in Brain-Heart Infusion (BHI) broth for 14 to 16 h at 30°C in a standing incubator. A 1:10 dilution of the culture was grown for 2 h at 37°C in a shaking incubator prior to infection. Both RAW 264.7 macrophages and BMDM were infected at a multiplicity of infection (MOI) of 10 as described.16

Immunofluorescence and microscopy. Immunostaining was conducted as previously described.44 In brief, after infections, cells were fixed using 2.5% paraformaldehyde for 10 min at 37°C. Extracellular L. monocytogenes were detected by immunostaining prior to permeabilization. Cells were then permeabilized and blocked using 0.2% saponin with 10% normal goat serum for 14 to 16 h at 4°C. All colocalization quantifications were done using a Leica DMIRE2 epifluorescence microscope equipped with a 100× oil objective, 1.4 numerical aperture. 100 intracellular bacteria were examined in each experiment. Images are single confocal z-slices taken using a Zeiss Axiovert confocal microscope and LSM 510 software. Velocity software (Improvision) was used to analyze images. Images were imported into Adobe Photoshop and assembled in Adobe Illustrator.

Light and electron microscopy. RAW 264.7 cells were seeded on grided coverslips and transfected with GFP-LC3. Twenty-four h later, cells were infected with NHS-647 labeled wild-type L. monocytogenes for 60 min as described and cells were washed with 0.2 M sodium cacodylate buffer and fixed with 2.5% paraformaldehyde in sodium cacodylate buffer (all reagents were from
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Acknowledgments

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