Pathogenic, but not non-pathogenic, *Rickettsia* manipulate inflammasome-

dependent IL-1 responses to facilitate their replication and host dissemination.

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Author Contributions

33   O.H.V., M.S.R., and A.F.A. planned the research, analyzed, and interpreted the data;

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Abstract

Rickettsia species (spp.) are strict obligate intracellular bacteria, symbiotic in their

arthropod vector, and some being pathogenic in their mammalian host, including humans.

One critical feature of these stealthy group of pathogens is their ability to manipulate

hostile cytosolic environments to their benefits. Although our understanding of *Rickettsia*

cell biology and pathogenesis are evolving, the mechanisms of host innate immune

defense evasion by pathogenic *Rickettsia* spp. remains to be elucidated. Here, we

showed that disease severity in wild-type (WT) C57BL/6J mice infected with *R. typhi*-

(etiologic agent of murine *typhus*) and *R. rickettsii* (etiologic agent of Rocky Mountain

Spotted Fever), but not with non-pathogenic *R. montanensis*, correlated with levels of

bacterial burden as detected in the spleens, as well as the serum concentrations of pro-

inflammatory cytokine IL-1α and to a lesser extent IL-1β. Antibody-mediated

neutralization of IL-1α confirmed a key role in controlling mortality rates and bacterial

burdens of rickettsiae-infected WT mice. As macrophages are a primary source of both

IL-1α and IL-1β cytokines, we determined the mechanism of the anti-rickettsial activities

using bone-marrow-derived macrophages. We found that pathogenic *R. typhi* and *R.*

rickettsii, but not non-pathogenic *R. montanensis*, induced autophagy, and avoided

autophagolysosomal destruction, while simultaneously eluded pro-IL-1α induction and

benefited from the dampening of IL-1α secretion, via Caspase-11-Gsdmd-dependent

mechanism, to facilitate intracytosolic replication. Adoptative transfer experiments

identified that IL-1α secretion by macrophages was critical for controlling rickettsiosis in

WT mice. In sum, we identified a previously unappreciated pathway by which pathogenic,

unlike non-pathogenic, rickettsiae preferentially target the Caspase-11-Gsdmd-IL-1α

signaling axis in macrophages, possibly via an autophagy-dependent mechanism, to

support their replication and dissemination within the host.

Significance Statement

Currently, no vaccines are available to prevent rickettsioses, and tick- and flea-borne

rickettsial infections in humans are on the rise globally. In fact, the insufficient

understanding of how pathogenic *Rickettsia* species circumvent host immune defense

mechanisms has significantly hindered the development of more effective therapeutics.

Here, we identified a previously unappreciated role for the Caspase-11-Gsdmd-IL-1α

signaling axis, to limiting the survival and dissemination of pathogenic *R. rickettsia* and

R. typhi species in macrophages and wild-type C57BL/6J mice. Adoptative transfer

studies further identified IL-1α-secreting macrophages as critical mediators in controlling

rickettsial infection in WT mice. Collectively, these findings provide insight into the

potential mechanism of how pathogenic, but not non-pathogenic *Rickettsia* spp., become

ubiquitinated, induce autophagy and benefit from the dampening of the Caspase-11-

Gsdmd-mediated release of IL-1α to support host colonization.

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Introduction

Invasive cytosolic bacteria, including *Listeria*, *Shigella*, *Burkholderia*, *Francisella*,

Orientia, and *Rickettsia* species (spp.) have developed strategies to induce their own

uptake by phagocytosis and to circumvent host innate immune defenses for their

intracellular survival (Personnic et al., 2016; Ray et al., 2009). Human infection with

Rickettsia spp. occurs via infected hematophagous arthropods such as ticks, fleas, and

human body lice (Sahni et al., 2018) either through the bite or deposited infected feces

into skin and mucosal surfaces. Upon entry, *Rickettsia* spp. encounter tissue-resident

immune cells, like macrophages (MΦ). Activated MΦ play a crucial role in either

terminating an infection at an early stage, which commonly is the fate of non-pathogenic

Rickettsia spp., or succumbing to bacterial replication and pathogen colonization as well

as host dissemination to distant organs (Sahni et al., 2018). After internalization into host

cells, *Rickettsia* spp. escape from phagosomes and subvert host cytosolic defense

mechanisms (*i.e.*, autophagy and inflammasomes) to establish an intracytosolic

replication niche. Recently, we reported that pathogenic *Rickettsia* spp. secret effectors

to promote host colonization by modulating endoplasmic reticulum structures or by

hijacking the autophagic defense pathway (Lehman et al., 2018; Rahman et al., 2010,

2013; Rennoll-Bankert et al., 2015, 2016; Voss et al., 2020). Subversion of autolysosomal

destruction to colonize the host cytosol exposes *Rickettsia* spp. to another cytosolic host

sensor-regulated defense mechanism, the inflammasomes (Ray et al., 2009; Sun et al.,

2017). Inflammasomes are immune signaling complexes categorized into canonical

[Caspase (Casp)-1] and non-canonical [murine Casp-11 or human Casp-4/5]

inflammasomes. The inflammasome complex assembly involves the adaptor protein ASC

and upstream sensors including NLRP1, NLRP3, NLRC4, AIM2, and pyrin, and is

activated by both exogenous pathogen-associated molecular pattern molecules (PAMPs)

and endogenous damage-associated molecular pattern molecules (DAMPs). Initiation of

the canonical inflammasome results in the activation of Casp-1. Active Casp-1 leads to

the maturation of proinflammatory cytokines IL-1β and IL-18 and the activation of

gasdermin D (Gsdmd), the executor of pyroptosis (Place and Kanneganti, 2018; Xue et

al., 2019). Although IL-1β is released by both canonical and non-canonical inflammasome

pathways, IL-1α is induced preferentially by the non-canonical inflammasome pathway

(Malik and Kanneganti, 2018; Tapia et al., 2019; Wiggins et al., 2019). IL-1α is expressed

by a wide range of hematopoietic and non-hematopoietic cell types, whereas IL-1β is

primarily produced by myeloid cells (Malik and Kanneganti, 2018). Importantly, although

IL-1α and IL-1β signal through the same receptor, IL-1R, these two cytokines are not

completely functionally redundant (Malik and Kanneganti, 2018). Given the importance

for both canonical and non-canonical inflammasome-mediated IL-1 signaling in limiting

pathogen dissemination, many bacteria have evolved strategies to block their activation

(Krakauer, 2019; Mitchell and Isberg, 2017; Seveau et al., 2018; Storek and Monack,

2015; Vladimer et al., 2013; Zheng et al., 2020). In fact, various pathogenic intracellular

bacteria utilize their own effector repertoire to evade these pathways to successfully

replicate and disseminate in their host cells (Sun et al., 2017; Takahama et al., 2018).

In the case of *Rickettsia*, our understanding of the role of inflammasomes in controlling

host colonization is only now emerging (Bechelli et al., 2018; Burke et al., 2020; Engström

et al., 2019; Smalley et al., 2016). Specifically, how pathogenic *Rickettsia* spp. manipulate

immune defenses to replicate within the host cytosol not only relies almost exclusively on

data from tick-transmitted rickettsiae [*e.g.*, members of spotted fever group (SFG) or

transition group (TRG)], but also shows that these pathogens likely employ species-

specific strategies to evade host cytosolic defense mechanisms. For instance, *R.*

australis, a pathogenic TRG member, benefited from ATG5-mediated autophagy

induction and suppression of inflammasome-dependent IL-1β production to colonize both

BMDMΦ (Bechelli et al., 2018) and mice (Rumfield et al., 2020). In contrast, *R. parkeri*, a

mildly pathogenic member of SFG (see Figure 1A), utilizes its surface cell antigen Sca5

(OmpB) for protection against autophagic recognition, and consequently benefits from

inflammasome-mediated host cell death that antagonizes the action of Type I IFN in

BMDMΦ and mice (Burke et al., 2020; Engström et al., 2019). In contrast, our recent

report on the flea-transmitted *R. typhi* [pathogenic member of typhus group (TG)], showed

that *R. typhi* is ubiquitinated upon host entry and escapes autolysosomal fusion to

establish an intracytosolic niche in non-phagocytic cells (Voss et al., 2020). These

unexpected findings on how SFG, TRG, and TG *Rickettsia* differentially promote their

host dissemination prompted us to explore the underlying mechanism(s) by which

pathogenic, but not non-pathogenic, *Rickettsia* spp. manipulate immune defenses to

establish a replication niche in phagocytic cells, like MΦ. Specifically, we sought to test

the hypothesis that pathogenic, but not non-pathogenic, *Rickettsia* spp. induce

autophagy, but evade autophagolysosomal destruction, to dampen inflammasome-

mediated IL-1 responses thereby promoting their intracytosolic replication as well as host

dissemination.

Results

***In vivo* models of rickettsiosis**.

At present, more than 30 *Rickettsia* spp. have been described globally, but less than

a dozen is known to cause disease in humans, with some being notoriously pathogenic

and associated with high morbidity and mortality, while others exert limited or no

pathogenicity (Figure 1A). We sought to test our hypothesis that pathogenic, but not non-

pathogenic, *Rickettsia* spp. manipulate immune responses in host defense cells, like MΦ,

to replicate and disseminate. We simultaneously evaluated the cytosolic host defense

responses between pathogenic [*R. rickettsii (Sheila Smith, SS)* and *R. typhi* (Wilmington)

and non-pathogenic (*R. montanensis*) strains *in vivo*. We first established a mouse model

of mild (~LD_{25}) or more severe (~LD_{50}) rickettsiosis in C57BL/6J WT mice. For both *R.*

rickettsii and *R. typhi* LD_{25} or LD_{50} were achieved with doses of 10^5 or 10^6 PFU,

respectively (Figures 1B-C), however, *R. montanensis*-infected mice showed no signs of

lethality at either 10^5 or 10^6 PFU (Figure 1D), Bacterial burden in spleens from infected

C57BL/6J WT mice (only dose of 10^6 PFU is shown) confirmed successful infection with

all three *Rickettsia* spp. at day 3 post-infection, while *R. typhi*- and *R. rickettsii*-infected

WT mice displayed significantly higher bacterial burden in the spleens as compared to

splenic tissues from *R. montanensis*-infected mice at day 7 (Figure 1E). This correlated

with the observed differences in the spleen sizes and weights of the infected animals

(Figure S1), suggesting more efficient clearance of *R. montanensis* compared to the

pathogenic strains. Given the earlier findings from other laboratories and ours (Bechelli

et al., 2018; Burke et al., 2020; Engström et al., 2019; Papp et al., 2016; Rumfield et al.,

2020; Smalley et al., 2016; Voss et al., 2020), we hypothesized that the observed

dissimilarities in pathogenicity among *Rickettsia* spp. is likely linked to differences in host

defense responses. Recent findings further suggest that the intracytosolic survival of

different *Rickettsia* spp. is either supported or suppressed by immune defense responses

(*e.g.*, IFN-I, TNF-α, or IL-1β) (Bechelli et al., 2018; Burke et al., 2020; Engström et al.,

2019; Papp et al., 2016; Rumfield et al., 2020; Smalley et al., 2016), leaving the precise

mechanism to be determined. Therefore, we first sought to evaluate the canonical and

non-canonical inflammasome responses at the level of IL-1β and IL-1α cytokine secretion

in the sera of *R. typhi*-, *R. rickettsii*-, and *R. montanensis*-infected animals. The increase

in mortality and elevated bacterial burden correlated with reduced serum levels of both

IL-1β and IL-1α cytokines (Figures 1F-G), suggesting that dampening of both canonical

and non-canonical inflammasome-dependent signaling responses is a potential

mechanism for lethality and dissemination of pathogenic *Rickettsia* spp.

Anti-rickettsial activity of IL-1α is involved in restricting *Rickettsia* infection.

To characterize further the role of IL-1α and IL-1β cytokines in restricting non-

pathogenic and pathogenic *Rickettsia* spp. *in vivo*, IL-1α or IL-1β function was neutralized

via tail vein (*i.v.*) injection, with anti(α)-IL-1α, αIL-1β, or αIgG-isotype control antibodies

(Abs) into C57BL/6J WT mice in our established model of mild rickettsiosis (LD$_{25}$; ~10^5

PFU, Figures 1B-D). Neutralization of IL-1α, and to a much lesser extent IL-1β, was

associated with a significant increase in the mortality of *R. typhi-*, *R. rickettsii-*, and *R.*

montanensis-infected mice (Figures 2A-C) and resulted in the development of

splenomegaly (Figure S2), which correlated with an increase in bacterial loads in the

spleen (Figure 2D). The efficiency of Ab-mediated blocking was confirmed by measuring

the levels of IL-1β and IL-1α cytokine in the sera of the rickettsiae-infected mice (Figures

2E-F). Next, we sought to determine the effect of administering recombinant (r)IL-1α or

rIL-1β proteins on *Rickettsia* dissemination *in vivo*. Accordingly, we administered (*i.v.*)

endotoxin-free rIL-1α and rIL-1β proteins following infection with *R. typhi*, *R. rickettsii*, and

R. montanensis. Pretreatment of mice with rIL-1α, and to a lesser extent rIL-1β, protected

C57BL/6J WT mice from pathogenic *Rickettsia*-induced lethality (Figures S3A-C),

significantly reduced development of splenomegaly, and caused a decrease in the

bacterial burden in the spleens of infected animals (Figures S3D-F). Moreover, the

observed phenotypes correlated with the measured IL-1α and IL-1β serum concentrations

(Figures S3G-H). Collectively, these findings suggest that IL-1α, and to a lesser extent,

IL-1β, are involved in restricting the replication and dissemination of non-pathogenic and

pathogenic *Rickettsia* spp.

Pathogenic *Rickettsia* species dampen pro-IL-1α induction and Caspase-11-

dependent IL-1α secretion to establish a replication niche in macrophages.

As MΦ are one of the cell types first encountered during infection by *Rickettsia* spp.

and are considered to play a crucial role in either terminating the infection early at the

skin site or allow pathogen colonization and subsequent dissemination within the infected

host (Sahni et al., 2018), we tested the hypothesis that pathogenic, but not non-

pathogenic, rickettsiae dampen MΦ immune responses. In this effort, we infected

BMDMΦ derived from WT mice with pathogenic *R. typhi* and *R. rickettsii* or non-

pathogenic *R. montanensis* and assessed first the canonical and non-canonical

inflammasome-dependent IL-1 responses. Our assays revealed that *R. typhi*- or *R.*

rickettsii-infected BMDMΦ WT produced lower levels of IL-1β and IL-1α, and showed

significantly lesser induction of host cell death, as compared to *R. montanensis*-infected

BMDMΦ WT (Figures 3A-I, black squares). In addition, the reduced levels of IL-1

responses and host cell death correlated with an elevated bacterial burden (Figure 3J,

black squares). Importantly, and in agreement with our *in vivo* data (Figure 1E), *R. typhi*-

or *R. rickettsii*-infected BMDMΦ WT displayed, over the course of infection, a higher

bacterial burden than *R. montanensis*-infected BMDMΦ WT (Figure 3J, 2 *vs.* 24 h black

squares), suggesting more efficient clearance of *R. montanensis* compared to the

pathogenic strains (Figures 3J and 1E). To determine the importance of IL-1α and IL-1β

in restricting the replication of pathogenic and non-pathogenic *Rickettsia* spp. in MΦ, we

infected BMDMΦ derived from WT, IL-1α-, or IL-1β-deficient mice with all three *Rickettsia*

spp. and assessed the cytokine levels of IL-1β and IL-1α in cultured supernatants as well

as bacterial burdens. As anticipated, infection of IL-1β$^{-/-}$ or IL-1α$^{-/-}$ BMDMΦ with *Rickettsia*

spp. did not result in the secretion of either IL-1β or IL-1α, respectively, when compared

to infected WT BMDMΦ (Figures S4A-F). Moreover, infections with *R. montanensis*

resulted in overall higher IL-1 responses and lower bacterial burden when compared to

infections performed with *R. typhi* or *R. rickettsii* in WT, IL-1β$^{-/-}$, or IL-1α$^{-/-}$ BMDMΦ

(Figures S4A-G). Of note, the bacterial burden of all three *Rickettsia* spp. in infected IL-

$1\alpha^{-/-}$ BMDMΦ was higher than the levels detected in $IL-1\beta^{-/-}$ or WT BMDMΦ (Figures

S4G), suggesting that IL-1α and to significantly lesser extent IL-1β, plays a role in

restricting rickettsiae survival. As our findings suggest that pathogenic, but not non-

pathogenic, *Rickettsia* spp. can dampen IL-1α and IL-1β secretion, we explored the

mechanism of IL-1 signaling responses in greater detail. First, we assessed the protein

expression levels of pro-IL-1β and -IL-1α in WT BMDMΦ upon *Rickettsia* infection and

showed that pro-IL-1β levels were induced by all three *Rickettsia* spp. to similar levels

(~5-fold) when compared to uninfected WT BMDMΦ (Figure S4H). Intriguingly, only *R.*

montanensis-infected WT BMDMΦ produced significantly higher levels of pro-IL-1α, as

compared to *R. typhi-* or *R. rickettsii*-infected MΦ (Figure S4H). As IL-1 signaling

responses require canonical and non-canonical inflammasome pathways, which in turn

involves the proteolytic processing of both cytokines by activated Caspase (Casp)-1

(canonical) and Casp-11 (non-canonical) respectively, we assessed the potential role of

Casp-1 and Casp-11 in regulating replication of non-pathogenic *vs.* pathogenic *Rickettsia*

in BMDMΦ. In this effort, BMDMΦ derived from WT, $Casp-1^{-/-}$, $Casp-11^{-/-}$, and $Casp-1/11^{-}$

$^{/-}$ mice were infected with *R. typhi*, *R. rickettsii*, and *R. montanensis* and the levels of IL-

1β and IL-1α, as well as bacterial burdens, were evaluated over the course of infection.

Our assays revealed that Casp-11 was involved in the secretion of cleaved IL-1α, and to

a lesser extent cleaved IL-1β, upon infection of BMDMΦ with non-pathogenic and

pathogenic *Rickettsia* spp. (Figures 3A-B, D-E, and G-H; $Casp-11^{-/-}$; $Casp-1/11^{-/-}$). In

addition, Casp-11 deficiency resulted in a significant decrease in host cell death (Figures

3C, F, and I). Casp-1 deficiency ($Casp-1^{-/-}$) caused a significant decrease in IL-1β

production [Figures 3A, D, and G (green lines)], while IL-1α secretion as well as the level

of cell death remained unaffected during infection with all three *Rickettsia* spp. [Figures

3B-C, E-F, and H-I (green lines, symbols)]. Analysis of bacterial burdens further revealed

a prominent role for Casp-11, but not Casp-1, in restricting the replication of both

pathogenic and non-pathogenic *Rickettsia* spp. (Figure 3J; WT (square symbols); Casp-

1[-/-] (sphere symbols); Casp-11^{-/-} (triangles symbols); Casp-1/11[-/-] (diamond symbols)]. As

our findings indicate that infections with *R. typhi*- and *R. rickettsii* resulted in a significant

reduction of IL-1α secretion, likely via Casp-11-dependent mechanism, we assessed the

expression and activation status of Casp-1 and Casp-11 via Western blot analyses. As

anticipated, *R. montanensis* infection resulted in a robust activation of Casp-1, as

indicative of the detection of the Casp-1-p20 fragment (Figure 3K). In contrast, infection

with *R. typhi* and *R. rickettsii* spp. resulted in a lower activation of Casp-1 (~5-fold) (Figure

3K). Intriguingly, only infection with *R. montanensis* resulted in a robust induction of Casp-

11 (~8 fold) as compared to infection data using both pathogenic *Rickettsia* spp. (Figure

3K). As IL-1 cytokine secretion dependents on Gsdmd, the pore-forming executor of

pyroptosis (Batista et al., 2020; Kanneganti et al., 2018; Liu et al., 2016; Tsuchiya et al.,

2021), we assessed the proteolytic processing of Gsdmd and showed that only *R.*

montanensis infection resulted in a robust cleavage of Gsdmd (~8 fold), as indicative by

the detection of the Gsdmd-p30 fragment (Figure 3K). In support of our findings, we

showed that infection of Gsdmd^{-/-} BMDMΦ with non-pathogenic and pathogenic

Rickettsia spp. released significantly lower levels of IL-1β and IL-1α, as compared to WT

BMDMΦ (Figures S5A-B). Furthermore, analysis of bacterial burdens provided additional

evidence that Gsdmd plays a role in restricting the replication of *R. typhi*, *R. rickettsii*, and

R. montanensis, (Figure S5C). These findings suggest that pathogenic, unlike non-

pathogenic, *Rickettsia* spp. differentially modulate pro-IL-1 induction and dampen IL-1

cytokine secretion, likely via a Casp-11-Gsdmd-dependent mechanism, to support

replication in MΦ.

Ubiquitination and autophagy induction contribute to the survival of pathogenic

***Rickettsia* species in macrophages.**

Preceding findings suggest that intracellular pathogens, like rickettsiae, not only

encounter inflammasome-dependent defense mechanisms but are also confronted by

another cytosolic defense pathway, autophagy (Bechelli et al., 2018; Smalley et al.,

2016). Both responses not only are key to mount the appropriate host defense responses

(Krakauer, 2019; Seveau et al., 2018) but are also functionally interconnected. In fact,

recent reports indicated that autophagy acts on intracellular microbes upstream of the

inflammasome and thereby functions as a negative regulator by degrading inflammasome

components (Krakauer, 2019; Seveau et al., 2018; Sun et al., 2017; Takahama et al.,

2018). In the case of rickettsiae, however, the role of autophagy in regulating

inflammasome responses to facilitate their host colonization remains inconclusive. For

instance, *R. australis*, a pathogenic TRG member, benefited from ATG5-dependent

autophagy induction and suppression of inflammasome-dependent IL-1β production to

colonize MΦ (Bechelli et al., 2018; Smalley et al., 2016). In contrast, *R. parkeri*, a mildly

pathogenic member of SFG, demonstrated that its surface protein OmpB is critical for

protecting against autophagic recognition, while evasion of autophagy was critical for

invasion of BMDMΦ and WT mice by *R. parkeri* (Burke et al., 2020; Engström et al.,

2019). Intriguingly, our recent report on *R. typhi* showed that *R. typhi* is ubiquitinated upon

host entry, induces autophagy, but escapes autophagolysosomal maturation for

intracellular colonization in non-phagocytic cells (Voss et al., 2020). Given these reports

by others and our recent findings, we hypothesized that pathogenic, but not non-

pathogenic, *Rickettsia* spp. induce autophagy and down-regulate IL-1β and IL-1α

cytokine responses to establish a replication niche in MΦ. To test this hypothesis, we first

evaluated the ubiquitination status of *R. typhi*, *R. rickettsii*, or *R. montanensis*, during

invasion of BMDMΦ derived from WT mice. Our data showed, similar to infection studies

using *R. australis* (Bechelli et al., 2018), both pathogenic *R. rickettsii*, and *R. typhi* strains

were ubiquitinated upon entry into WT BMDMΦ (Figures S6A-B). In contrast, but similar

to infection studies using *R. parkeri*, non-pathogenic *R. montanensis* was not

ubiquitinated during infection of WT BMDMΦ (Figures S6A-B), suggesting that *R.*

montanensis is likely destroyed by phagolysosomal fusion before escaping into cytosol

of MΦ. Furthermore, we evaluated the status of autophagy markers p62 (SQSTM1) and

autophagic vesicle formation marker LC3B (Klionsky et al., 2016) during infection of WT

BMDMΦ by Western blot analyses and showed that, unlike *R. montanensis*, infection with

both pathogenic *Rickettsia* spp. increased autophagic flux, as evidenced by an enhanced

induction of LC3B and the simultaneously down-regulation of p62 expression (Figure

S6C). To further confirm the observation that pathogenic, but not non-pathogenic,

Rickettsia spp. could modulate autophagy flux, we evaluated the status of LC3B

during infection of ATG5$^{fl/fl}$ or ATG5$^{fl/fl}$-LysM-Cre BMDMΦ by immunofluorescence assay

(IFA). We showed that, unlike *R. montanensis*, *R. typhi*, and *R. rickettsii* colocalized with

LC3B upon entry of ATG5$^{fl/fl}$ MΦ, but not in ATG5$^{fl/fl}$-LysM-Cre MΦ (Figures 4A-D). Given

that *R. typhi* was shown to be capable of avoiding autolysosomal destruction in non-

phagocytic cells (Voss et al., 2020), we evaluated the colocalization pattern of rickettsiae

with the lysosomal marker Lamp2 and showed that, unlike non-pathogenic *R.*

montanensis, both *R. typhi*, and *R. rickettsii* spp., did not colocalize with Lamp2 in ATG5^{fl/fl}

MΦ (Figures 4A-D), while all three rickettsiae strains colocalized with Lamp2 in ATG5^{fl/fl}-

LysM-Cre MΦ (Figures 4A-D), suggesting that pathogenic *Rickettsia* spp. abate

autophagosomal maturation. Given these data, we sought to study further the autophagy

induction by *Rickettsia* spp. utilizing an inhibitor of autophagy, 3-methyladenine (3-MA).

Similar to our infection studies using ATG5-deficient MΦ, treatment of WT BMDMΦ with

3-MA significantly decreased the number of LC3B^{+}-bacteria (Figures S7A-G).

Importantly, 3-MA treatment increased the number of Lamp2^{+}-pathogenic rickettsiae

(Figures S7A-G), providing further support to our hypothesis that pathogenic *Rickettsia*

spp. rely on the initiation of autophagy and escape from autophagolysosomal destruction

to establish a replication niche. To test if autophagy was involved in the dampening of the

inflammasome-dependent IL-1 cytokine responses, we evaluated the IL-1β and IL-1α

cytokine levels in cultured supernatants of rickettsiae-infected ATG5^{fl/fl} and ATG5^{fl/fl}-LysM-

Cre BMDMΦ. Lack of autophagy was associated with an increase in the secretion of IL-

1β or IL-1α upon infection with non-pathogenic as well as pathogenic *Rickettsia* spp.

(Figure 4E). Collectively, our data are in agreement with previous reports (Bechelli et al.,

2018; Voss et al., 2020), indicating that, unlike non-pathogenic *R. montanensis* spp., both

pathogenic *R. typhi*, and *R. rickettsii* spp., induce autophagy but avoid

autophagolysosomal destruction, as well as dampen anti-rickettsial inflammasome-

dependent IL-1 cytokine responses during establishment of an intracytosolic replication

niche in MΦ.

Secretion of IL-1α by macrophages is crucial in restricting the survival and

dissemination of pathogenic and non-pathogenic *Rickettsia* species. To examine

whether secretion of IL-1 by MΦ limits the replication of *Rickettsia* spp. *in vivo*, we first

injected (*i.v.*) WT mice with PBS- or dichloromethylene biphosphate (Cl_2MBP)-liposomes

to deplete endogenous macrophages as described previously (Voss et al., 2016). Next,

PBS- or Cl_2MBP-liposomes treated WT mice were injected (*i.v.*) with BMDMΦ isolated

from WT, IL-1β$^{-/-}$, or IL-1α$^{-/-}$ mice prior to infection with *R. typhi*, *R. rickettsii*, or *R.*

montanensis. Strikingly, adoptive transfer of IL-1α$^{-/-}$ BMDMΦ, but not IL-1β$^{-/-}$, or WT MΦ,

significantly increased the mortality of Cl_2MBP- but not PBS-treated WT mice injected

with all three *Rickettsia* spp., reaching levels similar to the survival percentages observed

in IL-1α Ab-neutralization studies (Figures 5A-D, Figures S8A-D and Figure 2). Moreover,

transfer of IL-1α$^{-/-}$ BMDMΦ resulted in the development of splenomegaly (Figures S8E-

F) and an increase in bacterial burden in the spleens of Cl_2MBP-treated WT mice (Figure

5E), which correlated with a decrease in IL-1α serum concentrations without affecting IL-

1β serum levels (Figures 5F-G). In contrast, transfer of IL-1β$^{-/-}$ BMDMΦ, had an overall

lesser effect on the severity of rickettsiosis, as evidenced by a lower mortality rate, smaller

spleen size, and lower bacterial burden in Cl_2MBP-treated WT mice (Figures 5A-D, and

Figure S8), which is in agreement with our IL-1β Ab-neutralization data (Figure 2). In

addition, transfer of IL-1β$^{-/-}$ BMDMΦ, resulted in a decrease in IL-1β serum concentrations

without affecting IL-1α serum levels (Figures 5F-G). In sum, our data presented herein

suggest a model by which pathogenic *Rickettsia* spp. become ubiquitinated, induce

autophagy, and avoid autophagolysosomal destruction, while elude pro-IL-1α induction

and diminish IL-1α secretion, likely by dampening the Casp-11-Gsdmd pathways, to

facilitate intracytosolic replication in MΦ and ultimately cause host dissemination (Figure

5H).

Discussion

Obligate intracytosolic bacterial pathogens, which successfully reside and replicate

within the host cytosol, overcome mechanisms of innate immune defense surveillance,

including inflammasomes and autophagy. However, in the case of strict obligate

intracellular *Rickettsia* spp., the roles for both inflammasome and autophagy to restrict

their replication in endothelial cells and immune cells, like MΦ, is only now emerging,

although without consistent mechanistical insights (Bechelli et al., 2018; Burke et al.,

2020; Engström et al., 2019; Moderzynski et al., 2016; Papp et al., 2016; Rumfield et al.,

2020; Smalley et al., 2016). Given these knowledge gaps and our current lack of

understanding on how TG *Rickettsia* spp. modulate inflammasome and autophagy

pathways to facilitate host dissemination, we established an animal model of rickettsiosis

using C57BL/6J WT mice by comparing both mild ($\sim LD_{25}$) and more severe disease

($\sim LD_{50}$) development for two pathogenic spp., *R. rickettsii*, and *R. typhi*. In fact, data of

disease severity correlated with the levels of bacterial burden detected in the mice

spleens. We also observed that infections with pathogenic, but not non-pathogenic,

Rickettsia spp. resulted in a reduced serum response of both pro-inflammatory cytokines,

IL-1β and IL-1α, which is likely the result of pathogenic *Rickettsia* spp. to evade canonical

and non-canonical inflammasome-dependent defense sensing, of which the former is in

agreement with recent studies using *R. australis* (Rumfield et al., 2020). Thus, our data

suggests that a dampening of both canonical and non-canonical inflammasome-

dependent signaling contributes to the enhanced survival and dissemination of

pathogenic *Rickettsia* spp. in our *in vivo* experiments.

Our data further suggest that IL-1α, and to significantly lower extent IL-1β, plays a role

in limiting rickettsial infection *in vivo*. By testing the putative anti-rickettsial capabilities of

these cytokines through employing Ab-neutralization and recombinant protein assays, we

showed that IL-1α, and to a much lesser level IL-1β, was able to restrict the replication

and dissemination of both non-pathogenic and pathogenic *Rickettsia* spp. *in vivo*. Our

current understanding by which *Rickettsia* spp. evade host-induced anti-bacterial

activities, and in particular, how cytosolic rickettsiae overcome host immune surveillance

in defense cells, like MΦ, is primarily based on inconsistent reports (Bechelli et al., 2018;

Burke et al., 2020; Engström et al., 2019; Smalley et al., 2016). Thus, we sought to

address the hypothesis that pathogenic *R. typhi*, and *R. rickettsii* spp. but not non-

pathogenic *R. montanensis* dampen immune defense responses in order to establish an

intracytosolic replication niche in MΦ. In agreement with our *in vivo* infection models, *R.*

montanensis-infected WT BMDMΦ produced higher levels of IL-1α and IL-1β cytokines

and displayed reduced bacterial loads during the course of infection, compared to *R.*

typhi- or *R. rickettsii*-infected BMDMΦ. These data support the notion that non-

pathogenic, but not pathogenic, *Rickettsia* spp. are more efficiently cleared by MΦ, a

mechanism that further supports the previously published findings with SFG *Rickettsia*

using THP-1 cells, a human macrophage-like cell line (Curto et al., 2016).

After internalization by MΦ, intracellular pathogens encounter host innate defense

mechanisms, notably autophagy and inflammasome-mediated responses (Krakauer,

2019; Seveau et al., 2018). Intriguingly, both pathways are functionally linked, and recent

reports suggest a mechanism by which autophagy acts on intracellular microbes

upstream of the inflammasome and thereby functions as a negative regulator by

degrading inflammasome components (Krakauer, 2019; Seveau et al., 2018; Sun et al.,

2017; Takahama et al., 2018). However, the role of autophagy in controlling host

colonization of *Rickettsia* spp. remained a matter of debate (Bechelli et al., 2018;

Engström et al., 2019). For example, pathogenic *R. australis* benefited from autophagy

induction and suppression of inflammasome-dependent IL-1β secretion to colonize

BMDMΦ (Bechelli et al., 2018), while mildly pathogenic *R. parkeri* utilization of its surface

protein OmpB was critical for its evasion of autophagy and invasion of C57BL/6J BMDMΦ

and WT mice (Burke et al., 2020; Engström et al., 2019). Given that OmpB (Sca5) is

predicted to be expressed in most if not all *Rickettsia* spp. (Voss and Rahman, 2021),

likely implies that the observed OmpB-dependent route of autophagy evasion is a

species-specific mechanism employed by *R. parkeri*. This idea is further supported by

previously published findings for *R. typhi* (Voss et al., 2020) and *R. australis* (Bechelli et

al., 2018), which showed that both pathogenic *Rickettsia* spp. benefited from autophagy

to colonize host cells. In an attempt to decipher the mechanism of host-defense evasion,

we tested if pathogenic, but not non-pathogenic, *Rickettsia* spp. induce autophagy and

down-regulate inflammasome responses to establish a replication niche in MΦ. Our data

reveals that, like *R. parkeri*, non-pathogenic *R. montanensis* is not ubiquitinated during

infection of MΦ, while both pathogenic *R. typhi*, and *R. rickettsii* are ubiquitinated upon

MΦ entry, which is in agreement with reports on pathogenic *R. australis* (Bechelli et al.,

2018). In addition, we showed that, unlike *R. montanensis*, *R. typhi*, and *R. rickettsii*

colocalized with LC3B, but not with the lysosomal marker Lamp2, after MΦ entry.

Importantly, our presented data using the pharmacological inhibitor of autophagy, 3-MA,

or ATG5-deficient MΦ further strengthen our hypothesis that pathogenic, but not non-

pathogenic, *Rickettsia* spp. induce autophagy but avoid autophagolysosomal destruction

and subsequently dampening anti-rickettsial inflammasome-dependent IL-1 cytokine

responses to establish an intracytosolic replication niche in MΦ.

Of interest, our findings also raised another intriguing question as to why pathogenic

R. typhi, and *R. rickettsii* spp. seem to possess the ability to actively induce autophagy,

while non-pathogenic *R. montanensis* did not. As *Rickettsia*-specific immunodominant

outer membrane proteins (*e.g.*, Scas) are predicted to be expressed on either pathogenic

or non-pathogenic *Rickettsia* spp. (Voss and Rahman, 2021), one alternative explanation

is the presence of an effector repertoire that differs depending on the rickettsial

pathogenicity. In fact, we recently reported that pathogenic *R. typhi* induces autophagy

upon infection of non-phagocytic cells, while subsequently avoiding autophagosomal

destruction, via the secretion of its phosphatidylinositol 3-kinase (PI3K) effector,

Rickettsia intracellular secreted kinase-1 (Risk1) and phospholipases (e.g., patatin (Pat)-

1 and -2) (Voss et al., 2020; Voss and Rahman, 2021). This mechanism of host invasion

seems fairly consistent with rickettsial close relatives, such as *Anaplasma*

phagocytophilum and *Ehrlichia chaffeensis* (Lin et al., 2016; Rikihisa, 2017, 2019;

Rikihisa and Lin, 2010), or other intracellular pathogens such as *Shigella* (Campbell-

Valois et al., 2015; Ogawa et al., 2005). So, it is tempting to speculate that effectors, like

Risk1 and Pat1/2 (either alone or in combination with other currently unknown effectors),

could account for the observed phenotypic difference between pathogenic and non-

pathogenic *Rickettsia* spp. However, the precise composition of the effector repertoire for

each *Rickettsia* spp. is currently a matter of active research, and therefore, the precise

mechanism remains to be defined.

Given that IL-1 signaling is modulated through inflammasome-dependent Casp-1,

Casp-11, and Gsdmd activation, we tested the role of both caspases as well as Gsdmd,

and found that non-pathogenic, but not pathogenic, *Rickettsia* spp. ensued Casp-1

activation and Casp-11 induction, which ultimately resulted in the proteolytic processing

of Gsdmd and release of IL-1α and IL-1β cytokines. Intriguingly, the lack of Casp-11

induction by pathogenic, but not non-pathogenic, *Rickettsia* spp. suggest that the

membrane-bound LPS of *R. typhi*, and *R. rickettsii* spp. is less immunogenic than that of

R. montanensis, which is further supported by our recent reports (Guillotte et al., 2018;

Guillotte et al., 2021). Our findings further suggest that pathogenic, as compared to non-

pathogenic, *Rickettsia* spp., benefit from the dampening of the Casp-11-Gsdmd-IL-1α

signaling axis to establish a replication niche in MΦ as evidenced by the increased

replication in MΦ from Casp-11$^{-/-}$, Casp-1/11$^{-/-}$, or Gsdmd$^{-/-}$ mice compared to WT and

Casp-1$^{-/-}$ BMDMΦ. Finally, we sought to determine the role of IL-1 cytokine responses by

MΦ in restricting the replication of *Rickettsia* spp. and showed that transfer of IL-1α$^{-/-}$

BMDMΦ, and to much lesser extent the administration of IL-1β$^{-/-}$ BMDMΦ, exacerbated

the disease progression in WT mice injected with either pathogenic or non-pathogenic

Rickettsia spp. It is worth noting that IL-1α is produced by other immune cells, such as

neutrophils. Although our study did not evaluate a potential contributing role of

neutrophils, preceding findings suggest that neutrophils did not alter the course of

rickettsiosis or contributed to the restriction of bacterial growth (Papp et al., 2016).

Overall, our findings present a previously unappreciated model of host invasion by which

pathogenic, but not non-pathogenic, *Rickettsia* spp. become ubiquitinated, initiate

autophagy, but avoid autophagolysosomal destruction, while elude pro-IL-1α induction

and diminish IL-1α secretion; likely via the dampening of the Casp-11-Gsdmd signaling

pathway, to facilitate their replication in MΦ and ultimately cause host dissemination

(Figure 5H).

Materials and Methods

Animals

All experiments were conducted in fully AAALAC accredited program using 8-10 weeks

old female C57BL/6J WT mice in a specific pathogen-free environment according to the

University of Maryland School of Medicine Institutional Animal Care and Use Committee

(IACUC) in compliance with the National Institutes of Health Guide.

Antibodies and reagents

Anti(α)-IL-1α (clone ALF-161), αIL-1β (clone B122), or an isotype control IgG (Armenian

hamster IgG) antibody (Ab) were purchased from BioXCell. Mono- and polyubiquitinylated

conjugated Ab (FK2) (αUb) was obtained from Enzo Life Sciences. Anti-LC3B (E5Q2K)

Ab was from Cell Signaling Technology. αCaspase (Casp)-1 Ab was purchased from

Adipogen, while αCasp-11 [EPR18628] and αGSDMD [EPR19828] Abs were obtained

from Abcam. Elongation factor Ts (EF-Ts) Ab was obtained from Primm Biotech as

previously described (Voss et al., 2020). The p62 (SQSTM1) Ab, and 3-methyladenine

(3-MA) were purchased from Sigma. LAMP2 (H4B4) and GAPDH (FL-335) Abs were from

Santa Cruz Biotechnology. ProLong Gold antifade mounting medium with DAPI (4′,6-

diamidino-2-phenylindole), paraformaldehyde (PFA), Halt protease and phosphatase

inhibitor cocktail, and Alexa 488/594-conjugated secondary Abs were purchased from

Thermo Fisher Scientific. Endotoxin-free recombinant mouse IL-1α and IL-1β proteins

were purchased from BioLegend.

Bacterial strains, cell culture, and infection

Vero76 cells (African green monkey kidney, ATCC, RL-1587) were maintained in minimal

Dulbecco's modified Eagle's medium (DMEM) supplemented with 10% heat-inactivated

fetal bovine serum (FBS) at 37°C with 5% CO_2. *R. montanensis* strain M5/6 and *R.*

rickettsia strain Sheila Smith (*SS*) were obtained from Dr. Ted Hackstadt (Rocky Mountain

Laboratories, NIH, MT, USA) and *R. typhi* strain Wilmington was obtained from CDC. All

Rickettsia strains were propagated in Vero76 cells grown in DMEM supplemented with

5% FBS at 34°C with 5% CO_2. All *Rickettsia* were purified as previously described

(Rennoll-Bankert et al., 2015). For infection of BMDMΦ, purified *Rickettsia* were used at

a multiplicity of infection (MOI) of 50 for various length of times. Rickettsiosis in mice was

induced by tail vein injection (*i.v.*) of purified *Rickettsia* (10^5-10^6 PFU), resuspended in

PBS. At Days 1, 3, and 7 after administration, blood was collected, and serum cytokine

levels were measured by flow cytometry. Splenic tissue specimens were collected at the

indicated times and used for bacterial burden analysis by qPCR described below.

Differentiation of bone marrow-derived macrophages

Bone marrow cells were isolated from femurs and tibias of WT, ATG5$^{fl/fl}$, ATG5$^{fl/fl}$-LysM-Cre, IL-1α$^{-/-}$, IL-1β$^{-/-}$, Gsdmd$^{-/-}$, Casp-1$^{-/-}$, Casp-11$^{-/-}$, Casp-1/Casp-11$^{-/-}$ mice. Femurs from Casp-1$^{-/-}$, Casp-11$^{-/-}$, Casp-1/Casp-11$^{-/-}$ were kindly provided by Dr. Amal Amer (The Ohio State University, OH, USA), femurs from ATG5$^{fl/fl}$ and ATG5$^{fl/fl}$-LysM-Cre mice were provided by Dr. Christina Stallings (Washington University School of Medicine, MO, USA), while bones from IL-1α$^{-/-}$ and IL-1β$^{-/-}$ mice were obtained from Dr. Thirumala-Devi Kanneganti (St. Jude Children's Research Hospital, TN, USA). Femurs from Gsdmd$^{-/-}$ were kindly provided by Dr. Matthew Welch (University of California, Berkeley, CA, USA). Differentiation was induced by culturing bone marrow cells in RPMI 1640 medium supplemented with 10% FBS and 30% L929-conditioned medium (a source of macrophage colony stimulating factor) and cultured for 7 days as described previously (Voss et al., 2016).

Measurement of cytokines and chemokines

IL-1 cytokine concentrations in the sera of mice or supernatants from cultured BMDMΦ were assessed using the LEGENDplex mouse inflammation kit (BioLegend) following the manufacturer's instructions as described previously (Voss et al., 2016).

RNA isolation and quantitative real-time PCR

BMDMΦ samples were collected at 2, 6, 24, and 48 h post-infection, while spleens were collected at day 3 or 7 post infection. RNA was extracted from 1×10^6 BMDMΦ or 100 µl of organ homogenate using the Quick-RNA miniprep kit (ZymoResearch). The iScript

Reverse Transcription Supermix kit (Bio-Rad; 1708841) was used to synthesize cDNAs

from 200 ng of RNA according to the manufacturer's instructions. Quantitative real-time

PCR was performed using SYBR Green (Thermo Fisher Scientific), 2 μl cDNA and 1 μM

each of the following oligonucleotides for rickettsial citrate synthase gene (*gltA*) forward

(F): 5'-CATAATAGCCATAGGATGAG-3'; reverse (R): 5'-ATGATTTATGGGGAACTACC-

3' and analyzed as described previously (Smalley et al., 2016). Oligonucleotides for

GAPDH were obtained from Qiagen.

Immunofluorescence

Eight-well chamber slides were seeded with BMDMΦ and infected with partially

purified pathogenic and non-pathogenic *Rickettsia* spp. as described previously (Rennoll-

Bankert et al., 2015). Briefly, partially purified *Rickettsia* were added to BMDMΦ and

incubated for various length of time at 34°C with 5% CO_2. Following incubation, cells were

washed three times with 1 x PBS and fixed with 4% paraformaldehyde (PFA) for 20 min

at room temperature. Cells were than permeabilized in blocking buffer (0.3% saponin and

0.5% normal goat serum in 1 x PBS) for 30 min and incubated for 1 h with the following

primary Abs diluted in Ab dilution buffer (0.3% saponin in 1 x PBS): αEF-Ts (1:500), αUb

(1:100), αLC3B (1:100), and αLAMP2 (1:100). Cells were then washed with 1 x PBS and

incubated for 1 h with αAlexa Fluor 594 or αAlexa Fluor 488 secondary Abs diluted

1:1,500 in Ab dilution buffer. Next, cells were washed with 1 x PBS and mounted with

ProLong Gold antifade mounting medium containing DAPI. Images were acquired using

the Nikon W-1 spinning disk confocal microscope (University of Maryland Baltimore,

Confocal Core Facility) and analyzed using Fiji software. Approximately 100 host cells

were enumerated for each experiment and each experiment was repeated five times.

Extract preparation, and Western blot analysis.

Rickettsia-infected BMDMΦ cells were lysed for 2 h at 4°C in ice-cold lysis buffer (50 mM

HEPES [pH 7.4], 137 mM NaCl, 10% glycerol, 1 mM EDTA, 0.5% NP-40, and

supplemented with protease and phosphatase inhibitory cocktails) as described

previously (9). Equal amounts of protein were loaded for SDS-PAGE and membranes

were probed with αp62, αLC3B, αCasp-1, αCasp-11, αGSDMD, αIL-1α, αIL-1β, αEF-Ts,

and αGAPDH Abs, followed by enhanced chemiluminescence with secondary Abs

conjugated to horseradish peroxidase.

Neutralization of endogenous IL-1α and IL-1β

For *in vivo* neutralization of IL-1α and IL-1β, C57BL/6J WT mice were *i.v.* injected with

250 mg of αIL-1α (clone ALF-161, BioXCell), αIL-1β (clone B122, BioXCell), or an IgG-

isotype control (Armenian hamster IgG, BioXCell) Ab 24 h before the induction of mild

rickettsiosis using 10^5 PFU of *R. typhi*, *R. rickettsii*, or *R. montanensis*.

Adoptive transfer of bone marrow-derived macrophages

C57BL/6J WT mice were injected (*i.v.*) twice with PBS- or dichloromethylene biphosphate

(Cl_2MBP)-liposomes 72 and 48 h prior to macrophage transfer as described previously

(Voss et al., 2016). Next, C57BL/6J WT mice were injected (*i.v.*) with WT, IL-1β$^{-/-}$, or IL-

1α$^{-/-}$ BMDMΦ [5 x 10^6 cells/mouse] followed by infection (24 h post-MΦ transfer) with *R.*

typhi, *R. rickettsii*, *R. montanensis*, or PBS (dose 10^5 PFU).

Statistical analysis

Endpoint studies of mice subjected to mild (10^5 PFU) and severe (10^6 PFU) rickettsiosis

were analyzed by using Kaplan-Meir survival curves and the log-rank test (GraphPad

Prism Software, version 8). The statistical significance was assessed using ANOVA with

Tukey's multiple comparisons post-test (GraphPad). Data are presented as mean ± SEM,

unless stated otherwise. Alpha level was set to 0.05.

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Conflicts of Interest

The authors declare no conflict of interest. The funding sources had no role in the design

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Figure Legend

Figure. 1. *In vivo* models of rickettsiosis.

(**A**) *Rickettsia* spp. and their level of pathogenicity to humans (Sahni et al., 2018; Voss

and Rahman, 2021).

(**B-D**) Establishment of a model of rickettsiosis (LD_{25} and LD_{50}) for *R. typhi* [B]*, R. rickettsii*

[C] or *R. montanensis* [D] in C57BL/6J WT mice. Animals were injected via tail vein (*i.v.*)

with different doses [10^5-10^6 PFU] of *R. typhi*, *R. rickettsii*, *R. montanensis*, or PBS (n=12

for each treatment). Survival was monitored for 7 days.

(**E**) Bacterial burden was tested in spleens of *R. typhi*-, *R. rickettsii*-, *R. montanensis*-, or

PBS-injected WT mice (n=5 per each treatment) shown in (B-D) by *GltA* RT-qPCR at day

3 and 7 (n=5 for each treatment) using the host housekeeping gene, *Gapdh*, for

normalization.

(**F-G**) Serum samples from rickettsiae-infected mice described in (B-D) were analyzed for

IL-1β (F) and IL-1α (G) production using the Legendplex kits (BioLegend) followed by flow

cytometry analysis.

Error bars in (E-G) represent means ± SEM from five independent experiments; NS, non-

significant; *$p ≤ 0.05$; **$p ≤ 0.01$; ***$p ≤ 0.001$; ****$p ≤ 0.005$.

Figure. 2. Neutralization of IL-1α activity augments mortality of pathogenic and

non-pathogenic _Rickettsia_-induced rickettsiosis.

(**A-C**) C57BL/6J WT mice were injected via tail vein (_i.v._) with 10^5 PFU of _R. typhi_ [A], _R._

rickettsii [B], _R. montanensis_ [C], or PBS (A-C; n=12 for each treatment) followed by a

subsequent injection (_i.v._) with αIL-1β, αIL-1α or IgG-isotype control antibody (Ab) [250

μg Ab/mouse]. Survival was monitored for 7 days.

(**D**) Bacterial burden was tested in spleens of Ab-treated _R. typhi_-, _R. rickettsii_-, _R._

montanensis-, or PBS-injected WT mice shown in (A-C) by _GltA_ RT-qPCR at day 7 (n=5

for each treatment) using the host housekeeping gene, _Gapdh_, for normalization.

(**E-F**) Serum samples from mice described in (A-C) were analyzed for IL-1β (E) and IL-

1α (F) production at day 7 (n=5 for each treatment) using the Legendplex kits (BioLegend)

followed by flow cytometry analysis.

Error bars in (D-F) represent means ± SEM from five independent experiments; NS, non-

significant; *$p ≤ 0.05$; **$p ≤ 0.01$; ***$p ≤ 0.001$; ****$p ≤ 0.005$.

Figure. 3. Pathogenic, but not non-pathogenic, _Rickettsia_ species limit Caspase-1-

and Caspase-11-dependent IL-1 signaling to facilitate their intracellular replication

in macrophages.

(**A-I**) BMDMΦ from WT, Casp-1$^{-/-}$, Casp-11$^{-/-}$, or Casp-1/11$^{-/-}$ mice were infected with *R.*

typhi (A-C), *R. rickettsii* (D-F) or *R. montanensis* (G-I) [MOI=50] for 0, 6, 24, and 48 h.

Culture supernatants were analyzed for production of IL-1β (A, D, G) and IL-1α (B, E, H)

using Legendplex kits (BioLegend) followed by flow cytometry. BMDM cell death at 24 h

post-infection, was measured by LDH release assay (C, F, I).

(**J**) Bacterial burdens in infected BMDMΦ were evaluated 2 and 24 h post-infection by

GltA RT-qPCR. Expression of the host housekeeping gene *Gapdh* was used for

normalization.

(**K**) Western analysis of Casp-1, Casp-11, and GSDMD induction and processing at 24 h

post-infection with *R. typhi*, *R. rickettsii*, or *R. montanensis* using αCasp-1, αCasp-11, and

αGSDMD antibodies. Reblotting with rickettsial specific αEF-Ts and host cell specific

αGAPDH antibodies served as infection and equal loading controls respectively.

Error bars in (G) represent means ± SEM from five independent experiments; NS: non-

significant; *$p \leq 0.05$; **$p \leq 0.01$; ***$p \leq 0.005$. Immunoblot data are a representative of

three independent experiments.

Figure. 4. Pathogenic *Rickettsia* species induce autophagy and evade

autophagolysosomal destruction to establish a replication niche in macrophages.

BMDMΦ from ATG5$^{fl/fl}$ or ATG5$^{fl/fl}$-LysM-Cre mice were infected with *R. typhi*, *R. rickettsii*,

or *R. montanensis* [MOI=50] for 2 h.

(**A-C**) *Rickettsia*-infected ATG5$^{fl/fl}$ and ATG5-deficient BMDMΦ were fixed with 4% PFA

and *Rickettsia* spp. were detected using the rickettsial specific Alexa Fluor 594-

conjugated EF-Ts, while LC3B, and Lamp2 expression was assessed using Alexa Fluor

488-conjuagted αLC3B, or αLamp2 antibodies respectively.

(**D**) Graphs show the numbers of engulfment of cells in which *Rickettsia* spp. colocalized

with LC3B, or Lamp2. DNA was stained using DAPI (blue). Colocalization data were

analyzed using Coloc 2 plugin Fiji software. Bars in panels A-C, 10 µm.

(**E**) Culture supernatants of *Rickettsia*-infected ATG5$^{fl/fl}$ and ATG5-deficient BMDMΦ were

analyzed 24 h post-infection for the production of IL-1β and IL-1α using Legendplex kits

(BioLegend) followed by flow cytometry.

Error bars (D, E) represent means ± SEM from five independent experiments; NS: non-

significant; *$p \leq 0.05$; **$p \leq 0.01$; ***$p \leq 0.005$.

Figure. 5. Macrophages-dependent secretion of IL-1α contributes more than IL-1β

for controlling the survival and dissemination of pathogenic and non-pathogenic

***Rickettsia* species.**

(**A-D**) Dichloromethylene biphosphate (Cl$_2$MBP)-treated C57BL/6J WT mice were

injected *i.v.* with WT, IL-1β$^{-/-}$, or IL-1α$^{-/-}$ BMDMΦ [5 x 10^6 cells/mouse] followed by infection

(24 h post-MΦ transfer) with *R. typhi* [B], *R. rickettsii* [C], or *R. montanensis* [D] (dose 10^5

PFU) (B-D; n=12 for each treatment). Survival was monitored for 7 days.

(**E**) Bacterial burden was tested in spleens from mice described in (A-D) by *GltA* RT-

qPCR at day 7 (n=5 for each treatment) using the housekeeping gene, *Gapdh*, for

normalization.

(**F-G**) Serum samples from mice described in (B-D) were analyzed for IL-1β (F) and IL-1α (G) production at day 7 (n=5 for each treatment) using the Legendplex kits (BioLegend) followed by flow cytometry analysis.

Error bars in (E-G) represent means ± SEM from five independent experiments; NS, non-significant; *$p \leq 0.05$; **$p \leq 0.01$; ***$p \leq 0.001$; ****$p \leq 0.005$.

(**H**) Proposed working model on how pathogenic *Rickettsia* spp. become ubiquitinated, induce autophagy, and escape autophagolysosomal destruction, while dampen Casp-1 and Casp-11-dependent IL-1 signaling responses to establish a replication niche in MΦ and ultimately causing host dissemination. However, non-pathogenic *Rickettsia* spp. likely get destroyed by phagolysomal fusion that may induce inflammasome mediated IL-1 response.

Fig. S1. Splenic data during infection of pathogenic and non-pathogenic *Rickettsia* species.

(**A**) Representative images of spleens (at day 7) from C57BL/6J WT mice injected *i.v.* with *R. typhi*, *R. rickettsii*, *R. montanensis*, or PBS (dose 10^6 PFU).

(**B**) Spleen weight from injected animals was evaluated at day 7 day (n=5).

Error bars in (B) represent means ± SEM from five independent experiments; *$p \leq 0.05$; ***$p \leq 0.001$.

Fig. S2. Splenic data after IL-1 signaling neutralization during infection of pathogenic and non-pathogenic *Rickettsia* species.

(**A**) Representative images of spleens (day 7) from C57BL/6J WT mice injected *i.v.* with

R. typhi, *R. rickettsii*, *R. montanensis*, or PBS (dose 10^5 PFU) followed by administration

of αIL-1β, αIL-1α, or IgG isotype control antibody (Ab) [250 μg Ab/mouse] (24 h post-Ab

injection).

(**B**) Spleen weight from injected animals was evaluated at day 7 (n=5).

Error bars in (B) represent means ± SEM from five independent experiments; *$p \leq 0.05$;

**$p \leq 0.01$; ***$p \leq 0.001$.

Fig. S3. Administration of recombinant IL-1α rescues fatal *Rickettsia*-induced

rickettsiosis.

(**A-C**) C57BL/6J WT mice were injected *i.v.* with recombinant (r)IL-1β or rIL-1α protein

[500 ng/mouse] followed by infection (24 h post protein injection) with 10^6 PFU of *R. typhi*

[A], *R. rickettsii* [B], *R. montanensis* [C], or PBS (A-C; n=15 for each treatment). Survival

was monitored for 7 days.

(**D**) Bacterial burden was tested in spleens of protein-treated, *R. typhi*-, *R. rickettsii*-, *R.*

montanensis- or PBS-injected WT mice shown in (A-C) by *GltA* RT-qPCR at day 7 (n=5

for each treatment) using the housekeeping gene, *Gapdh*, for normalization.

(**E**) Representative images of spleens from C57BL/6J WT mice injected *i.v.* with rIL-1β or

rIL-1α protein followed by administration of *R. typhi*, *R. rickettsii*, *R. montanensis* or PBS

(dose 10^6 PFU) at day 7.

(**F**) Spleen weight from injected animals was evaluated at day 7 day (n=5).

(**G-H**) Serum samples from mice described in (A-C) were analyzed for IL-1β (G) and IL-

1α (H) production at day 7 (n=5 for each treatment) using the Legendplex kits (BioLegend)

followed by flow cytometry analysis.

Error bars in (D, F-H) represent means ± SEM from five independent experiments; NS,

non-significant; *$p \leq 0.05$; **$p \leq 0.01$; ***$p \leq 0.001$; ****$p \leq 0.005$.

Fig. S4. IL-1α, but not IL-1β, contributes to the survival of *Rickettsia* species in

macrophages.

(**A-F**) BMDMΦ from WT, IL-1β$^{-/-}$, or IL-1α$^{-/-}$ mice were infected with *R. typhi*, *R. rickettsii*,

or *R. montanensis* [MOI=50] for 0, 6, 24, and 48 h. Culture supernatants were analyzed

for production of IL-1β (A, C and E) and IL-1α (B, D and F) using Legendplex kits

(BioLegend) followed by flow cytometry.

(**G**) Bacterial burden in rickettsiae-infected BMDMΦ from WT, IL-1β$^{-/-}$, or IL-1α$^{-/-}$ mice was

evaluated at 2 and 24 h post-infection by *GltA* RT-qPCR. Expression of the housekeeping

gene *Gapdh* was used for normalization.

(**H**) BMDMΦ from WT mice were either left uninfected (-) or infected with *R. typhi*, *R.*

rickettsii, or *R. montanensis*, [MOI=50] for 24 h. Lysates were immunoblotted with αIL-1α,

αIL-1β, αET-Ts, and αGAPDH antibodies. Densitometry was performed using Fiji

software and data represent the fold-change ratios of pro-IL-1β/GAPDH or pro-IL-

1α/GAPDH between uninfected and infected cells are shown. Immunoblot data are a

representative of three independent experiments.

Error bars in (A-G) represent means ± SEM from five independent experiments; NS: non-

significant; *$p \leq 0.05$; **$p \leq 0.01$; ***$p \leq 0.005$; ****$p \leq 0.001$.

Fig. S5. Gsdmd is involved in the release of IL-1α and IL-1b by macrophages upon *Rickettsia* infection.

(**A-B**) BMDMΦ from WT and Gsdmd$^{-/-}$ mice were infected with *R. typhi*, *R. rickettsii*, or *R. montanensis* [MOI=50] for 24 h. Culture supernatants were analyzed for production of IL-1β (A) and IL-1α (B) using Legendplex kits (BioLegend) followed by flow cytometry.

(**C**) Bacterial burden in rickettsiae-infected BMDMΦ from WT and Gsdmd$^{-/-}$ mice was evaluated at 2 and 24 h post-infection by *GltA* RT-qPCR. Expression of the housekeeping gene *Gapdh* was used for normalization.

Error bars in (A-C) represent means ± SEM from five independent experiments; NS: non-significant; *$p \leq 0.05$; **$p \leq 0.01$; ***$p \leq 0.005$.

Fig. S6. Pathogenic, but no non-pathogenic, *Rickettsia* species become ubiquitinated and induces autophagy in macrophages upon infection.

BMDMΦ from WT mice were infected with *R. typhi*, *R. rickettsii*, or *R. montanensis* [MOI=50] for 2 h.

(**A-B**) *Rickettsia*-infected WT BMDMΦ were fixed with 4% PFA, while *Rickettsia* spp. and their ubiquitination status was detected using a rickettsial specific Alexa Fluor 594-conjugated EF-Ts and Alexa Fluor 488-conjuagted αUb antibody respectively.

Graph in (B) shows the numbers of ubiquitin positive (Ub$^+$) engulfment *Rickettsia* spp. DNA was stained using DAPI (blue). Colocalization data were analyzed using Coloc 2 plugin Fiji software. Bars in panel A, 10 μm.

(**C**) BMDMΦ from WT mice were either left uninfected (-) or infected with *R. typhi*, *R.*

rickettsii, or *R. montanensis*, [MOI=50] for 24 h. Lysates were immunoblotted with αp62,

αLC3B, αET-Ts, and αGAPDH antibodies.

Densitometry was performed using Fiji software and data represent the fold-change ratios

of p62/GAPDH or LC3B/GAPDH between uninfected and infected cells are shown.

Immunoblot data are a representative of three independent experiments.

Error bars in (B) represent means ± SEM from five independent experiments; **$p \leq 0.01$.

Fig. S7. Pharmacological modulation of autophagy regulates the ability of

***Rickettsia* species to evade autophagolysosomal destruction and their ability to**

establish a replication niche in macrophages.

(**A-F**) BMDMΦ from WT mice were either left untreated (NT; A-C) or pretreated with 3-

methyladenine (3-MA, 5 mM; D-F) for 1 h followed by *R. typhi*, *R. rickettsii*, or *R.*

montanensis [MOI=50] infection for additional 2 h. *Rickettsia*-infected WT BMDMΦ

[described in (A-F)] were fixed with 4% PFA and *Rickettsia* spp. were detected using a

rickettsial specific Alexa Fluor 594-conjugated EF-Ts Ab, while LC3B, and Lamp2

expression was assessed using Alexa Fluor 488-conjuagted αLC3B, or αLamp2 antibody

respectively.

(**G**) Graph shows the numbers of engulfment of cells in which *Rickettsia* spp. colocalized

with either LC3B, or Lamp2. DNA was stained using DAPI (blue). Colocalization data

were analyzed using Coloc 2 plugin Fiji software. Bars in panels (A-I), 10 µm.

Error bars (G) represent means ± SEM from five independent experiments; NS: non-

significant; **$p \leq 0.01$.

Fig. S8. Survival and splenic data after adoptive transfer of WT, IL-1β$^{-/-}$, or IL-1α$^{-/-}$

macrophages and infection of pathogenic and non-pathogenic *Rickettsia* species

into PBS- or dichloromethylene biphosphate (Cl$_2$MBP)-treated C57BL/6J WT mice.

(**A-D**) PBS-treated C57BL/6J WT mice were injected *i.v.* with WT, IL-1β$^{-/-}$, or IL-1α$^{-/-}$

BMDMΦ [5 x 10^6 cells/mouse] followed by infection (24 h post-MΦ transfer) with *R. typhi*

[B], *R. rickettsii* [C], *R. montanensis* [D], or PBS (dose 10^5 PFU) (B-D; n=12 for each

treatment). Survival was monitored for 7 days.

(**E**) Representative images of spleens (day 7) from PBS- or Cl$_2$MBP-treated C57BL/6J

WT mice injected *i.v.* with WT, IL-1α$^{-/-}$, or IL-1β$^{-/-}$BMDMΦ [5 x 10^6 cells/mouse] followed

by administration (24 h post-MΦ transfer) of *R. typhi*, *R. rickettsii*, *R. montanensis*, or PBS

(dose 10^5 PFU).

(**F**) Spleen weight from injected animals was evaluated at day 7 (n=5).

Error bars in (F) represent means ± SEM; from five independent experiments; NS, non-

significant; *p ≤ 0.05; **p ≤ 0.01.

Fig. 1

Fig. 2

Fig. 3

Fig. 5

A

B C57BL/6 WT

- BMDMΦ WT + *R. typhi*
- BMDMΦ IL-1β⁻/⁻ + *R. typhi*
- BMDMΦ IL-1α⁻/⁻ + *R. typhi*

C C57BL/6 WT

- BMDMΦ WT + *R. rickettsii (SS)*
- BMDMΦ IL-1β⁻/⁻ + *R. rickettsii (SS)*
- BMDMΦ IL-1α⁻/⁻ + *R. rickettsii (SS)*

D C57BL/6 WT

- BMDMΦ WT + *R. montanensis*
- BMDMΦ IL-1β⁻/⁻ + *R. montanensis*
- BMDMΦ IL-1α⁻/⁻ + *R. montanensis*

E C57BL/6 WT Spleen

- BMDMΦ WT + *R. typhi*
- BMDMΦ IL-1β⁻/⁻ + *R. typhi*
- BMDMΦ IL-1α⁻/⁻ + *R. typhi*
- BMDMΦ WT + *R. rickettsii (SS)*
- BMDMΦ IL-1β⁻/⁻ + *R. rickettsii (SS)*
- BMDMΦ IL-1α⁻/⁻ + *R. rickettsii (SS)*
- BMDMΦ WT + *R. montanensis*
- BMDMΦ IL-1β⁻/⁻ + *R. montanensis*
- BMDMΦ IL-1α⁻/⁻ + *R. montanensis*

F C57BL/6 WT

G C57BL/6 WT

- BMDMΦ WT + *R. typhi*
- BMDMΦ IL-1β⁻/⁻ + *R. typhi*
- BMDMΦ IL-1α⁻/⁻ + *R. typhi*
- BMDMΦ WT + *R. rickettsii (SS)*
- BMDMΦ IL-1β⁻/⁻ + *R. rickettsii (SS)*
- BMDMΦ IL-1α⁻/⁻ + *R. rickettsii (SS)*
- BMDMΦ WT + *R. montanensis*
- BMDMΦ IL-1β⁻/⁻ + *R. montanensis*
- BMDMΦ IL-1α⁻/⁻ + *R. montanensis*

H

Fig. 4

Fig. S1

A

C57BL/6 WT
Spleen

B

C57BL/6 WT
Spleen

- PBS
- *R. typhi* (10⁶ PFU)
- *R. rickettsii (SS)* (10⁶ PFU)
- *R. montanensis* (10⁶ PFU)

Fig. S2

A

C57BL/6 WT

Spleen

R. typhi + αIL-1α

R. typhi + αIL-1β

R. typhi + αIgG

R. rickettsii (SS) + αIL-1α

R. rickettsii (SS) + αIL-1β

R. rickettsii (SS) + αIgG

R. montanensis + αIL-1α

R. montanensis + αIL-1β

R. montanensis + αIgG

Day 7

B

C57BL/6 WT

Spleen

R. typhi + αIgG
R. typhi + αIL-1β
R. typhi + αIL-1α
R. rickettsii (SS) + αIgG
R. rickettsii (SS) + αIL-1β
R. rickettsii (SS) + αIL-1α
R. montanensis + αIgG
R. montanensis + αIL-1β
R. montanensis + αIL-1α

Weight (g)

0.4 0.3 0.2 0.1 0

Day 7

Fig. S3

Fig. S4

Fig. S5

A

B

C

Fig. S6

A

BMDMΦ WT + *R. typhi*

| Ub | EF-Ts | MERGE |

BMDMΦ WT + *R. rickettsii (SS)*

| Ub | EF-Ts | MERGE |

BMDMΦ WT + *R. montanensis*

| Ub | EF-Ts | MERGE |

B

- BMDMΦ WT + *R. typhi*
- BMDMΦ WT + *R. rickettsii (SS)*
- BMDMΦ WT + *R. montanensis*

# of Ub⁺-*Rickettsia*

2h

C

BMDMΦ WT

-	+	-	-	*R. typhi*
-	-	+	-	*R. rickettsii (SS)*
-	-	-	+	*R. montanensis*

kDa
62 — p62

Ratio
(p62/GAPDH)   1   0.24   0.13   0.98

16
14 — LC3B

Ratio
(LC3B/GAPDH)   1   4.3   8.2   1.2

36 — EF-Ts

36 — GAPDH

Fig. S7

A *R. typhi* (NT)
LC3B EF-Ts MERGE
LAMP2 EF-Ts MERGE

B *R. rickettsii (SS)* (NT)
LC3B EF-Ts MERGE
LAMP2 EF-Ts MERGE

C *R. montanensis* (NT)
LC3B EF-Ts MERGE
LAMP2 EF-Ts MERGE

D *R. typhi* (3-MA)
LC3B EF-Ts MERGE
LAMP2 EF-Ts MERGE

E *R. rickettsii (SS)* (3-MA)
LC3B EF-Ts MERGE
LAMP2 EF-Ts MERGE

F *R. montanensis* (3-MA)
LC3B EF-Ts MERGE
LAMP2 EF-Ts MERGE

G

# of LC3B⁺ *Rickettsia*
**
**
NS
NS
2h

# of Lamp2⁺ *Rickettsia*
**
**
NS
NS
2h

▲ *R. typhi* (NT)
▲ *R. rickettsii (SS)* (NT)
▲ *R. montanensis* (NT)
■ *R. typhi* (3MA)
■ *R. rickettsii (SS)* (3MA)
■ *R. montanensis* (3MA)

Fig. S8