Bacterial Growth Rate and Host Factors as Determinants of Intracellular Bacterial Distributions in Systemic Salmonella enterica Infections

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Received 24 July 2009/Returned for modification 6 September 2009/Accepted 11 September 2009

Bacteria of the species Salmonella enterica cause a range of life-threatening diseases in humans and animals worldwide. The within-host quantitative, spatial, and temporal dynamics of S. enterica interactions are key to understanding how immunity acts on these infections and how bacteria evade immune surveillance. In this study, we test hypotheses generated from mathematical models of in vivo dynamics of Salmonella infections with experimental observation of bacteria at the single-cell level in infected mouse organs to improve our understanding of the dynamic interactions between host and bacterial mechanisms that determine net growth rates of S. enterica within the host. We show that both bacterial and host factors determine the numerical distributions of bacteria within host cells and thus the level of dispersiveness of the infection.

Bacteria of the species Salmonella enterica are a threat to public health, causing enteric systemic diseases (typhoid and paratyphoid fever), gastroenteritis and nontyphoidal sepsis in humans and similar diseases in many other animal species worldwide. The emergence of multidrug-resistant Salmonella strains and the insufficient efficacy of some of the currently available Salmonella vaccines highlight the urgent need for improved prevention strategies to combat salmonellosis in humans and animals.

S. enterica typhoidal infections have a truly dispersive nature. In mouse infections, the clonal and independent expansion of bacteria derived from the initial inoculum is paralleled by an increase in the number of infected cells and of the multicellular pathological lesions that form at foci of infection (11, 15, 16). Control of the growth and spread of the bacteria requires recruitment and activation of phagocytes at the foci of infection with an influx of bone marrow-derived cells into the tissues and the concerted action of key cytokine networks: tumor necrosis factor alpha, gamma interferon (IFN-γ), and interleukin-12 (IL-12), IL-18 and IL-15 (7–9). In addition, reactive oxygen intermediates and reactive nitrogen intermediates act in phagocytes to control the growth of ingested bacteria (10, 17).

A key feature of the spread of S. enterica in the tissues is the heterogeneous numerical distribution of intracellular bacteria with low bacterial numbers seen at any one time in the majority of infected phagocytes, while a minority of phagocytes can be heavily infected (16). The combination of intracellular bacterial distributional data with “branching process” mathematical models allowed the discrimination of a number of mechanistic hypotheses on the cause of this strikingly skewed distribution of bacteria among host cells (1). In particular, the analysis gave scant support to the hypothesis that highly infected cells were intrinsically more susceptible to infection. Rather, the model supported the idea that all phagocytes were equivalently susceptible and that the skewed distribution was generated by the epidemic spread of the bacteria through the host cell population. The model gave further discrimination at the level of specific characteristics of within-cell bacterial division and cell death, with most support offered for a model with a constant rate of stochastic cell lysis of infected phagocytes, independent of intracellular bacterial numbers, and density-dependent slowing in intracellular bacterial division rates (1).

The use of our mathematical models as analytical platforms which allow us to elicit information about unobserved processes from observed data (1, 3) can be extended to generate and test predictions on the mechanistic bases of microbial and host determinants of bacterial spread and infection dynamics. For example, our previous model (1) predicts faster-growing strains to have distributions of intracellular bacteria that are more skewed toward higher counts. The relationship between bacterial growth and distributional bias can be understood as a consequence of an increase in the risk of host-cell lysis for a given bacterial load in those infections in which the bacteria grow more slowly; under these conditions, the intracellular bacterial load takes longer to reach a given size, so the likelihood of lysis before reaching that size will be greater.

In this report, we test whether variations in net bacterial growth determined by microbial factors or host immune control mechanisms affect intracellular bacterial loads per host phagocyte. The data indicate that intracellular bacterial loads in vivo correlate with the intrinsic growth rate of the bacteria in a given host-pathogen combination and/or experimental condition.
Ablation of host resistance factors affects *S. enterica* distribution: roles of phagocyte NADPH oxidase and IFN-γ. To determine the role of host immunological factors in shaping the intracellular numerical distribution of *S. enterica* cells in the murine liver, we infected mice deficient either in phagocyte NADPH oxidase or in the receptor for the phagocyte-activating cytokine IFN-γ.

During a systemic *S. enterica* infection, reactive oxygen intermediates generated via the phagocyte NADPH-oxidase (phox) are produced at the foci of infection and are highly bactericidal in the early stages of the infection, becoming bacteriostatic as the infection progresses (3, 10, 17). To reveal if the oxidative burst plays an important role in determining the bacterial distributions in host cells, we injected *ggp91phox*−/− phox mice, functionally deficient in the oxidative burst, together with matched wild-type C57BL/6 controls with log10 5.93 CFU of *S. enterica* SL3261. We determined that at 5 days postinfection (p.i.), the mean bacterial load per liver was on average log10 2.2 CFU greater (*P* = 1.47 × 10−9) in the *ggp91phox*−/− phox mice than in the wild-type mice (*ggp91phox*+/+ phox mice, log10 7.81 ± 0.19 CFU; wild-type mice, log10 5.61 ± 0.07 CFU [mean ± standard deviation]). The distributions of the numbers of bacteria per cell were also different between wild-type and *ggp91phox*−/− phox mice (Fig. 1A), with the *ggp91phox*−/− phox phagocytes exhibiting higher bacterial loads on average. We can summarize the relationships depicted in Fig. 1 through the use of odds ratios (ORs). For example, for a single group (e.g., C57BL/6), the odds of having two bacteria per cell relative to one bacteria per cell are simply the number of cells containing two bacteria divided by the number containing a single bacterium. Therefore, the odds give a comparative measure of how likely the two events (two bacteria per cell versus one bacterium per cell) are within each group. If we have more than one group (i.e., C57BL/6 versus *ggp91phox*−/− phox mice), we can use the ratio of the odds between each group to summarize the relative odds.

Therefore, an OR of 1 means that the odds of having two bacteria per cell compared to one bacterium per cell are the same for both the C57BL/6 mice and the *ggp91phox*−/− phox mice. An OR value of <1 would indicate that there is a larger odds of having more bacteria per cell in the knockout mice than in the wild-type mice, and an OR value of >1 indicates the opposite. All ORs in Table 1 are relative to the group containing a single bacterium. The top row in Table 1 shows the trend in higher intrabacterial numbers for the *ggp91phox*−/− phox phagocytes (*P* = 1.07 × 10−7).

IFN-γ is produced by NK cells, T lymphocytes, and macrophages and is important in controlling early *Salmonella* growth in the host, principally via bacteriostatic mechanisms (4, 5, 12, 13). IFN-γR−/− mice, which lack the receptor for IFN-γ signaling, and C57BL/6 wild-type control mice were infected with log10 5.81 CFU of *S. enterica* SL3261. At 12 days p.i., the mean bacterial load per organ was on average log10 3.76 CFU greater (*P* = 9.56 × 10−9) in the IFN-γR−/− mice than in the wild-type mice (IFN-γR−/− mice, log10 9.17 ± 0.05 CFU; wild-type mice, log10 5.41 ± 0.59 CFU [mean ± standard deviation]). The distributions for intracellular bacterial loads between the wild-type and IFN-γR−/− mice are shown in Fig. 1B. The trend in the data (middle row in Table 1) is that the IFN-γR−/− phago-
cytes exhibit higher intrabacterial loads than those from the wild-type mice \( (P < 2.2 \times 10^{-16}) \).

These results indicate that when bacterial growth is accelerated because of the lack of immune control mechanisms in the \( \text{gp91}^{-/-} \text{phox} \) and IFN-\( \gamma R^{-/-} \) mice, the distribution of bacteria within host phagocytes is skewed toward higher numbers of bacteria per cell.

Exacerbation of the net bacterial growth of virulent \( S. \) enterica in host phagocytes results in higher intracellular densities. The experiments described above indicate that exacerbation of the growth of a slow-growing \( S. \) enterica strain (SL3261) due to impairment of the immune system results in increased intracellular numerical distributions. We also know from our previous work that virulent, fast-growing strains show a skew toward higher intracellular intensities than slow-growing attenuated strains (1). Here we wish to address the question of whether further acceleration of the already rapid growth of a virulent strain in innately susceptible mice would result in higher intracellular bacterial densities than those normally seen in virulent infections. To address this question, we used a system in which parenteral coadministration of an attenuated \( S. \) enterica vaccine strain (SL3261) at a high dose can increase the growth rate of a virulent strain (C5) in the tissues (2). This effect is dependent on the release of the immunosuppressive cytokine IL-10 by way of stimulation of Toll-like receptor 4 (TLR4) acting through signaling pathways involving both TRIF and MyD88 adaptor molecules (2).

Mice were injected with log\( _{10} \) 3.17 CFU of nalidixic acid-resistant C5 (“single” infection) or log\( _{10} \) 3.17 CFU of nalidixic acid-resistant C5 and log\( _{10} \) 6.08 CFU of rifampin-resistant SL3261 (“double” infection). We determined that at 3 days p.i., the mean load of C5 per organ in the double-infection mice was greater than that in the single-infection mice: log\( _{10} \) 8.1 CFU and 6.2 CFU, respectively. (At 3 days p.i., the mean load of SL3261 per organ in the double-infection mice was log\( _{10} \) 6.1 CFU.) The ORs and distributions are shown in Table 1, bottom row, and Fig. 1C, respectively. The plot shows a shift toward higher bacterial loads per cell for the double compared to the single infections, backed up by the chi-square test for linear trend \( (P = 4.58 \times 10^{-6}) \). These results suggest that the increased growth rate of the C5 strain in the double infection relates to increased numbers of bacteria per phagocyte.

The work presented in this paper shows that intracellular bacterial loads in vivo increase with the intrinsic growth rate of the bacteria in a given mouse strain. The distribution of intracellular density for a given \( S. \) enterica strain becomes skewed to higher numbers if the infection is performed in immunodeficient animals (e.g., \( \text{gp91}^{-/-} \text{phox} \) and IFN-\( \gamma R^{-/-} \) mice), where

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**TABLE 1.** Differences between groups in the proportion of total infected host CD18\(^{+} \) phagocytes containing various numbers of bacteria as tested by a chi-square test for trend

<table>
<thead>
<tr>
<th>Group comparison</th>
<th>OR for no. of bacteria/phagocyte shown:</th>
<th>( P ) value</th>
</tr>
</thead>
<tbody>
<tr>
<td></td>
<td>1</td>
<td>2</td>
</tr>
<tr>
<td>1</td>
<td></td>
<td></td>
</tr>
<tr>
<td>C57BL/6 vs ( \text{gp91}^{-/-} \text{phox} ) (day 5 p.i.)</td>
<td>0.68</td>
<td>0.69</td>
</tr>
<tr>
<td>C57BL/6 vs IFN-( \gamma R^{-/-} ) (day 12 p.i.)</td>
<td>0.69</td>
<td>0.37</td>
</tr>
<tr>
<td>Single vs double infection (day 3 p.i.)</td>
<td>0.76</td>
<td>0.49</td>
</tr>
</tbody>
</table>

*Each column shows the OR between the groups (i.e., control versus test) relative to one bacterium per cell. The chi-square test for trend assesses the existence of this trend in the ORs.*
the bacteria increase in numbers at a higher rate. S. enterica strains with increased ability to grow in the tissues show distributional patterns skewed toward greater intensities of intracellular infection (i.e., higher numbers of bacteria per cell on average). These intracellular bacterial distributions are consistent with a model in which the burst rate of infected cells is independent of the number or net growth rate of the bacteria within the cells (1). Our findings indicate that subtle interactions between bacteria and the host immune system, in addition to the intrinsic net growth rate of a bacterial strain, determine the spread of Salmonella in the tissues.

ACKNOWLEDGMENTS

We thank J. Blackwell for the breeding pair of gg91Δgp91phox mice and G. Dougan for the IFN-γR−/− mice.

This work was funded by The Wellcome Trust through a Ph.D. training studentship awarded to G.L.F. and supported by a Biotechnology and Biological Sciences Research Council (BBSRC) grant BBS/B/02266 awarded to P.M. and D.J.M. and Medical Research Council (MRC) grant G0801161 awarded to A.J.G., P.M., and D.J.M.

The authors have no conflicting financial interests.

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DYNAMICS IN S. ENTERICA INFECTIONS 5611

Editor: A. J. Bäumler