Single passage in mouse organs enhances the survival and spread of *Salmonella enterica*

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Intravenous inoculation of *Salmonella enterica* serovar Typhimurium into mice is a prime experimental model of invasive salmonellosis. The use of wild-type isogenic tagged strains (WITS) in this system has revealed that bacteria undergo independent bottlenecks in the liver and spleen before establishing a systemic infection. We recently showed that those bacteria that survived the bottleneck exhibited enhanced growth when transferred to naive mice. In this study, we set out to disentangle the components of this *in vivo* adaptation by inoculating mice with WITS grown either *in vitro* or *in vivo*. We developed an original method to estimate the replication and killing rates of bacteria from experimental data, which involved solving the probability-generating function of a non-homogeneous birth–death–immigration process. This revealed a low initial mortality in bacteria obtained from a donor animal. Next, an analysis of WITS distributions in the livers and spleens of recipient animals indicated that *in vivo*-passaged bacteria started spreading between organs earlier than *in vitro*-grown bacteria. These results further our understanding of the influence of passage in a host on the fitness and virulence of *Salmonella enterica* and represent an advance in the power of investigation on the patterns and mechanisms of host–pathogen interactions.

1. Introduction

*Salmonella enterica* is a facultative intracellular pathogen capable of causing a spectrum of diseases in humans and other animals. The cumulative global death toll from non-typhoidal *Salmonella* (NTS) gastroenteritis, NTS bacteremia and typhoid fever is substantial [1]. Current measures to control *S. enterica* infections are suboptimal, and the increasing prevalence of multi-drug-resistant strains threatens to limit treatment options [2]. Consequently, there is a need to develop new therapeutic interventions. Experimental infection of mice with *S. enterica* serovar Typhimurium remains an important source of information about the *in vivo* dynamics of infection for both enteric and systemic salmonelloses. Variations in microbial loads in the organs of animals can be quantified post-mortem by plating homogenized tissues on solid culture medium, and counting the numbers of colony-forming units (CFUs) after incubation. While this method provides accurate estimates of the net growth rates of bacterial populations, it bears no information about the respective rates of the underlying processes of bacterial replication, death and migration. For this purpose, various experimental methods for tracking subpopulations of bacteria have been developed [3]. In particular, the use of wild-type isogenic tagged strains (WITS) has enabled a detailed analysis of the bottlenecks undergone by bacterial populations during the course of infection [4,5]. Libraries of WITS are constructed by inserting specific 40 base pair-long oligonucleotides into a non-coding region of the bacterial chromosome. As a result, within a
library, all WITS are phenotypically identical, but they can be identified by quantitative PCR. As this allows the quantification of multiple WITS in a mixed culture, it is possible to compare the neutral genetic diversity in mice inoculated with the same mixture of WITS. In particular, we recently demonstrated key differences in the killing and spread of S. Typhimurium following immunization of mice with either live or killed vaccines [6].

All WITS experiments consist of infecting mice with a known mixture of tagged wild-type strains and, after a suitable time, recovering the live bacteria from the tissues of interest. The bacteria are then plated for enumeration of CFUs and processed by quantitative PCR (qPCR) in order to assess the relative abundance of the WITS. A critical step in the analysis of these data is the use of mechanistic mathematical models that relate the bacterial numbers and WITS composition to demographic parameters: replication rates, death rates and migration rates. Although the population dynamics of bacteria in single organs can be described with simple stochastic models [4,5], statistical inference on model parameters can rapidly become intractable when movements between multiple compartments are accounted for [6].

Another common point to most published studies of S. enterica in mice—and more generally of any bacterial pathogen in animal models—is that the bacteria in the inoculum have been grown in vitro. This may result in genetic or epigenetic differences with bacteria that would enter the host via natural routes. Our seminal WITS study [4] showed that in vitro-grown S. Typhimurium undergoes high mortality upon entering the liver and spleen; but after a few hours, a drop in bactericidal activity allows bacteria to grow exponentially. Although we showed that the initial control is mediated by the host’s production of reactive oxygen intermediates [4], it is not clear whether the subsequent shift in dynamics is due to bacterial adaptation. In order to better understand the infection dynamics of in vivo-passaged bacteria, we recently compared the dynamics of S. Typhimurium colonization in the organs of mice following inoculation with either standard in vitro-grown bacteria or bacteria freshly extracted from the organs of infected mice [7]. We found that bacteria transferred after spending between 0.5 and 24 h in the donor host grew faster in the recipient host than in vitro-grown bacteria. There was however no apparent change in the initial drop in total bacterial numbers (first 6 h), leading to the hypothesis that in vivo adaptation did not make S. Typhimurium resistant to the early bactericidal activity.

In order to unravel the differences between the kinetics of in vitro-grown and in vivo-adapted S. Typhimurium, we repeated the transfer experiments from [7] using WITS. More specifically, our objective was to answer two questions: does in vivo adaptation affect the initial rates of bacterial replication and death in the liver and spleen? Do in vivo-adapted bacteria start moving between the liver and spleen earlier than in vitro-grown bacteria? We inoculated groups of mice intravenously with inocula comprising of either an even mixture of eight S. Typhimurium WITS grown in vitro, or an even mixture of eight WITS, each of them recovered from the spleen of a donor mouse infected with that single WITS. Organs (liver and spleen) of recipient mice were harvested at 0.5, 6, 24, 48 and 72 h post-inoculation (p.i.), live bacteria from each organ were enumerated on agar plates (figure 1), and the WITS composition determined by qPCR. The early dynamics of infection in each organ were modelled as a continuous-time Markovian process, with transition probabilities governed by three rates: immigration, replication and death.

We then estimated the parameters of this model with respect to the experimental observations at 0.5 and 6 h p.i. using Bayesian statistics. However, instead of resorting to numerical simulation of the dynamic process, as in reference [6], we derived an analytical expression of the probability-generating function (PGF) that led to a faster and more accurate estimation of the likelihood function. A detailed description of the mathematical and computational methods, which contain substantial improvements from [6], is provided in appendix A.

2. Results

2.1. Early dynamics (0–6 h p.i.)

Mice inoculated with in vitro-grown S. Typhimurium received on average 135 bacteria (±10%). After 30 min, we recovered on average 64 CFU from the organs, equally
split between the liver and spleen (resp. 31 and 33 CFU on average, \( n = 5 \) mice). Within 6 h, the average bacterial loads had dropped to 12 in the liver and 29 in the spleen. All eight WITS were recovered from most organs after 30 min (out of five mice, one animal had one WITS missing from its spleen and another animal had two missing from its liver), whereas all organs harvested after 6 h contained three to six WITS (figure 2). In contrast, the average inoculum size of \textit{in vivo}-grown bacteria was around 31 CFU (range 23–40), and we recovered on average 18 CFU after 30 min (60% of which in livers). By 6 h p.i., however, bacterial loads had increased to 20 CFU in livers and 11 CFU in spleens. On average, around five out of eight WITS were recovered from the livers of mice inoculated with \textit{in vivo}-grown bacteria, and under four WITS from the spleens, with no substantial change between 0.5 and 6 h p.i. (figure 2).

We then estimated the parameters of stochastic models of bacterial dynamics relative to the data on WITS frequencies in mouse organs at 0.5 and 6 h p.i. Because individual \textit{S. Typhimurium} bacteria have been shown to form independent foci of infection in mouse organs [8], we modelled the dynamics of a single WITS in a single organ (liver or spleen) governed by immigration from the bloodstream (from a finite inoculum), replication and death. We assumed that replication and death rates remained constant over the period of time considered (6 h).

The results shown in figures 3, 6 and 7 suggest that, within the liver and the spleen, the \textit{per capita} net growth rate during the early period is greater for \textit{in vivo}-grown bacteria than for those grown \textit{in vitro}, with the death rates for the \textit{in vivo} group being less than those for the \textit{in vitro} group.

2.2. Expansion phase (6–72 h p.i.)

In line with our previous study [7], we found that bacterial loads in livers and spleens increased steadily in both experimental groups from 6 to 72 h p.i. (figure 4). The net growth rate during that period was greater for \textit{in vivo}-grown bacteria (average doubling time 4.6 h) than for \textit{in vitro}-grown bacteria (average doubling time 6.3 h). A linear regression of log(CFU) against time confirmed that the difference in growth rates was statistically significant (\( p = 5 \times 10^{-7} \)).

In order to detect spillover of bacteria from the organs back into the bloodstream, we compared the distribution of WITS between the liver and spleen within each mouse. In both experimental groups, the correlation of WITS abundances between the liver and spleen was initially low (and non-significant) for the first 6 h but, by 72 h p.i., the correlation had increased to the point that the bacterial populations in the liver and spleen were virtually indistinguishable (figure 5). However, this increase occurred much...
more rapidly in recipient mice infected with in vivo-grown bacteria than in mice infected with in vitro-grown bacteria. This indicates that spillover started between 6 and 24 h p.i. in the former group and between 24 and 48 h p.i. in the latter group. It is worth noting that, by 24 h p.i., the total bacterial loads in four out of five mice infected with in vivo-grown bacteria had exceeded the bacterial loads in their counterparts (figure 4).

3. Discussion

These results cast a new light on the dynamics of bacterial infection inside hosts. By combining experiments with tagged strains, mathematical models and statistical analysis, we have unravelled two effects of the adaptation of S. Typhimurium to in vivo growth. Following their transfer from infected animals to naive animals, bacteria were not only able to survive the initial bottleneck better than in vitro-grown bacteria, but they also started their systemic spread much earlier (probably 24 h earlier). In particular, we have produced strong evidence against our previous hypothesis that in vivo adaptation had no effect on the initial killing of bacteria upon entering the organs [7]. Instead, we suggest that combined reductions in the replication and death of bacteria in the first 6 h of infection underlie variations in total bacterial numbers similar to those observed in mice infected with in vitro-grown bacteria.

Although the artificial transfer of bacteria from the organs of a donor mouse to the bloodstream of a recipient animal bypasses key steps in the natural route of transmission of a food-borne pathogen, our findings highlight potential pitfalls in experimental models of infection that use in vitro-grown bacteria. Whether S. enterica going through oral–faecal transmission would exhibit the same adaptations as our in vivo-grown strains is not known at this point, but it would be legitimate to expect discrepancies with in vitro-grown bacteria. However, the passage protocol that we followed could bear some resemblance with other routes of infection with S. enterica occurring naturally. Contamination of open wounds with S. enterica is a public health concern in developing countries, and bacterial contamination of blood products, albeit rare, remains a source of deadly S. enterica infection [9].

This study illustrated the benefit of adopting the Bayesian approach to data analysis. In particular, estimation of the posterior probability distributions for the parameters of the
Table 1. Primers used for qPCR.

| primer | tag | sequence 5’ to 3’ |
|--------|-----|-------------------|
| aijg497 | 1   | acgcacaccccacacgtc |
| aijg498 | 2   | acgcacaccccacacgtc |
| aijg503 | 11  | atcacaacaccccacacgtc |
| aijg504 | 13  | gcccaacaccccacacgtc |
| aijg507 | 17  | tcacccaccccacacgtc |
| aijg509 | 19  | gcacccaccccacacgtc |
| aijg510 | 20  | actcacaaccccacacgtc |
| aijg511 | 21  | acgcacaccccacacgtc |
| aijg520 | common | caagggacaccccactggtacgtc |

plates by washing with 2 ml PBS. Bacteria were thoroughly mixed by vortexing, harvested by centrifugation and stored at −80°C prior to DNA extraction.

4.1.5. Determination of wild-type isogenic tagged strains proportions in bacterial samples by qPCR

DNA was prepared from aliquots of bacterial samples using a DNAeasy blood and tissue kit (Qiagen). DNA concentration was determined using a NanoDrop 1000 spectrophotometer (Thermo Scientific). Approximately 10^6 total genome copies were analysed for the relative proportion of each WITS by qPCR using a NanoDrop 1000 spectrophotometer (Thermo Scientific). Approximately 10^6 total genome copies were analysed for the relative proportion of each WITS by qPCR in separate 20 μl reactions (primers; table 1). Reactions contained 10 μl of QuantiTect® SYBR® Green PCR kit reagent (Qiagen), 1 μM each primer, 4 μl sample and DNase-free water to 20 μl. Reaction conditions were 95°C for 15 min, 35 cycles of 94°C for 15 s, 61°C for 30 s and 72°C for 30 s. The copy number of each WITS genome in the sample was determined by reference to standard curves for each primer pair. It was not possible to perform a full standard curve for each primer pair on every rotor; however, individual standards were included on each rotor run to ensure that the values obtained were in the range expected. Standard curves were generated for each batch of PCR reagents by performing qPCRs in duplicate on four separate dilution series of known concentrations of WITS genomic DNA.

4.2. The early-dynamics model and its parameters

During the early period (0–6 h.p.i.), it is assumed that the only events that take place in the liver are the following

\[ \begin{align*}
\text{birth:} & \quad \alpha n^{0,0} \\
\text{death:} & \quad n^{0,0} \to 0. \\
\text{immigration:} & \quad 0 \to n^{0,0} \tag{4.1}
\end{align*} \]

where \( \alpha \) is the birth rate, \( \mu \) the death rate and \( n(t) \) is the rate at which new bacteria feed into the liver from the blood at time \( t \). A similar set of parameters exist for the spleen. No emigration of bacteria from the liver and spleen to the blood takes place during the early period. The master equation for this branching process is (with subscript ‘L’ omitted)

\[
\frac{dP_k(t)}{dt} = \begin{cases} 
\mu (k + 1) P_{k+1}(t) + \alpha (k - 1) P_{k-1}(t) + \nu(t) P_k(t) & \text{if } k > 0, \\
-((\alpha + \mu) k + \nu(t)) P_k(t) & \text{if } k = 0
\end{cases}
\]

\[
(4.1)
\]
where \( P_k(t) \) is the probability of having \( k \) bacteria present at time \( t \).

We can derive an expression for \( v(t) \) in terms of \( t \) as follows. First, the rate with which the expected value of \( X_0 \) in the blood, \( E[X_{\text{blood},t}] \), decreases can be expressed as

\[
\frac{dE[X_{\text{blood},t}]}{dt} = -c_1 E[X_{\text{blood},t}] - c_0 E[X_{\text{blood},t}] = -c E[X_{\text{blood},t}],
\]

(i.e. \( c = c_1 + c_0 \)) where \( c_1 \) and \( c_0 \) are the rate constants for bacteria moving from the blood to the liver and spleen, respectively; consequently,

\[
E[X_{\text{blood},t}] = n_{B0} e^{-ct},
\]

where \( n_{B0} = E[X_{\text{blood},0}] \). We ignore bacterial replication and death in the blood, on the basis that bacteria are known to reside there for a very short period of time (which we checked \( a \) posteriori with our parameter estimates). Given also the uncertainty in inoculum sizes and the lack of data on bacterial loads in the blood, it appeared very unlikely we would be able to recover any information on the values of additional parameters from the data. The rate \( v(t) \) with which bacteria move from the blood to the liver at time \( t \) is proportional to \( E[X_{\text{blood},t}] \) with rate constant \( c_L \),

\[
v(t) = c_L E[X_{\text{blood},t}] ;
\]

therefore, from (4.2),

\[
v(t) = c_L n_{B0} e^{-ct},
\]

from which we have that \( v(t_0) = c_L n_{B0} \). If we let \( \beta_k \) denote \( v(t_0) \), then (4.3) can be rewritten as

\[
v(t) = \beta_k e^{-ct},
\]

where \( \beta_k = v(t_0) \) and \( c \) is an immigration constant. We assume that, for the \( w \)th WITS, \( n_{B0} = m_{wi} \).

An analogous case exists for the spleen, and we will use \( \theta \) to represent the vector of parameters for both liver and spleen:

\[(\alpha_s, \mu_s, \ell_s, \alpha_r, \mu_r, \ell_r, \phi_s)\].

4.2.1. Data

Data were provided from the mouse experiments using \( S. enterica \) WITS grown in vitro or in vivo. The observed data were not the number of WITS \( n \), but the corresponding number \( u \) of CFU; however, for the early-dynamics model, we have used \( u \) as a proxy for \( n \).

For each of the in vitro and in vivo groups, eight WITS were present in the inocula, and the number \( u \) of CFU (and thus the number of WITS \( n \)) present in the liver and spleen 0.5 h and 6 h p.i. were recorded. Five mice were used for each time point.

Let \( m_1, \ldots, m_6 \) denote the frequencies of the eight WITS injected. If \( D_{ji}^{(w)} \) denotes the liver and spleen WITS frequencies from the \( i \)th mouse for time point \( t \) following inoculation

\[
D_{ji}^{(w)} = \{n_{ji}^{(w-1)}, \ldots, n_{ji}^{(w-8)}\} \cup \{n_{wi}, n_{ji}^{(w-1)}, \ldots, n_{ji}^{(w-8)}\},
\]

where \( n_{wi}^{(w-1)} \) is the frequency of the \( w \)th WITS present in the liver of the \( i \)th mouse for time point \( t \), then the total data \( D \) across all mice and time points is

\[
D = D_{1}^{(w)} \cup \cdots \cup D_{s}^{(w)} \cup D_{1}^{(w)} \cup \cdots \cup D_{s}^{(w)},
\]

for both the in vitro and in vivo groups. For each group, there are three estimates of \( m_1, \ldots, m_6 \).

4.2.2. Parameter estimation

Parameters \( \theta \) for both the in vitro- and in vivo-grown \( S. enterica \) Typhimurium can be estimated using Bayesian inference. More precisely, we can estimate the posterior distribution \( p(\theta|D, m_1^{(w)}, \ldots, m_6^{(w)}) \) via the relationship

\[
p(\theta|D, m_1^{(w)}, \ldots, m_6^{(w)}) = \frac{p(\theta)p(D|m_1^{(w)}, \ldots, m_6^{(w)}, \theta)}{\int p(\theta)p(D|m_1^{(w)}, \ldots, m_6^{(w)}, \theta) d\theta} (4.5)
\]

As the mice and WITS are independent of each other, the likelihood \( p(D|m_1^{(w)}, \ldots, m_6^{(w)}, \theta) \) can be factorized as follows

\[
p(D|m_1^{(w)}, \ldots, m_6^{(w)}, \theta) = \prod_{i=1}^{5} p(D_{ji}^{(w)}|m_1^{(w)}, \ldots, m_6^{(w)}, \theta), (4.6)
\]

where

\[
p(D_{ji}^{(w)}|m_1^{(w)}, \ldots, m_6^{(w)}, \theta) = \prod_{w=1}^{W} p(n_{wi}|m_{wi}, \theta) = \prod_{w=1}^{W} \left[ \prod_{i=1}^{5} p(n_{ji}^{(w)}|m^{(w)}_{ji}, \theta) \right]. (4.7)
\]

Consequently, determining the posterior probability distribution requires the estimation of \( p(n_{ji}^{(w)}|m^{(w)}_{ji}, \theta) \) for each \( n_{ji}^{(w)} \in D \).

This is described in appendix A.

A robust method for the estimation of the denominator of (4.5) is Markov chain Monte Carlo (MCMC)-based nested sampling [12]. Here, the multivariate integral in the denominator of (4.5) is equated to the univariate integral \( \int \phi^{-1}(\xi) d\xi \), where \( \phi^{-1}(\xi) \) is that likelihood \( \lambda \) such that \( p(\xi|\theta_0) > \lambda \). In contrast to the multivariate integral, the univariate integral can be readily estimated by standard numerical methods.

Nested sampling is a sequential process. Starting with a population of particles \( \{ \xi \} \) drawn from the prior distribution \( \pi(\theta) \), the point \( \theta_{\min} \) with the smallest likelihood \( \lambda_{\min} \) is recorded along with the associated probability \( \xi \). Point \( \theta_{\min} \) is then replaced by a new point drawn randomly (via MCMC) from the restricted prior \( \pi(\theta|\xi > \lambda_{\min}) \). As this process is repeated, the population of points moves progressively higher in likelihood, and the associated restricted priors are nested within each other. The resulting sequence of points \( \{ \lambda_{\min}, \xi \} \) produces the plot required for \( \int \phi^{-1}(\xi) d\xi \).

A drawback of the original version of nested sampling is that it will underestimate the integral if a likelihood function is multimodal. Feroz et al. [13] developed a version of nested sampling that can cope with multimodal likelihood functions, but Brewer et al. [14] designed a computationally more elegant approach to this problem called diffusive nested sampling.

Rather than confining sampling to a succession of nested restricted priors, diffusive nested sampling uses one or more particles to explore a mixture of nested priors, with each successive distribution occupying about \( e^{-1} \) times the enclosed prior mass of the previous distribution. This not only allows lower (earlier) levels to be resampled to improve accuracy, but also allows sampling across multimodal likelihood functions. We performed diffusive nested sampling with 10,000 iterations of a single particle and a maximum of 30 nested levels. For the sake of computational expediency, parameter space was restricted to \([0,2]\) for each parameter. The uniform prior was used. This parameter space was sufficiently large to illustrate the differences of interest between the posterior distributions in spite of the truncation of \( c_i \) in figure 6f.

In order to monitor the progress of the estimation of \( p(\theta|D, m_1^{(w)}, \ldots, m_6^{(w)}) \), posterior distributions based on subsets of \( D \) were used: \( p(\theta|D_{1:5}^{(w)}, D_{6}^{(w)}, m_1^{(w)}, \ldots, m_6^{(w)}) \). These distributions, computed from likelihood \( p(\theta|D_{1:5}^{(w)}, D_{6}^{(w)}, m_1^{(w)}, \ldots, m_6^{(w)}) \), required less time to compute but could be estimated in parallel to each other and then combined as described in appendix A.

The resulting posterior probability distributions for parameters \( \alpha_s, \mu_s, \ell_s, \alpha_r, \mu_r, \ell_r, \phi_s \) associated with the in vitro and in vivo groups are shown in figures 6 and 7. Posterior \( p(\xi|D, m_1^{(w)}, \ldots, m_6^{(w)}) \) for parameter \( \xi \in \{\alpha_s, \mu_s, \ell_s, \alpha_r, \mu_r, \ell_r, \phi_s\} \) was produced by averaging the posteriors obtained with
 respect to the three inoculum sizes used for each group (figures 8 and 9). Separation between the in vitro and in vivo distributions for parameter $\xi$ is measured by AUC, which is equal to the probability that $\xi$ randomly chosen from the in vivo distribution will be less than $\xi$ randomly chosen from the in vitro distribution.

Kaiser et al. [15] have also modelled birth–death–immigration in order to estimate parameters but they used a more simplified model regarding immigration. In contrast, we allowed for the fact that immigration is inhomogeneous as there is a finite number of bacteria immigrating from the bloodstream into the organs. Furthermore, their parameters were estimated using maximum-likelihood without taking into account parameter uncertainties.

Table 2 lists the resulting mean values for the parameters contained in $\theta$ according to $p(\xi, m_1, \ldots, m_9)$.

**Ethics.** All animal work was approved by the ethical review committee of the University of Cambridge and was licensed by the UK Government Home Office under the Animals (Scientific Procedures) Act 1986.
Authors’ contributions. A.J.G. conceived and planned the experiment. A.J.G. and P.M. performed the experimental work. A.J.G., P.M. and D.J.M. obtained the funding for the experimental work. A.J.G., R.D. and O.R. analysed the data. R.D., A.G. and O.R. developed the Bayesian model. A.J.G., R.D., O.R., P.M., D.J.M. contributed to the writing of the manuscript.

Competing interests. We declare we have no competing interests.

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Appendix A. The probability of a number of bacteria

The following sections describe the steps taken to derive an expression for the number of bacteria \( n \) at time \( t \) starting from a PGF. Figure 10 highlights the main steps of the derivation.

A.1. Probability-generating function

Our approach to the estimation of \( p(n|m, \theta) \) has been to use a PGF.

A PGF for the branching process can be defined as

\[
G(z, t) = \sum_{n=0}^{\infty} z^n p(n|m, \theta),
\]

where \( z \) is a real or complex number. A virtue of using a PGF is that, in principle, probabilities can be extracted from PGFs by differentiation; for example, in the case of (A 1), we have

\[
p(n|m, \theta) = \left. \frac{\partial^n}{\partial z^n} G(z, t) \right|_{z=0}.
\]

The following partial differential equation can be derived from (A 1) (theorem A.2):

\[
\frac{\partial}{\partial t} G(z, t) = [\alpha(t) - \mu(t)](z - 1) G(z, t) + \nu(t)(z - 1) G(z, t).
\]

If there is no immigration (i.e. \( \nu(t) = 0 \)) and the branching process begins from a single particle (i.e. \( X_0 = 1 \)), then (A 3) can be solved [16] to give

\[
G(z, t) = 1 + \frac{1}{e^{\sigma(t)} - 1 - \int_0^t \alpha(\tau) e^{\sigma(\tau)} d\tau}
\]

where \( \sigma(t) = \int_0^t [\mu(\tau) - \alpha(\tau)] d\tau \).

In order to allow for immigration (i.e. \( \nu(t) > 0 \)), we consider a single bacterium appearing in the liver from the
If we denote the PGF for this delayed process by \( G(z, t, u) \) for \( t < u \), then we can derive an expression for \( G(z, t, u) \) in a manner analogous to that for (A 4), in which the lower limits for the integrals of (A 4) and definition of function \( \sigma(t) \) are replaced with \( u \):

\[
G(z, t, u) = 1 + \frac{1}{e^{\sigma(t)} / (z - 1) - \int_0^t \alpha(\tau) e^{\sigma(\tau)} d\tau}, \quad (A 5)
\]

where

\[
\sigma(t, u) = \int_u^t [\mu(\tau) - \alpha(\tau)] d\tau. \quad (A 6)
\]

According to reference [16], we can write the PGF for when \( X_0 = \xi \) as follows

\[
H(z, t|\xi) = E[z^X|X_0 = \xi] = G(z, t, 0)\exp \left\{ \int_0^t [G(z, t, u) - 1]v(u) du \right\}. \quad (A 7)
\]

**Figure 9.** Box plots of the component distributions used for the posterior distributions for (a) \( \alpha_S \), (b) \( \mu_S \) and (c) \( c_S \) shown in figure 7.

**Table 2.** Mean values and 95% credible intervals (highest probability density intervals) for parameters \( a_L, \mu_L, \alpha_L, \alpha_S, \mu_S \) and \( c_S \) associated with the in vitro and in vivo groups. Values are restricted to the interval \([0, 2]\) for each parameter. Uniform prior distributions over \([0, 2]\) were used for every parameter.

| parameter | meaning                  | mean and 95% HPD interval in vitro | mean and 95% HPD interval in vivo |
|-----------|--------------------------|-----------------------------------|-----------------------------------|
| \( \alpha_L \) | birth rate in liver       | 0.758 (0.10 – 1.25)               | 0.486 (0.10 – 0.97)               |
| \( \mu_L \)  | death rate in liver       | 1.187 (0.58 – 1.86)               | 0.433 (0.06 – 1.06)               |
| \( \alpha_S \) | birth rate in spleen      | 0.793 (0.26 – 1.38)               | 0.404 (0.06 – 1.06)               |
| \( \mu_S \)  | death rate in spleen      | 1.041 (0.43 – 1.70)               | 0.429 (0.06 – 1.06)               |
| \( c_S \)    | blood-to-spleen rate      | 0.850 (0.35 – 1.34)               | 0.852 (0.15 – 1.66)               |

blood not at time 0 but at some later time \( u > 0 \). If we denote the PGF for this delayed process by \( G(z, t, u) \) for \( t < u \), then we can derive an expression for \( G(z, t, u) \) in a manner analogous to that for (A 4), in which the lower limits for the integrals of (A 4) and definition of function \( \sigma(t) \) are replaced with \( u \).
Use probability generating function $G(z, t)$ (Equation ▶ pending ▶)

Re-express $G(z, t)$ as expectation $H(z, t(z))$ (Equation ▶ pending ▶)

Approximate inversion of $H(z, t(z))$ using Cauchy contour integral (Equation ▶ pending ▶)

Result is $\tilde{p}(X = nX_0 = \xi)$ (Equation ▶ pending ▶)

**Figure 10.** The main steps taken for deriving an expression for the number of bacteria $n$ at time $t$ starting from a probability generating function. $\xi$ is the number of bacteria when $t = 0$, and $z$ is a real or complex number.

We can solve (A 7) by letting the birth and death rates be constant over time, as follows.

Let $\alpha(t) = \alpha$ and $\mu(t) = \mu$, then (A 6) becomes

$$
\sigma(t, u) = \int_0^t \mu(\tau) - \alpha(\tau) \, d\tau = \int_0^t (\mu - \alpha) (t - u),
$$

and the integral of (A 5) becomes

$$
\int_0^t \alpha(\tau) e^{\sigma(\tau)} \, d\tau = \int_0^t \alpha e^{(\mu-\alpha)(t-u)} \, d\tau = \frac{\alpha}{\mu - \alpha} e^{(\mu-\alpha)(t-u)} - 1.
$$

This results in (A 5) becoming

$$
G(z, t, u) = 1 + \frac{1}{e^{(\mu-\alpha)(t-u)} / (z - 1) - \alpha / (\mu - \alpha) e^{(\mu-\alpha)(t-u)}} - 1
$$

$$
= 1 + \frac{(z - 1)(\mu - \alpha) e^{(\mu-\alpha)(t-u)}}{\mu - az + \alpha(z - 1) e^{(\mu-\alpha)(t-u)}},
$$

(A 8)

From (A 8) and (4.4), we can write the integral of (A 7) as

$$
\int_0^t [G(z, t, u) - 1] \nu(u) \, du = \frac{\beta e^{-\alpha(\xi)} (z - 1)(\mu - \alpha) e^{(\mu-\alpha)(t-u)}}{\mu - az + \alpha(z - 1) e^{(\mu-\alpha)(t-u)}} \, \nu(u) \, du,
$$

(A 10)

from which we can derive the expression (theorem A.3)

$$
\int_0^t [G(z, t, u) - 1] \nu(u) \, du = \frac{\beta e^{-\alpha(\xi)} (z - 1)(\mu - \alpha) e^{(\mu-\alpha)(t-u)}}{\mu - az + \alpha(z - 1) e^{(\mu-\alpha)(t-u)}} \, \nu(u) \, du,
$$

(A 11)

Finally, substituting (A 9) and (A 11) into (A 7) leads to the relationship

$$
H(z, t|\xi) = \left( 1 + \frac{(z - 1)(\mu - \alpha) e^{(\mu-\alpha)t}}{\mu - az + \alpha(z - 1) e^{(\mu-\alpha)t}} \right)^\xi
$$

$$
\times \exp \left\{ \frac{\beta e^{-\alpha(\xi)} (z - 1)(\mu - \alpha) e^{(\mu-\alpha)t}}{\mu - az + \alpha(z - 1) e^{(\mu-\alpha)t}} \right\} F_1 \left( 1, \frac{-c}{\mu - \alpha} + 1; \frac{-c}{\mu - \alpha} + 2, \frac{\alpha(z - 1) e^{(\mu-\alpha)t}}{az - \mu} \right)\right\}
$$

(A 12)
A.2. Inversion of the probability-generating function

Extracting probabilities from PGFs is called inversion, and in the case of PGF $H(z, t|\xi)$, we have

$$p(X_t = n|X_0 = \xi) = \frac{1}{n!} \frac{\partial^n}{\partial z^n} H(z, t|\xi) \bigg|_{z = 0}. \quad (A\,13)$$

Although inversion of a PGF via differentiation is analytically correct, it can be a formidable task to undertake, depending on the complexity of the PGF. An alternative approach is to use the inversion formula based on the Cauchy contour integral [17],

$$p_n(t) = \frac{1}{2\pi i} \oint_{\Gamma} G(z, t) e^{-z t} dz, \quad (A\,14)$$

where $i = \sqrt{-1}$ and $\Gamma$ is a closed contour around 0 in the disc of convergence. If we choose $\Gamma$ to be a circle of radius $r (0 < r < 1)$ and use the change of variable $z = re^{it}$, then [17]

$$p_n(t) = \frac{1}{2\pi r n!} \int_0^{2\pi} G(re^{it}, t) e^{-rn\,e^{it}} \, dt. \quad (A\,15)$$

A trapezoidal approximation of the integral in (A15) leads to the following approximation of $p_n(t)$ [17]

$$\hat{p}_n(t) = \frac{1}{2\pi r n!} \sum_{j=0}^{2n-1} G(re^{j\pi/n}, t) e^{-j\pi r t}, \quad (A\,16)$$

with error $\varepsilon = p_n(t) - \hat{p}_n(t)$ given by

$$\varepsilon = \sum_{j=0}^{2n} p_n(1 + 2j/r)(t) r^{2j/n}. \quad (A\,17)$$

Here, $\ell$ is an integer to control the round-off error, and we can set $\ell = 1$ [18,19]. The error is related to the radius $r$ of the disc of convergence for (A14) by [17, 18]

$$\varepsilon \leq \frac{r^{2n}}{1 - r^{2n}}. \quad (A\,17)$$

If $r$ is sufficiently small such that (A17) becomes $\varepsilon \leq r^{2n}$, then we will have $\varepsilon \leq 10^{-8}$ when $r = 10^{-n/2n}$ [17].

We can reduce the computation of (A16) by a factor of 2 by taking the real-valued part of it [17–19]

$$\hat{p}_n(t) = \Re \left\{ \frac{1}{2\pi r n!} \sum_{j=0}^{2n-1} G(re^{j\pi/n}, t) e^{-j\pi t} \right\}$$

$$= \frac{1}{2\pi r n!} \Re \left( \sum_{j=0}^{2n-1} G(re^{j\pi/n}, t) e^{-j\pi t} \right)$$

$$= \frac{1}{2\pi r n!} \left\{ G(r, t) + (-1)^n G(-r, t) + 2 \sum_{j=1}^{n-1} (-1)^j R(G(re^{j\pi/n}, t)) \right\}. \quad (A\,18)$$

In the context of conditional probability $p(X_t = n|X_0 = \xi)$ and PGF $H(z, t|\xi)$, (A18) becomes

$$p(X_t = n|X_0 = \xi) = \frac{1}{2\pi r n!} \left\{ H(r, t|\xi) + (-1)^n H(-r, t|\xi) + 2 \sum_{j=1}^{n-1} (-1)^j R(H(re^{j\pi/n}, t|\xi)) \right\}. \quad (A\,19)$$

A.3. Combining posterior probabilities

Because of the probabilistic independences present within the data, we were able to combine posterior distributions of the form $p(\theta|D_{0,5}, D_{0,5}, m^{[1]}, \ldots, m^{[k]})$ by application of theorem A.1

$$p(\theta \in \Phi|D_{0,5}, m^{[1]}, \ldots, m^{[k]}) = k p(\theta \in \Phi)^{-1}$$

$$\times \prod_{i=\{1,2,3,4\}} \prod_{j=\{4,3,2,1\}} p(\theta \in \Phi|D_{0,5}, D_{0,5}, m^{[1]}, \ldots, m^{[k]}),$$

where $\Phi$ is a path-connected subset of parameter space and $k$ is the normalization constant. Note that any permutation of $\{1, 2, 3, 4\}$ could be used for $j$.

A.4. Accuracy

The expected number of bacteria at time $t$ is given by

$$E[X_t|X_0 = \xi] = \sum_{n=0}^{\infty} np(X_t = n|X_0 = \xi),$$

but it is also given by

$$E[X_t|X_0 = \xi] = \frac{\partial}{\partial z} G(z, t) \bigg|_{z = 1},$$

and if $E[X_0] = \xi$, then (theorem A.4)

$$E[X_t|X_0 = \xi] = (\xi + f) e^{(\alpha - \mu)t} - f e^{-ct},$$

where $f = \beta/(c + \alpha - \mu)$.

An assessment of the accuracy of using (A19) can be made by comparing the true expected value based on

$$E_{true}[X_t|X_0 = \xi] = (\xi + f) e^{(\alpha - \mu)t} - f e^{-ct},$$

with the expectation estimated using those values of $p(X_t = n|X_0 = \xi)$ obtained from (A19)

$$E[X_t|X_0 = \xi] = \sum_{n=0}^{\infty} np(X_t = n|X_0 = \xi).$$

As an example of such a comparison, the expected values obtained when using $\alpha_1 = 0.394$, $\mu_1 = 0.804$, $c_1 = 0.704$ and $n_{B,0} = 124$ were

$$E_{true}[X_t|X_0 = 0] = 21.02081255 \quad \text{and} \quad E[X_t|X_0 = 0] = 21.02081257.$$

Theorem A.1. Let $\theta$ be a point in parameter space and $\Phi$ a path-connected subset of that space. Let $A_1, \ldots, A_S$ be sets of data that are independent of each other given $\theta \in \Phi$, then

$$p(\theta \in \Phi|A_1, \ldots, A_S) = kp(\theta \in \Phi)^{1-S}$$

$$\times \prod_{i=1}^{S} p(\theta \in \Phi|A_i), \quad (A\,20)$$

where $k$ is the normalization constant.
From the master equation (4.1), we have

\[ p(\theta \in \Phi | A_1, \ldots, A_s) = \frac{p(\theta \in \Phi)p(A_1, \ldots, A_s) \theta \in \Phi)}{Z_{1-s}}, \quad (A21) \]

where \( Z_{1-s} \) is a normalization constant ensuring that \( \sum_{\theta} p(\theta \in \Phi | A_1, \ldots, A_s) = 1 \). Now,

\[ p(\theta \in \Phi | A_s) = \frac{p(\theta \in \Phi)p(A_s | \theta \in \Phi)}{Z_s}, \quad (A23) \]

where \( Z_s \) is a normalization constant, thus,

\[ p(A_s | \theta \in \Phi) = \frac{Z_s p(\theta \in \Phi | A_s)}{p(\theta \in \Phi)}. \quad (A24) \]

Proof.

[16, p. 201] Consider the PGF \( G(z, t) = \sum_{k=0}^{+\infty} z^k P_k(t) \).

From the master equation (4.1), we have

\[ \frac{\partial G}{\partial t} (z, t) = \sum_{k=0}^{+\infty} z^k \frac{dP_k(t)}{dt} = \sum_{k=0}^{+\infty} z^k \left( \mu(k+1)P_{k+1}(t) + \alpha(k-1)P_{k-1}(t) + \beta e^{-\alpha} P_k(t) - ((\alpha + \mu)k + \beta e^{-\alpha})P_k(t) \right), \]

and then

\[ \frac{\partial G}{\partial t} (z, t) = \sum_{k=0}^{+\infty} z^k \mu(k+1)P_{k+1}(t) + \sum_{k=0}^{+\infty} z^k \alpha(k-1)P_{k-1}(t) + \sum_{k=0}^{+\infty} z^k \beta e^{-\alpha} P_k(t) \]

\[ - \sum_{k=0}^{+\infty} z^k \beta e^{-\alpha} P_k(t) \]

\[ = \mu \frac{\partial G}{\partial z} (z, t) + \alpha z \frac{\partial G}{\partial z} (z, t) + \beta e^{-\alpha} zG(z, t) - (\alpha + \mu)z \frac{\partial G}{\partial z} (z, t) - \beta e^{-\alpha} G(z, t). \]

Hence, the differential equation

\[ \frac{\partial G}{\partial t} (z, t) = (\alpha z - \mu)(z - 1) \frac{\partial G}{\partial z} (z, t) + \beta e^{-\alpha}(z - 1) G(z, t). \quad (A26) \]

Note: In the above proof, we can use \( \alpha(t) \) in place of \( \alpha \) and \( \mu(t) \) in place of \( \mu \).

Lemma A.1.

\[ \int_0^1 \phi(t)(1-t)^n (1-xt)^b dt = B(b+1, c+1)_{\alpha} \psi \phi(-a, b) \]

\[ + b + c + 2; x). \quad (A27) \]

where \( B(a, b) \) is the beta integral and \( \psi \phi \) is the hypergeometric function given by

\[ B(a, b) = \int_0^1 t^{a-1}(1-t)^{b-1} dt, \]

\[ \psi \phi(a, b; c; x) = \sum_{k=0}^{+\infty} (-a)_k (b)_k \frac{x^k}{k!}. \]

Proof. Because

\[ (1-xt)^b = \sum_{k=0}^{+\infty} \left( \begin{array}{c} a \\ k \end{array} \right) (-xt)^k = \sum_{k=0}^{+\infty} (-a)_k \frac{x^k}{k!}, \quad (A28) \]

we have

\[ \int_0^1 \phi(t)(1-t)^n (1-xt)^b dt = \sum_{k=0}^{+\infty} (-a)_k \frac{x^k}{k!} \int_0^1 \phi(t)(1-t)^n dt. \quad (A29) \]

Now

\[ B(b+k+1, c+1) = \frac{\Gamma(b+k+1)\Gamma(c+1)}{\Gamma(c+b+k+2)} \]

\[ = \frac{(b+k)_k \Gamma(b+1)\Gamma(c+1)}{(c+b+2)_k} \]

\[ = \frac{(b+k)_k B(b+1, c+1)}{(c+b+2)_k} \]

hence

\[ \int_0^1 \phi(t)(1-t)^n (1-xt)^b dt = B(b+1, c+1)_{\alpha} \phi(-a, b) \]

\[ + b + c + 2; x). \quad (A30) \]
Theorem A.3.

\[
\int_0^t [G(z, t, u) - 1] \nu(u) du = B e^{-ct}(z-1)(\alpha - \mu) \left( \frac{1}{\mu - \alpha} \right) 2F_1 \left( 1, \frac{-c}{\mu - \alpha} + 1; \frac{-c}{\mu - \alpha} + 2; \frac{\alpha(z - 1)}{\alpha z - \mu} \right) - e^{(\alpha - \mu + c)t} 2F_1 \left( 1, \frac{-c}{\mu - \alpha} + 1; \frac{-c}{\mu - \alpha} + 2; \frac{\alpha(z - 1)e^{(\alpha - \mu)t}}{\alpha z - \mu} \right).
\]

Proof. We have

\[
\int_0^t [G(z, t, u) - 1] \nu(u) du = \int_0^t \beta e^{-ct}(z-1)(\mu - \alpha) e^{(\alpha - \mu)(t-u)} (\mu - \alpha)(z-1)[1 - e^{(\alpha - \mu)(t-u)}] du.
\]

Consider the variable change \( x = e^{(\alpha - \mu)(t-u)} \), so that \( u = (1/(\mu - \alpha)) \log(x) + t \) and \( dx = (\mu - \alpha) x du \), then

\[
\int_0^t [G(z, t, u) - 1] \nu(u) du = \int_0^1 \beta e^{-ct} x e^{(\alpha - \mu)(z-1)} x(1 + \alpha(z - 1) x) \left( 1 + \psi \right)^{-1} dx,
\]

where \( \psi = \alpha(z - 1)/(\mu - \alpha) \).

To compute (A31), we can use the identity (lemma A.1)

\[
\int_0^1 (1-t)^x (1-xt)^y dt = B(b+1, c+1)_{2}F_1(-a, b+1; b+c+2; x),
\]

as follows

\[
\frac{\beta e^{-ct} \psi}{\alpha} \int_0^1 x^{(\alpha - \mu)(z-1)}(1 + \psi x)^{-1} dx = \int_0^1 x^{(\alpha - \mu)(z-1)}(1 + \psi x)^{-1} dx - \int_0^1 x^{(\alpha - \mu)(z-1)}(1 + \psi x)^{-1} dx
\]

\[
= \frac{\beta e^{-ct} \psi}{\alpha} \left( \int_0^1 x^{(\alpha - \mu)(z-1)}(1 + \psi x)^{-1} dx - \int_0^1 y^{(\alpha - \mu)(z-1)}(1 + \psi y)^{-1} dy \right)
\]

\[
= \frac{\beta e^{-ct} \psi}{\alpha} B \left( \frac{-c}{\mu - \alpha} + 1, 1 \right) _2F_1 \left( 1, \frac{-c}{\mu - \alpha} + 1; \frac{-c}{\mu - \alpha} + 2; - \psi \right)
\]

Finally, given that

\[
B \left( \frac{-c}{\mu - \alpha} + 1, 1 \right) = \frac{\alpha - \mu}{c + \alpha - \mu},
\]

we have

\[
\int_0^t [G(s, t, u) - 1] \nu(u) du = \frac{\beta e^{-ct}(s-1)(\alpha - \mu)}{\mu (s - \alpha)} (c + \alpha - \mu) _2F_1 \left( 1, \frac{-c}{\mu - \alpha} + 1; \frac{-c}{\mu - \alpha} + 2; \frac{\alpha(s - 1)}{\alpha s - \mu} \right) - e^{(\alpha - \mu + c)t} 2F_1 \left( 1, \frac{-c}{\mu - \alpha} + 1; \frac{-c}{\mu - \alpha} + 2; \frac{\alpha(s - 1)e^{(\alpha - \mu)t}}{\alpha s - \mu} \right).
\]

Theorem A.4.

The expected number of bacteria at time \( t \) is given by

\[
E[X_t] = (\xi + f) e^{(c + \alpha - \mu)t} - f e^{-ct},
\]

\[
\frac{\partial}{\partial s} G(z, t) = \sum_{n=0}^{\infty} p_n(t) n z^{n-1},
\]

where \( f = \beta/(c + \alpha - \mu) \).

Proof. From the PGF of the branching process (A1), we have
thus
\[ \frac{\partial}{\partial t} G(z, t) \bigg|_{t=1} = \sum_{n=0}^{\infty} \nu_p(t) = E[X_1], \quad (A35) \]
hence
\[ \frac{\partial}{\partial t} E[X_1] = \frac{\partial}{\partial t} \left( \frac{\partial}{\partial z} G(z, t) \bigg|_{t=1} \right) = \frac{\partial^2}{\partial t \partial z} G(z, t) \bigg|_{t=1}. \quad (A36) \]
Now, if rates $\mu$ and $\alpha$ are assumed to be constant over time, and $v(t)$ is written as $\beta e^{-\lambda t}$ (4.4), then (A3) can be written as
\[ \frac{\partial}{\partial t} G(z, t) = (\alpha z - \mu)(z - 1) \frac{\partial}{\partial z} G(z, t) + \beta e^{-\lambda t}(z - 1)G(z, t), \]
in that case
\[ \frac{\partial^2}{\partial t \partial z} G(z, t) = \frac{\partial}{\partial z} \left( \frac{\partial}{\partial z} G(z, t) \right) = (\alpha z - 1) \frac{\partial}{\partial z} G(z, t) + (\alpha z - \mu) \frac{\partial^2}{\partial z^2} G(z, t) + \beta e^{-\lambda t} G(z, t) + \beta e^{-\lambda t} \]
\[ \times (z - 1) \frac{\partial}{\partial z} G(z, t); \]
therefore
\[ \frac{\partial^2}{\partial t \partial z} G(z, t) \bigg|_{t=1} = (\alpha - \mu) \frac{\partial}{\partial z} G(z, t) \bigg|_{t=1} + \beta e^{-\lambda t} G(1, t) \bigg|_{t=1} = (\alpha - \mu) \frac{\partial}{\partial z} G(z, t) \bigg|_{t=1} + \beta e^{-\lambda t}, \]
because $G(1, t) = 1$. From (A35) and (A36), we can rewrite this as the differential equation
\[ \frac{d}{dt} E[X_1] = (\alpha - \mu)E[X_1] + \beta e^{-\lambda t}. \quad (A38) \]
Solving (A38) as a first-order differential equation gives
\[ E[X_t] = \varphi e^{(\alpha - \mu)t} - \frac{\beta e^{-\lambda t}}{c + \alpha - \mu}, \quad (A39) \]
where $\varphi$ is a constant. This constant can be dealt with as follows. If $\xi$ is the initial number of bacteria, then $E[X_0] = \xi$, consequently, setting $t$ in (A39) equal to 0 gives
\[ \varphi = \xi + \frac{\beta}{c + \alpha - \mu}, \]
and the resulting expression for the expected number of bacteria at time $t$ is
\[ E[X_t] = (\xi + f) e^{(\alpha - \mu)t} - f e^{-\lambda t}, \quad (A40) \]
where $f = \beta/(c + \alpha - \mu)$.

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