Need for CD8 T cell clusters to eliminate a malaria liver stage arises in part due to heterogeneity in killing efficacy of individual effector T cells

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Abstract

Vaccination strategies in mice inducing high numbers of memory CD8 T cells specific to a single epitope are able to provide sterilizing protection against infection with Plasmodium sporozoites. We have recently found that Plasmodium-specific CD8 T cells cluster around sporozoite-infected hepatocytes but whether such clusters are important in elimination of the parasite remains incompletely understood. Here we used our previously generated data in which we employed intravital microscopy to longitudinally image 32 GFP-expressing Plasmodium yoelii parasites in livers of mice that had received activated Plasmodium-specific CD8 T cells after sporozoite infection. We found great heterogeneity in the dynamics of the normalized GFP signal from the parasites (termed "vitality index" or VI) that was weakly correlated with the number of T cells near the parasite. We also found that a simple model assuming mass-action, additive killing by T cells well describes the VI dynamics for most parasites predicting highly variable killing efficacy of individual T cells. Given the estimated median per capita kill rate of $k = 0.031$/h we predict that a single T cell is typically incapable to kill the the parasite within 48 hour lifespan of the liver stage. Stochastic simulations of T cell clustering and killing of the liver stage also suggested that 1) three or more T cells per liver stage are required to ensure sterilizing protection; 2) both variability in killing efficacy of individual T cells and resistance to killing by individual parasites may contribute to the observed variability in VI decline, and 3) stable VI of some clustered parasites cannot be explained by measurement noise. Taken together, our analysis for the first time provides estimates of efficiency at which individual CD8 T cells eliminate intracellular infection in vivo.

Keywords: CD8+ T cell, Plasmodium sporozoites, liver stages, intravital imaging, mathematical modeling

Abbreviations: Py - Plasmodium yoelii, GFP - green fluorescent protein, VI - vitality index, DDR - density-dependent recruitment.

1 Introduction

Malaria is a mosquito-born disease caused by parasites from genus Plasmodium; the Plasmodium parasites of humans are responsible for more than 200 million infections and 500,000 deaths annually [1]. Infection starts when mosquitoes inject sporozoites (a specific stage of Plasmodium parasites) into dermal tissue [2]. The sporozoites move in the tissue, find blood vessels, invade into the blood vessels, and disseminate in the body with the blood. Some sporozoites invade the liver, infect hepatocytes and form liver stages. It takes approximately 2 days (in mice) or 6-7 days (in humans) for liver stages to develop into merozoites (another stage of malaria parasites) [3]. Merozoites infect red blood cells and ultimately cause clinical symptoms of malaria. Several vaccine candidates aim at preventing the disease; some of these aim at removing all liver stages by inducing large numbers of Plasmodium-specific memory CD8 T cells [4–6].

Multiple strategies have been used to generate large numbers of Plasmodium-specific CD8 T cells including priming mice with dendritic cells (DCs) coated with Plasmodium peptides and boosting with Listeria monocytogenes (LM), expressing Plasmodium peptides, immunization with radiation-attenuated sporozoites (RAS), and adoptive transfer of in vitro activated CD8 T cells [4, 7–12]. While these strategies have shown good protection following exposure to Plasmodium sporozoites (e.g., [4, 13]), specific mechanisms by which vaccine-induced CD8 T cells find the inflected cells and critical parameters required for parasite's killing such as the number and duration of CD8 T cell contacts with parasitized cells, remain largely unknown.

Intravital microscopy has been used to gain quantitative insights into the process by which CD8 T cells kill their targets in vivo. In particular, as far as we are aware, Mempel *et al.* [14] were the first to directly observe killing of targets (peptide-pulsed B cells) by CD8 T cells in vivo. Interestingly, the authors found that formation of the conjugate between the T cell and its target eventually resulted in arrest of the target cell movement and indication of the target cell death within 20-30 min after initial contact [14]. In contrast, killing of cancer cells by adoptively transferred activated CD8 T cells on average took 6 hours [15]. As far as we are aware we were the first to document kinetics of killing of individual parasitized cells by CD8 T cells in vivo [16]. In that study by using intravital microscopy we followed the kinetics of formation of clusters of Plasmodium-specific CD8 T cells around Plasmodium liver stages in murine livers; interestingly, a formation of larger clusters (3 or more cells present within 40 μm of the parasite) was associated with a higher chance of parasite's death during the imaging period [16]. Also, based on the kinetics of the loss of fluorescence signal from the GFP-expressing parasites we observed four different patterns of parasite's death but the actual killing kinetics was not quantified [16]. Recent work extended our observations to CD8 T cell-mediated killing of virus-infected cells suggesting that after initial contact, it takes on average 30 minutes for the T cell to kill its target [17]. Interestingly, while the initial analysis suggested that there may be cooperation between individual CD8 T cells bound to the same virus-infected cells, further analysis suggested that such a conclusion may be an artifact of the data analysis that ignored prolonged "zombie" contacts of CD8 T cells with already dying targets [17, 18]. Another study suggested that killing of cancer cells may require several contacts by the same or different CD8 T cells occurring within a short (< 1 h) time period [19].

Following our previous work here we provide comprehensive quantitative analysis of the data on the kinetics of CD8 T cell-mediated killing of Plasmodium liver stages. In these experiments we could accurately monitor the number of Plasmodium-specific CD8 T cells located in the vicinity of GFP-expressing liver stages and "health" of the liver stages (indicated by the relative magnitude of

the GFP signal) for several hours for 32 individual parasites [16]. Most of the liver stages (24/32) had at least a single CD8 T cells nearby at some point of imaging, and our recently developed density-dependent recruitment model of T cell cluster formation could reasonably well describe the kinetics of accumulation of Plasmodium-specific CD8 T cells near individual parasites over time. By fitting a simple mathematical model to the VI decline data we found that per capita killing efficiency of Plasmodium-specific CD8 T cells in vivo varied dramatically between different parasites. Interestingly, we did not find any evidence that CD8 T cells cooperate in parasite's killing as the basic, mass action-based model could describe the data well for most parasites. Stochastic simulations suggested that given high variability in T cell killing efficacy, three or more T cells per liver stage are needed to ensure sterilizing protection. We found found that large variability in VI dynamics can be explained by many T cells being noncytolytic and constant VI for some parasites cannot come from insufficient imaging time.

2 Materials and methods

2.1 Experimental Data

Experimental data for our analyses have been generated in our previously published work [16] except the novel data on the dynamics of the vitality index (VI, see below) in control mice. In short, there were two sets of experiments performed (**Figure 1**A). In control experiments, Balb/c mice were infected with 3×10^5 GFP-expressing Plasmodium yoelii (Py) sporozoites i.v., and 24h later the livers of mice were surgically exposed and imaged using a spinning disk confocal microscope. In total, 38 parasites in 2 different mice were followed for 6 hours. Imaging data from 22 of such parasites were analyzed longitudinally. Specifically, the vitality index (VI) of each parasite at different times was calculated in ImageJ as the $\log_{10}$ of the parasite brightness to the background brightness in the GFP channel using maximal z projection. In control experiments parasites were defined as superficial or deep based on their higher or lower z position in the stack of images, respectively (e.g., **Supplemental Figure S1**). In treatment experiments, mice were infected with 3×10^5 GFP-expressing Py sporozoites. Twenty hours later, 9×10^6 activated Py-specific CD8 T cells were transferred into infected mice (for details of how activated Py-specific CD8 T cells were generated see [16]). Four to eight hours later, livers of mice were surgically exposed and imaged using a spinning disk confocal microscope. In total, 32 parasites were followed in 4 mice. VI was calculated for each parasite, and by segmenting the movies with Imaris (https://imaris.oxinst.com), the number of T cells found within 40 μm of the liver stage over time was quantified [20–22]. Following previous analysis we assume that the parasite is considered dead if the VI becomes less than 0.2 [16]. Our main results, however, were not particularly sensitive to this assumption (see Results section).

We provide all numeric experimental data as the supplement to the paper. These data include the following.

(a) For control experiments, imaging was performed from 24 hour to 30 hour and from 30 hour to 33 hour after infection in 2 mice, respectively. The data include VI over time for each parasite (**Figure 1**Bi and **Supplemental Figure S1**A).

(b) For treatment experiments, imaging was performed in different intervals that typically varied per mouse but also per parasite: 4 to 6.2 hours, 8 to 11.8 hours, 5 to 9.12 hours, 6 to 9.12

hours, 6.5 to 7.32 hours, and 7.82 to 11 hours in four different mice (**Figure 1**Bii-Biii and **Supplemental Figure S1**B-D). For every mouse and parasite ID, the data include the time since infection (hours), the number of T cells per parasite, GFP level of the background and the parasite, and the parasite's VI.

In cases when VI or T cell number per parasite could not be calculated (due to imaging artifacts), values were indicated as NA. These data were excluded in the analysis.

2.2 Mathematical models

2.2.1 Dose response models to predict parasite's VI from T cell numbers

In our data both parasite's VI and T cell number per parasite change over time. In addition to modeling the dynamics of VI change (see below) we aggregated the data and calculated the relationship between the VI and T cell numbers per parasite at a given time point t. For the analysis we normalized the VI for each parasite to its initial value found at the beginning of imaging. To describe the "dose" relationship between the VI and the number of CD8 T cells we used several alternative models. These include log-logistics model:

$$V(T(t), \beta_1, \beta_2, \beta_3, \beta_4) = \beta_2 + \frac{\beta_3 - \beta_2}{1 + \mathrm{e}^{\beta_1(\log(T(t) - \log(\beta_4)))}}, \tag{1}$$

where β_1 denoting the steepness of the dose-response curve, β_2, β_3 the lower and upper limit of the response and β_4 represent the effective dose T_{IC50}. Other models are

$$\begin{aligned}
V(T(t), \bar{\beta}) &= \beta_2 + (\beta_3 - \beta_2)\mathrm{e}^{-\mathrm{e}^{\beta_1(\log(T(t) - \log(\beta_4))}}, && (2)\\
V(T(t), \bar{\beta}) &= \beta_2 + (\beta_3 - \beta_2)(1 - \mathrm{e}^{-\mathrm{e}^{\beta_1(\log(T(t) - \log(\beta_4))}}), && (3)\\
V(T(t), \bar{\beta}) &= \beta_2 + (\beta_3 - \beta_2)\Phi(-\beta_1(\ln(T(t)) - \ln(\beta_4))), && (4)\\
V(T(t), \bar{\beta}) &= \beta_2 + (\beta_3 - \beta_2)\mathrm{e}^{-\frac{T(t)}{\beta_4}}, && (5)
\end{aligned}$$

where eqns. (2)–(5) are for Weibull I, Weibull II, log-normal, and exponential functional response, respectively; Φ is cumulative normal distribution function. We fitted these models to data using R package *drc*. In *drc*, parameters are estimated using maximum likelihood that is under the assumption of normally distributed response simplifies to nonlinear least squares [23]. From the parameter estimates we calculated T_{IC50} as number of CD8 T cells required for 50% inhibition of parasite's VI from its initial value. Typically, T_{IC50} was computed numerically by setting $V = 0.5$ in the model and solving for $T(t)$ with estimated parameters $\bar{\beta}$.

2.2.2 Mixed effect modeling of VI dynamics

To separate the effect of time (t), T cell number per parasite (T), and mouse effect (M) in the VI dynamics we performed linear mixed-effect modeling analysis. Using *lme4* package in R we considered

the following alternative models that take into account time since T cell transfer t and the number of T cells per parasite T:

$$
\begin{aligned}
V &\sim t, && (6)\\
V &\sim t+1|T, && (7)\\
V &\sim t\times T+1|T, && (8)\\
V &\sim t+1|T+1|t:T. && (9)
\end{aligned}
$$

To determine potential impact of individual mice on the VI dynamics we considered the following models:

$$
\begin{aligned}
V &\sim t+1|M+1|T, && (10)\\
V &\sim t+1|M+1|M/T, && (11)\\
V &\sim t\times T+1|M/T, && (12)\\
V &\sim t+1|M/T+1|t:T, && (13)
\end{aligned}
$$

where notations are defined as follows: $1|T$ is represent a random effect upon VI after a fixed effect, $1|M$ is defined a random effect of four different mice upon VI, $t \times T$ is defined main effect with interaction between time and T cells, $1|M/T$ indicates a nested random effect of T cells from different mice, $1|t:T$ is used to define a random effect with interaction between T cell number and time. This analysis was performed on 24 parasites that had at least one T cell within 40 μm of the parasite at some time during imaging. All models were compared with the null model (no T cells or mouse effect) using ANOVA, and the best model was determined based on the lowest Akaike Information Criterion (AIC) value [24, 25].

2.2.3 A forecasting statistical model to estimate next VI from previous VI and T cell numbers

To investigate whether CD8 T cells may impact dynamics of parasite's VI in subtle ways we borrowed a forecasting approach from economics and several alternative mathematical models from disease population ecology [26]. The basic idea of the model is to use information on the parasite's VI (V_t) and T cell number around the parasite (T_t) at time t to predict parasite's VI at time $t+1$. We consider the following alternative models:

$$
\begin{aligned}
V_{t+1} &= (1+r)V_t, && (14)\\
V_{t+1} &= (1+r)V_t - kV_t^{\alpha}T_t^{\beta}, && (15)
\end{aligned}
$$

where r is the growth rate of the VI and k is the killing rate of the VI by T cells in eqns. (14)–(15). Departures from the mass-action killing of the parasite by T cells are modelled with parameter β with $\beta > 1$ indicating cooperation at killing and $\beta < 1$ indicating competition at killing.

We fitted these model to the parasite's VI using linear regression (least squares) in R by taking V_t and T_t given in the data and predicting V_{t+1} also found in the data. Specifically, for V_{t+1} we took observed values for VI for a given parasite starting at time point $t = 2$ and regressed this vector against VI values starting at $t = 1$ until $t = N - 1$ where N is the number of data points for each specific parasite. To investigate if different dynamics of T cell numbers per parasite may allow for a better description of VI dynamics we allowed the number of T cells per parasite i) to change randomly, ii) to increase over time from the lowest number found in the data for a given parasite to 10 (maximal value in our data), and iii) to decrease over time from the highest number of T cells found in the data for a given parasite to zero (lowest value found in our data).

2.2.4 Mechanistic modeling of T cell clustering dynamics

We have recently shown that dynamics of CD8 T cell cluster formation around the liver stages is best described by the density-dependent recruitment (DDR) model in which T cells enter the cluster at a constant rate λ_0 and at the rate that depends on the number of T cells already in the cluster $\lambda_1 T(t)$; T cells leave the cluster at a constant per capita rate μ [16, 22, 27]. By fitting the DDR model to the kinetics of formation of clusters around individual liver stages we found that the model in which recruitment rates λ_0 and λ_1 decline with time describes the data better than the model with constant parameters [22]. Based on these results we propose the following model with time-dependent rates of T cell clustering in the DDR model:

$$\frac{\mathrm{d}T(t)}{\mathrm{d}t} = \mathrm{e}^{-\alpha t}[\lambda_0 + (\lambda_1 - \mu)T(t)], \tag{16}$$

where α is the rate at which λ_0, λ_1, and μ decline with time since T cell transfer. Interestingly, this model fitted the data with slightly lower quality as compared to the model in which recruitment-related parameters changed at 4 h post T cell transfer (AIC 182.1 vs. 177.7, ΔAIC = 4.4, see Kelemen *et al.* [22] for the latter model description). The solution of eqn. (16) with the initial condition $T(0) = 0$ is

$$T(t) = \frac{\lambda_0}{(\lambda_1 - \mu)} \left(\mathrm{e}^{\frac{\lambda_1 - \mu}{\alpha}(1 - \mathrm{e}^{-\alpha t})} - 1 \right), \tag{17}$$

where only 3 parameter combinations (λ_0, $\lambda_1 - \mu$, and α) determine the dynamics of the average cluster size. Unfortunately, experimentally measured cluster sizes for individual liver stages were insufficient to estimate all 3 parameters, in part because, faster recruitment rates λ_0 and λ_1 could be compensated by the faster decline in the recruitment rates given by α. Therefore, for further analyses we used a simplified DDR model in which we let $\alpha \to 0$:

$$T(t) = \frac{\lambda_0}{\mu - \lambda_1}(1 - e^{-(\mu - \lambda_1)t}), \tag{18}$$

It should be noted that to describe typical cluster dynamics data with finite cluster size $\mu > \lambda_1$ and that only λ_0 and the difference $\mu - \lambda_1$ can be estimated from the average cluster data. We found that predictions of the DDR model with constant and time-dependent parameters deviate insignificantly and thus, are not expected to influence estimate of the T cell killing rates. To estimate

model parameters (λ_0 and $\mu - \lambda_1$) we fitted eqn. (18) to the experimentally measured number of T cells per parasite over time for each parasite using least squares in Mathematica (using function NonlinearModelFit) or function nlsLM in R (using package minpack.lm) with control maxfev=10000 with maxiter=1024 [28].

2.2.5 Mechanistic modeling of VI dynamics

To further understand whether CD8 T cells compete or cooperate in killing of the parasite and to estimate the per capita killing efficiency of Plasmodium-specific CD8 T cells we used the following alternative models for the dynamics of parasite's VI

$$\frac{\mathrm{d}V_t}{\mathrm{d}t} = rV_t - kV_tT(t), \tag{19}$$

$$\frac{\mathrm{d}V_t}{\mathrm{d}t} = rV_t - kV_tT(t)^n, \tag{20}$$

where V_t represents the parasite's VI at time t (in hours), r is the rate of VI's growth, k is the killing efficiency of CD8 T cells and n is Hill coefficient, indicating deviation of the killing from mass-action (in eqn. (20)). Parameter n allows to detect cooperativity ($n > 1$) or competition ($n < 1$) between different T cells in killing. The dynamics of the number of CD8 T cells per parasite $T(t)$ is given in eqn. (18). The models were fitted to the dynamics of VI for all parasites. The models were fitted using least squares using the FindMinimum routine in Mathematica. For each model (three different functional responses) we performed the above procedure separately. We then used the AIC to select the best model from the two different functional CD8 T cell responses ($n = 1$ and $n \neq 1$):

$$\mathrm{AIC} = N \ln \left[\frac{SSR}{N} \right] + 2N_p, \tag{21}$$

where SSR is the sum of squared residuals from the fit, N is the number of data points and N_p is the number of model parameters fitted to data [24, 25].

2.2.6 Stochastic model of killing of the liver stage assuming variability in T cell killing efficacy and/or parasite resistance

We simulated T cell-mediated killing of the liver stages by selecting a given number of T cells per parasite (parameter n_T). Each of n_T T cells was assumed to either have maximal killing efficacy $k = 0.1$/h or to be nonlytic ($k = 0$) with probability f_K. Parasites may be either fully sensitive to killing or fully resistant to killing by T cells; this was determined randomly for each liver stage with the probability f_R. For each T cell cluster we allowed T cells to interact for dt h chosen uniformly between 0 and 1 h. We determined if the liver stage was eliminated by summing killing efficacies for n_T T cells in the cluster and the time dt T cells interacted with the liver stage assuming the killing process is exponentially distributed (per eqn. (19)). For each run we calculated the T cell killing rate as the ratio of the probability of liver stage death over the number of T cells and the duration of T cell interaction with the liver stage, $1/(n_T dt)$ or 0. We repeated simulations 10,000 times for the same number of T cells and calculated the average killing rate for a given set of model parameters.

2.2.7 Stochastic model of variability of parasite's VI over time

To investigate VI variability that many come from stochasticity of parasite's dynamics we performed stochastic simulations of the parasite's VI in the presence of different numbers of T cells near the parasite using Gillespie's algorithm [29]. Simulations were performed to mimic experimental design. Specifically, in experiments GFP signal from the parasite could theoretically vary between 0-255 in unit increments (8 bit), and typically, by the start of imaging, GFP signal rarely exceeded 200 with background being 10-20. For simplicity we assume that parasite's health signal starts at 100 with the background being 1, resulting in the initial VI being $\log_{10}(100/1) = 2$. Parasite's GFP signal was allowed to grow over time with a minimal growth rate ($r = 0.0001/\text{h}$) for twenty hours while background remained fixed. At this time, T cells were transferred into mice; T cells accumulated at the parasite at the rate defined by parameters λ_0 and $\mu - \lambda_1$ (see eqn. (18)) and killed the parasite at a rate k. The simulations were run for another 36 hours. Two hundred simulations were run using python package *gillespy2* with *Tau-Hybrid* solver. In another set of simulations instead of modeling increase in T cell numbers near the parasite we allowed T cell numbers to change randomly over time in the range observed for a given parasite.

3 Results

3.1 Experimental framework to quantify how *Plasmodium*-specific CD8 T cells kill *Plasmodium yoelii* parasites in the liver

To understand how Plasmodium-specific CD8 T cells may eliminate Plasmodium yoelii (Py) sporozoites from the liver we have performed intravital imaging experiments in which GFP-expressing parasites were imaged in the livers of live mice using intravital microscopy [16, **Figure 1**A]. From these imaging data, we calculated the relative brightness of the GFP signal from Py liver stages (denoted as vitality index or VI) in both control and treatment experiments (**Figure 1**Bi-Bii) and the number of Plasmodium-specific CD8 T cells located within 40 μm from the parasite at different times after T cell transfer in treatment experiments (**Figure 1**Biii).

In control experiments in which no T cells were transferred, VI remained constant for all except of one parasite that were followed longitudinally (**Supplemental Figure S1**A). Estimated growth rates of the VI on average did not significantly differ from 0 ($p = 0.92$ and $p = 0.13$ for mouse 1 and 2, respectively, Sign-Ranked test) suggesting that in the absence of T cells, the VI does not increase over several hours of the imaging experiments. This is perhaps expected given that the VI denotes the relative GFP intensity and true parasite's growth may be better estimated by the size of the liver stage [30]. Interestingly, the actual value of the VI varied for different parasites with the parasites in deeper tissues (as judged by the slice's z coordinate) but most were above of VI = 0.2 which was previously defined as a VI cutoff for a dead/dying parasite [16].

Importantly, VI was more variable over time and between individual parasites in mice that had received Py-specific T cells (**Figure 1**Bii, **Supplemental Figure S1**B, **Supplemental Figure S2** and **Supplemental Figure S3**). In these experiments 8 out of 32 of the liver stages were not surveyed by T cells over the imaging period (i.e., no T cells were within 40 μm of the parasite, **Supplemental Figure S1**C and **Supplemental Figure S4**); the change in the number of T cells in the vicinity of each parasite was variable with some parasites accumulating more T cells while

others loosing T cells, and some parasites being surveyed by a single T cell in a short time period (**Figure 1**Biii and **Supplemental Figure S4**). Interestingly, many parasites had stable VI despite having multiple T cells nearby (e.g., **Supplemental Figure S3**) and several parasites did not exhibit appreciable decline in VI over imaging time period (**Supplemental Figure S2**).

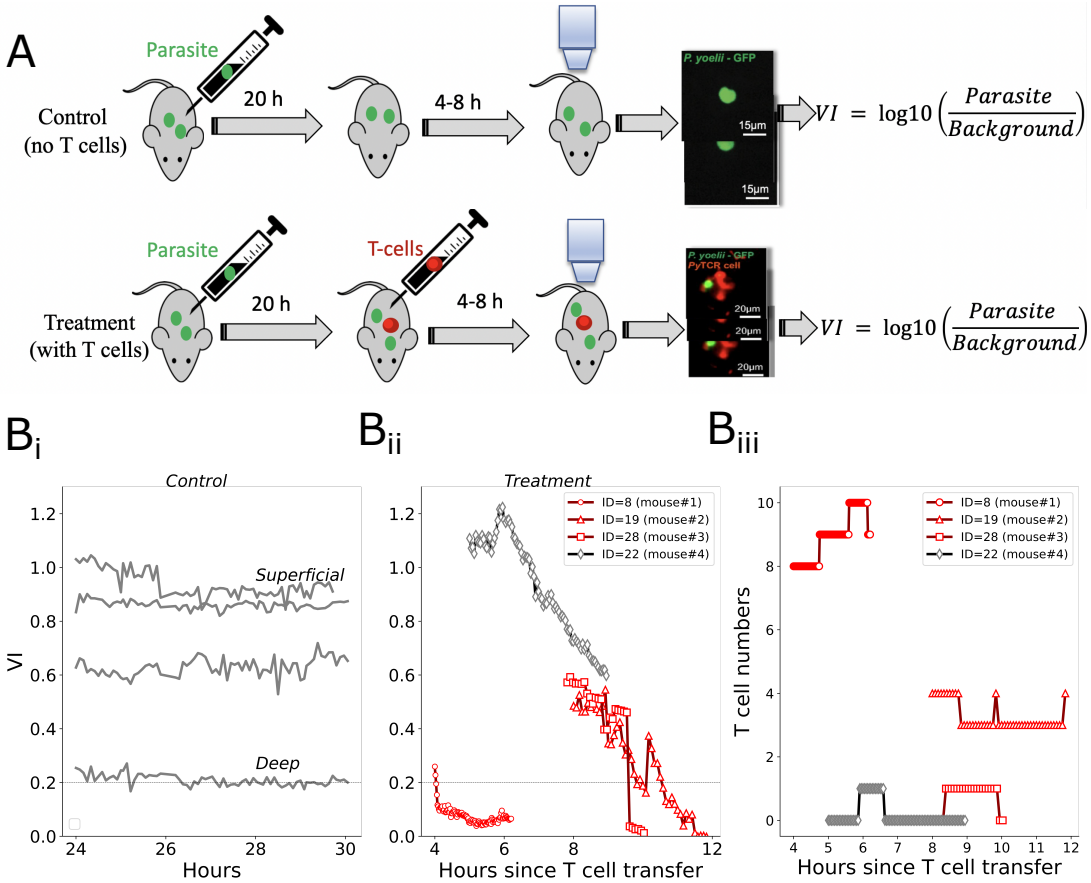


Figure 1: Experimental design to measure T cell impact on Plasmodium liver stages. **(A)** Experimental design. Mice were infected with 3×10^5 GFP-expressing Py sporozoites and divided into two groups as control or treatment. In the control group mice were left until imaging started 24-28 hours after the infection. In the treatment group, 9×10^6 Py-specific activated CD8+ T cells (PyTCR) were transferred into infected mice 20 hours after infection. Four to eight hours later, murine livers were surgically exposed and z-stacks of images were taken using spinning disk confocal microscope [16]. Vitality index (VI) of a given parasite was calculated as the $\log_{10}$ of the ratio between brightness of the GFP signal from the parasite to the brightness of the background based on maximal z projections. The number of T cells within 40 μm of each liver stage was also calculated. **(Bi,Bii)**: Example of the VI dynamics for control (Bi) or treatment (Bii) groups. "Superficial" and "deep" denote location of the parasite based on the z coordinate in the imaging data. **(Biii)** Change in the number of Py-specific CD8+ T cells near the Py-infected hepatocytes over time since T cell transfer. See **Supplemental Figure S1** for all data graphs.

3.2 The number of T cells per parasite negatively correlates with parasite's VI

To better understand how the number of CD8 T cells per parasite is related to the parasite's VI and how imaging of individual mice may influence the results, we performed several alternative analyses. First, we analyzed the relationship between the VI and the number of T cells per parasite for each mouse. Interestingly, we found that a higher number of T cells per parasite was negatively correlated

with the parasite's VI for three out of four mice (**Figure 2**A). There was no correlation between CD8 T cell numbers per parasite and parasite's VI for most parasite-T-cell combinations, in part, because for many parasites the number T cells did not vary over time or there were no T cells near the parasite. However, for eight parasites we found that T cell numbers in the cluster are negatively correlated with VI (**Figure 2**B) suggesting that at least for a subset of parasites CD8 T cells may suppress parasite's "health".

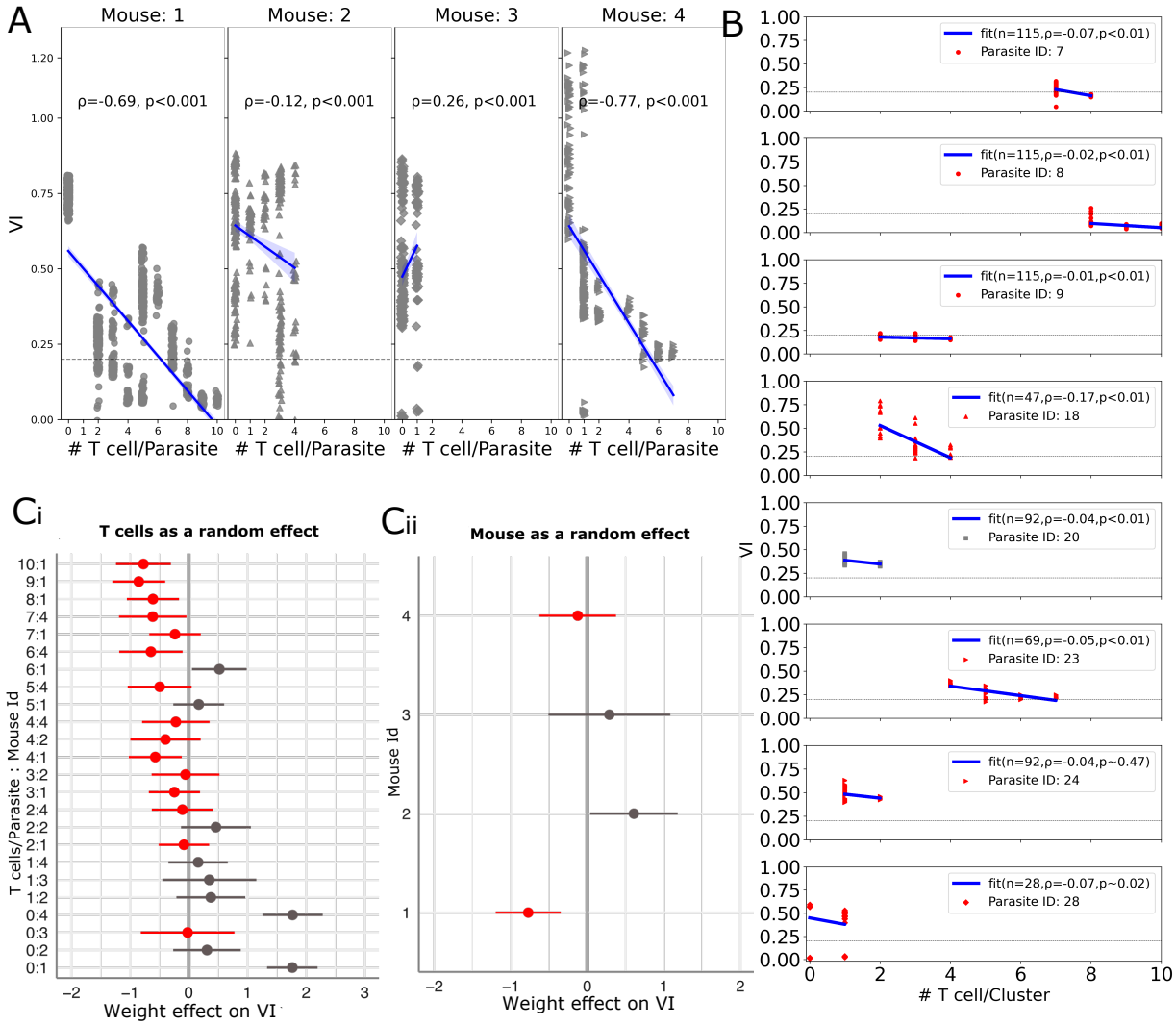


Figure 2: Higher CD8 T cell numbers per parasite are negatively correlated with the parasite's VI. (A) Correlation between parasite's VI and T cell numbers per parasite is shown for individual mice. The Spearman rank correlation coefficients ρ and corresponding p value were calculated using *scipy.stat* package in python and are shown on individual panels. (B) Correlation between parasite's VI and CD8 T cell numbers per parasite shown for subset of the data (8/32) for which such correlation was statistically significant (red and gray colors for the points correspond to dying and not dying parasites, respectively). Lines show linear regression with p value calculated using *statsmodels* package in python. (Ci) Prediction of the best fit linear mixed effects model assuming T cell numbers per parasite as a random effect (eqn. (11)) are shown for individual T cell number:mouse combinations. Negative values for effect (weight) correspond to T cell numbers that reduce VI over time. (Cii) Prediction of the best fit linear mixed effects model assuming mouse as a random effect (eqn. (10)) are shown for individual mice (negative and positive effect corresponds to the parasite's VI declining or increasing, respectively).

To understand how the time since T cell transfer may impact the relationship between T cell number per parasite and parasite's VI we fitted several alternative models to the parasite's VI normalized to its average value for each parasite for all mice but dividing the data into different time

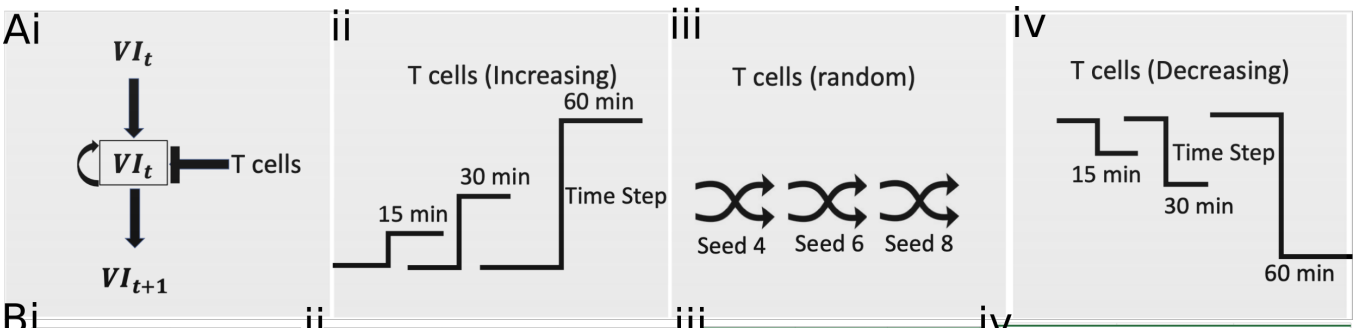
periods (see **Figure 1**Ciii, **Supplemental Figure S5**, and eqns. (1)–(5) in Materials and methods). Specifically, we divided the VI and T cell data for 32 parasites into four different cohort based on the time interval since T cell transfer (4-6 hours, 6-8 hours, 8-11 hours, and all data combined, 4-11 hours) and fitted five alternative models (eqns. (1)–(5)) to these data using least squares. All models described the data with similar quality and model predictions were typically similar for the alternative models with the exception of the exponential model that gave slightly different predictions (**Supplemental Figure S5**A-C). For each time period we then calculated the number of T cells, T_{IC50}, that was needed to reduce parasite's VI to 50% of its initial value. Interestingly, T_{IC50} was increasing with the time since T cell transfer from about 1 T cell per parasite at early time points (4-6 hours) to 13 T cells per parasite at later time points (8-11 hours, **Supplemental Figure S5**A-C). This result may indicate that there may be something special about parasites that had survived for 8-11 hours of T cell search for infection; perhaps such parasites are able to actively resist killing or that they are located in areas of the liver where T cells have lower access to. When analyzing all the data together we found that about 3 Py-specific CD8 T cells per parasite were needed to reduce the parasite's VI to 50% of its initial value (**Supplemental Figure S5**D); this estimate of the cluster size is similar to that calculated previously using an alternative approach [16].

Finally, to quantify the effect of the time since T cell transfer, the number of T cells per parasite, and the individual mouse we performed several linear mixed model-based analyses (see eqns. (6)–(13) and Materials and methods for more detail). By comparing among alternative models, the model in which VI was dependent on time since T cell transfer as a fixed effect and mouse being a random effect (eqn. (11)) described the data with best quality. In this model, based on total variance explained by the model the overall contribution of CD8 T cell number on parasite's VI was about 60% and mouse effect was about to 40%. Overall, higher T cell numbers were associated with decline in VI over time (**Figure 2**C); however, in mice 2&3 the VI did not significantly decline over time (**Figure 2**D). This analysis suggests that while CD8 T cell numbers per parasite do explain the dynamics of the parasite's VI (decline or growth), the effect is individual mouse-dependent highlighting the need to perform experiments in as many mice as possible.

3.3 A forecasting model with increasing T cell number per parasite better describes change in parasite's VI

Parasite's VI fluctuated over time for most parasites (e.g., **Figure 1**Bii). To investigate whether current VI and T cell number per parasite are predictive of the VI at a later time instance we borrowed an approach from economics dubbed "a forecasting model" (**Figure 3**Ai). We assumed how current and past VI are related, i.e., whether the next step VI is directly determined by the previous VI value eqns. (14)–(15) for the set of equations. In the model we then considered the impact of CD8 T cell number at the current time moment on the next time VI, and examined whether changes of T cell number per parasite improves the quality of the model fits of the VI data. We found that for T cell dynamics observed in experiments, adding T cell dynamics to the model fit improved the prediction of VI dynamics for 6 out of 19 parasites (**Figure 3**Bi).

We wondered if there may be errors in measuring of how many CD8 T cells are located near individual parasites. In our experiments the typical imaging depth is $h = 50$ μm, and given that we count T cells located within $r = 40$ μm from the parasite, the relative volume in which we typically count T cells near the deep parasite is $\pi r^2 h/(4/3\pi r^3) \approx 47\%$. This calculation suggests that we may be underestimating the number of T cells located near individual parasites, and it is possible that



Bi

Parasite ID	Initial T-cells	Anova (T-cells Vs Null) Experimental Data
1	5	0.61423
3	3	0.04*
4	5	0.0093*
5	2	0.00125*
7	7	0.2958
8	8	4.3E-08*
9	2	0.00997*
12	2	0.15373
13	0	0.92808
14	0	0.15435
17	3	0.92243
18	2	0.3656
19	4	0.16019
20	1	0.18949
22	0	0.64907
23	4	0.01812*
24	1	4.0E-06#
27	0	0.782644
28	0	0.727104
Total p(<0.05):		6

ii

Anova(increasing T-cell Vs Null)		
Time Step – 15 mins	Time Step – 30 mins	Time Step – 60 mins
0.6322	0.4855	0.3521
0.0005*	0.0027*	0.0017*
0.000067*	0.00056*	0.00087*
0.001052*	0.00053*	0.0008*
0.15265	0.32379	0.32379
8.34E-08*	3.99E-08*	3.99*
0.0000069*	0.000241*	0.003374*
0.12057	0.08353	0.1133
0.81775	0.79196	0.80223
0.004304*	0.00775*	0.018011*
0.10183	0.03804*	0.14389
0.029696*	0.36807	0.011355*
0.06904	0.05713	0.33334
0.000659*	0.002135*	0.03764*
0.04583*	0.04629*	0.02934*
0.00001736*	0.0002045*	0.093003
0.00032*	0.00402*	0.0003*
0.02375*	0.03878*	0.04732*
0.28474	0.23267	0.4632
12	12	11

iii

Anova (random T-cells Vs Null)		
Random seed-4	Random seed-6	Random seed-8
0.8096	0.3373	0.7777
0.0139*	0.026*	0.0096
0.0016*	0.0001*	0.01324
0.49711	0.27092	0.55263
0.53662	0.3796	0.13458
1.2E-06*	7.9E-07*	7.3E-09
0.04596*	0.13934	0.064771
0.004107*	0.0079*	0.11538
0.97186	0.91301	0.50321
0.64246	0.36752	0.00031*
0.34309	0.90727	0.96746
0.041532*	0.11282	0.32452
0.00084*	0.93893	0.99029
0.074165	0.143268	0.471
0.71035	0.85236	0.51198
0.57018	0.416445	0.45454
0.07534	3.5E-05*	4.0E-05*
0.59685	0.601323	0.5958
0.52672	0.7521	0.72184
7	5	2

iv

Anova (decreasing T-cell Vs Null)		
Time Step – 15 mins	Time Step – 30 mins	Time Step – 60 mins
0.6034	0.6189	0.6275
0.3124	0.1298	0.0249*
0.3741	0.04533*	0.00297*
0.11941	0.0657	0.096
0.73672	0.54395	0.54395
2.8E-05*	8.6E-06*	8.6E-06*
0.39182	0.3536	0.08714
0.423535	0.054537	0.319363
NA	NA	NA
NA	NA	NA
0.27103	0.99999	0.4509
0.011356*	0.011355*	0.3985
0.000832*	0.23168	0.299577
0.06985	0.99999	0.047638*
NA	NA	NA
0.44328	0.50619	0.0009*
3.9E-05*	3.9E-05*	4.0E-05*
NA	NA	NA
NA	NA	NA
4	4	6

Figure 3: Increasing T cell number in the cluster improves prediction of parasite's VI over time. (A) (i) Schematic diagram of the model to predict next VI (V_{t+1}) using its own previous value (V_t) and reduction of VI due to CD8 T cells present near the parasite. (ii) We increased the T cell number per parasite over time (with three different time steps) starting from the minimal number of T cells found for a given parasite to 10 – a maximum value observed in our data (see **Supplemental Figure S4** for the dynamics of T cell number for each parasite). (iii) We supplied a random T cell number over time (using three different random seeds) that were bounded by lowest and highest T cell number taken from experimental data. (iv) We decreased the T cell number over time (with three different time step) starting from the highest T cell number found in experiments for each parasite to zero. (B) We compared the fits of the forecasting null model where the next time step VI is only determined by the VI at the current step (eqn. (14)) with the model in which the dynamics of CD8 T cell numbers is included (eqn. (15)) using ANOVA in R. In fitting the model with changing CD8 T cell numbers per parasite we (i) took the actual T cell number data for each parasite, (ii) increased CD8 T cell numbers over time, (iii) chose random T cell numbers over time, and (iv) decreased T cell numbers over time. The analysis was done for 19 parasites for which there was at least 1 T cell nearby at several time points during the imaging period and for which T cell numbers were changing with time. Red and gray shading of rows denotes parasites that are dying (VI has declined or is declining to 0.2) or not dying, respectively. "NA" denotes situation when T cell number was zero. Linear regressions were done in R package *minpack.lm* with star $*$ denoting statistically significant difference in model fits at $p < 0.05$. Estimated model parameters are shown in **Supplemental Table S2**.

our determined change in T cell numbers per parasite may also be not fully accurate.

To investigate whether different T cell dynamics may improve prediction of the VI changes over time we simulated T cell dynamics for each parasite in three different ways: we assumed that 1) T cell number per parasite increases with time since T cell transfer from the minimal value found for a given parasite to 10 (maximum observed in our data), 2) T cell number is randomly chosen between minimal and maximal value, or 3) T cell number declines from the maximal value over time to zero. We found that increasing the number of T cells over time improved the description of the VI dynamics over the null model with no T cells in 12/19 parasites – a double when compared to the model fits when using actual data ($\chi_1 = 2.64$, $p = 0.10$; **Figure 3**Bii). This result was relatively independent on the rate at which T cell numbers were assumed to increase over time. In contrast, choosing random T cell numbers or decreasing T cell numbers over time resulted in fewer fits that improved prediction of parasite's VI over the null model (**Figure 3**Biii-Biv). These results suggest that there may be an increase in the number of T cells around individual parasites that is not fully detectable by the current imaging techniques at least for some (e.g., deep) parasites.

3.4 A simple model with mass-action killing describes well the VI dynamics for most parasites

Having performed several statistical analyses of the data we next turned to a more mechanistic modeling of T cell-mediated killing of the parasites by asking whether the kinetics of VI loss over time can be well described by different mathematical models. We focused this analysis on the subset of parasites for which there was at least one T cell present near the parasite during the imaging time period (24/32 parasites); this excluded 8 parasites from the analysis. Because imaging only allowed to observe T cell clusters at later points after T cell transfer and T cells in the cluster may start killing the parasite before imaging started, we needed a mathematical approximation to describe kinetics of T cell cluster formation after T cell transfer.

We have previously shown that "density-dependent recruitment" (DDR) model best describes clustering of CD8 T cells around Plasmodium liver stages [16, 22]; this model proposes that recruitment of T cells to the liver stage increases with the number of T cells already present near the liver stage. Analysis of kinetics of cluster formation for liver stages in the whole dataset suggested that parameters of the DDR model are likely to change with time indicating reduced rate of T cell recruitment at later times [22, eqn. (16)]. However, fitting the DDR model with time-dependent parameters (DDR-alpha model) to data for T cell clustering around individual liver stages typically resulted in overfitting and did not allow to estimate all 3 model parameter combinations (results not shown). Therefore, we fitted the version of the DDR model with constant parameters (eqn. (18)) to the measured numbers of CD8 T cells per parasite using nonlinear least squares and estimated model parameters (λ_0 and $\mu - \lambda_1$). The model fitted the data well (**Supplemental Figure S6**) and predicted relatively rapid formation of T cells clusters for most parasites as expected from our previous analysis [22]. Importantly, both estimated parameters varied dramatically between individual parasites (shown in a supplemental table available as a `csv` file) with median rates $\lambda_0 = 0.40/\text{h}$ and $\mu - \lambda_1 = 0.13/\text{h}$. By fitting the DDR model to the clustering data using nonlinear mixed effect approach we found that the data are best explained by variable between different liver stages initial recruitment rates λ_0 (median $\lambda_0 = 0.33/\text{h}$) and a constant cluster amplification rate $\mu - \lambda_1 = 0.29/\text{h}$ that are somewhat consistent with individual fits (results not shown).

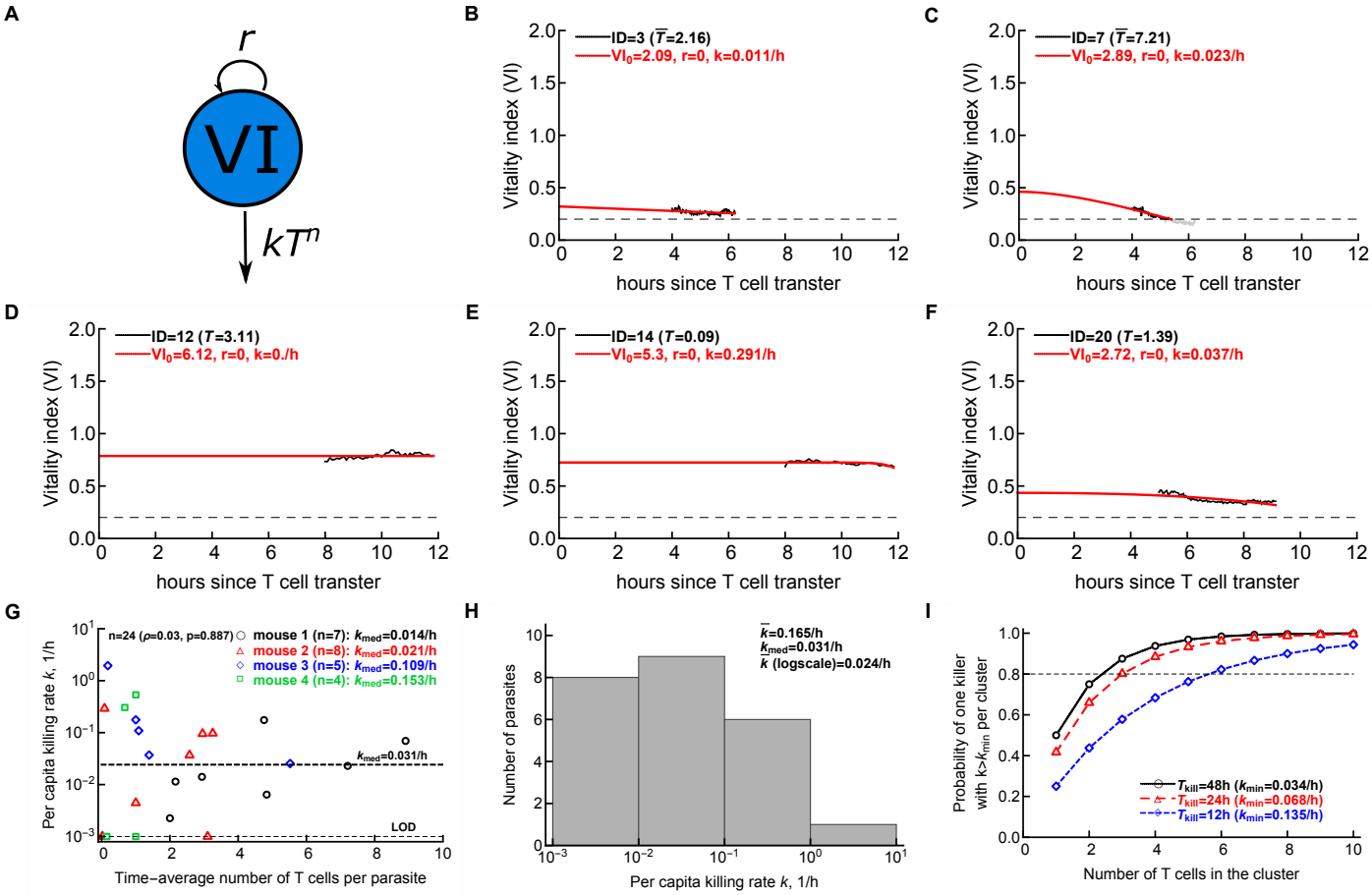


Figure 4: The best fit model suggests a relatively low killing efficacy of CD8 T cells in vivo. (A) Schematic of the model depicting the essential interaction between CD8+ T cells (T) and VI (V_t) where k, r, and n correspond to killing efficiency per T cell, growth rate of the parasites, and parameter indicating competition ($n < 1$) or cooperation ($n > 1$) between T cells located near the same parasite, respectively. Two alternative models (eqns. (19)–(20)) were fitted to the data on VI dynamics while taking into account change in the number of CD8 T cells per parasite as predicted by the density-dependent recruitment model (**Supplemental Figure S6**). (B-F) Experimental data on VI change in subset of parasites are shown by markers and lines are the best fit predictions of the simplest, mass-action model (eqn. (19)). Estimated killing rate k is shown on individual panels, and all fits are shown in **Supplemental Figure S7**. The dotted horizontal line denotes the death threshold VI = 0.2. (G) Estimates of per capita T cell killing efficacy is plotted against the time-average of the number of T cells near each liver stage for $n = 24$ parasites which had at least one T cell at some time during imaging. Estimates with $k = 0$ were assigned value of 10^{-3}/h (limit of detection, LOD) to display on the log-scale. Median estimates for the killing rate for individual mice or all data together (dashed line) are indicated on the panel. (H) Distribution of the estimated killing rates from G shown as a histogram. (I) Stochastic simulations on resampling of estimated killing efficacy per T cell from H predicting the the probability of liver stage elimination within different time intervals (48h, 24h, or 12h) as the function of the number of T cells in the cluster. Horizontal dashed line denotes 80% probability.

We then compared how well simple alternative models that assume different killing terms and that use the estimated dynamics of T cell numbers per parasite, fit the data on the dynamics of parasite's VI (**Figure 4**A). Specifically, we fitted the models to the change in VI over time using nonlinear least squares. These alternative models assumed 1) mass-action killing rate (eqn. (19)), 2) powerlaw killing term (eqn. (20)) that allows to detect cooperativity ($n > 1$) or competition ($n < 1$) between individual T cells in the cluster. In the fits we assumed that the parasite's growth rate $r = 0$ since our analysis of the data on VI dynamics in control mice found that this growth rate on average was not different from zero (**Supplemental Figure S1**A). In addition, we found that assuming $r > 0$ resulted in overfitting of the model to VI data (results not shown). Interestingly, we found that the model assuming mass-action killing described the data with sufficient quality for the majority of the liver stages (**Figure 4**B-F and **Supplemental Figure S7**). Some liver stages did not display any VI decline despite being surrounded by T cells (e.g., **Supplemental Figure S7**J, V, X) but most parasites did display some degree of death suggesting that our mathematical modeling-based approach allowed to detect minor killing signals in these data. Importantly, we found dramatically variable per capita T cell killing rates ranging from $k = 0/\text{h}$ to $k = 2/\text{h}$ with the median $k_{\text{med}} = 0.031/\text{h}$ (**Figure 4**G). Importantly, the estimated per capita killing rate did not depend on the average number of T cells observed for each liver stage for the imaging period ($\rho = 0.03$, $p = 0.89$) with some variability in median killing rates between individual mice (**Figure 4**G). The distribution of estimated killing rates is skewed with T cells around only few parasites show very high kill rates which for most parasites T cells have low killing efficacy (**Figure 4**G). Interestingly, we found higher average killing rates ($\bar{k} = 0.049/\text{h}$) for T cells around 8 parasites for which we found statistically significant correlation between VI and T cell number in a cluster (**Figure 2**B). This suggests that indeed, T cells in these clusters may be more efficient killers.

To confirm the low median killing rate of CD8 T cells we also fitted the mathematical model (eqn. (19)) to the VI dynamics using nonlinear mixed effect approach in R (using `nlme` routine). In this analysis we used average number of T cells per parasite for each of 24 parasites (and not their dynamics) and allowed for fixed and random effects for the T cell killing efficacy and initial VI. Interestingly, we found the best of the model when indeed both k and VI varied between parasites with the median killing rate being $k_{med} = 0.035/\text{h}$ that is consistent with the analysis found by fitting the models to the VI dynamics of individual parasites.

The kill rate of $k_{\text{med}} = 0.031/\text{h}$ by a "median" T cell suggests that it would take nearly 52 hours for such a cell to reduce parasite's VI from 100% to 20% and thus, to kill the parasite ($T_{\text{kill}} = 1/k_{\text{med}} \ln(100/20) = 51.8\text{h}$). Since this time is longer than the typical time of the liver stage (45-48h, [31]) this result suggests that a single CD8 T cells is typically insufficient to eliminate the liver stage. To understand how many T cells would be needed to eliminate the liver stage we resampled the estimated killing rates from **Figure 4**H for different number of T cells per parasite and estimated if for additive (mass-action) killing by n_T T cells, the parasite will die within 12, 24, or 48 h (**Figure 4**I). As expected, having more T cells in the cluster increases the chance of parasite's death. Importantly, even for the longest possible time of contact between T cells in the cluster and the parasite (48h) three T cells were required to ensure the death of the liver stage with over 80% probability (**Figure 4**G). These results strongly suggest that while a single CD8 T cell is clearly capable of eliminating the liver stage (e.g., **Figure S7**Q), clusters involving 3 or more T cells are needed to ensure elimination of a liver stage within 48 hours.

We also fitted an alternative model (eqn. (20)) to the VI data and found that for several parasites the alternative model provided somewhat better fits as judged by change in AIC (IDs = $7, 14, 18, 20, 23$). Visually this improvement in the fit allowed the model to more accurately describe

exponential decline in VI with time for this subset of the liver stages (results not shown). Interestingly, in all cases the best fit resulted in $n < 1$ (typically $n \approx 0$) suggesting competition between individual cells and saturation in killing after one T cell located the parasite. By fitting eqn. (20) to the VI dynamics data using nonlinear mixed effects approach improved the fit non-significantly while predicting $n = 0.75$. Thus, for most parasites the model assuming additive, mass-action-like killing was sufficient to accurately describe the data.

3.5 Stochastic simulations suggest that both variability in T cell killing efficacy and liver stage resistance to killing may contribute to the variability in estimated killing rates

The relationship between estimated per capita killing rate k and the average number of T cells observed during imaging for each liver stage (**Figure 4**G) had at least two interesting features: 1) the estimated killing rate varied dramatically between different liver stages, and 2) variability in the estimated killing rate is lower at larger number of T cells in the cluster. To investigate the potential causes of these two features we ran stochastic simulations (**Supplemental Figure S8**A). In the simulations we allowed n_T T cells to interact with the liver stage that may be fully susceptible or fully resistant to killing by T cells (with a probability f_R). T cells also may either be efficient killers (with $k = 1/\text{h}$) or be nonlytic ($k = 0$) sampled with a probability f_K. We then allowed clusters of T cells to interact with the parasite for uniformly chosen lengths of time dt and calculated whether such interaction resulted in parasite's death. Repeating the simulations for 10^4 liver stages for each parameter combination we could qualitatively recapitulate 1) variability in the estimated killing rate, and 2) decline in variability (estimated confidence intervals) with increasing cluster size (**Supplemental Figure S8**B-D). These simulations suggest that both variable T cell killing efficacy of individual cells and resistance of the liver stage to killing may contribute to the observed heterogeneity in the VI dynamics in vivo.

3.6 Stochastic model with independent and random T cell response is unable to explain the stability of VI most parasites

In our set of 32 parasites several parasites displayed no evidence of stable decline in VI despite being surrounded by one or several CD8 T cells for a period of time (e.g., parasite ID 11 and 12 in **Supplemental Figure S2**). Given that the estimated killing rate of CD8 T cells was relatively low (**Figure 4**G) we hypothesized if constant VI could be explained simply by insufficient imaging period of a few hours preventing us to see a noticeable decline in the VI.

To test this hypothesis we performed stochastic simulations of the parasite's GFP signal that would mimic our experimental design (see Materials and methods for detail). We started the simulation with the parasite's GFP signal being 100 that could change up or down by one (similar to information provided in the imaging data) and then calculated parasite's VI assuming background of one (i.e., the initial VI was $\log_{10}(100/1) = 2$). We allowed the parasite's VI to grow for 20 hours with a small growth rate $r = 0.0001/\text{h}$. After 20 hours T cells were transferred into the mice and started forming clusters around the parasite – the number of T cells per parasite was given by eqn. (18) with parameters chosen for individual parasites (**Supplemental Figure S6**). We started recording the VI 4-8 hours after T cell transfer and continued for another 2-4 hours. T cells were assumed to

reduce the VI according to the mass action model with $k = 0.031/\text{h}$. In this way we simulated 250 trajectories and estimated the rate at which VI was declining with time for individual runs taking the time period of imaging into account (**Figure 5**). The VI for individual runs was typically declining with time whether few or many T cells were located near the parasite (**Figure 5**A&C) even though there was large variability in the decline rates (**Figure 5**B&D). Importantly, none of the slopes of VI decline in simulations were close to the slow VI decline rate observed in the data for "non-dying" parasites. We also performed stochastic simulation with random CD8 T cells number within the specific range of per parasite data. But our simulation slope fails to capture the VI slope observed experimentally (**Supplemental Figure S9**). That suggests that our hypothesis that stable VI is due to stochasticity in the VI dynamics is not consistent with the data. The reasons why some parasites remain viable with no evidence of declining VI despite being surrounded by T cells remain unclear but may include at least three alternative explanations: 1) while being close, Py-specific CD8 T cells do not recognize the infection, 2) the parasite was actively inhibiting killing signals that CD8 T cells may be delivering to the infected cell, and 3) CD8 T cells in the cluster are nonlytic.

4 Discussion

It is well established that large numbers of Plasmodium-specific CD8 T cells are able to provide sterilizing protection against exposure to Plasmodium sporozoites but the mechanisms by which these T cells eliminate the parasites in the liver remain unclear. We used data from our previous intravital imaging of livers in live mice to accurately quantify kinetics at which Py-specific CD8 T cells eliminate Py parasites from the liver [16]. In several alternative statistical analyses we found that presence of Py-specific CD8 T cells typically results in a faster loss of the VI signal from the parasites that we interpret as the process of parasite's dying. We estimated that on average 3 T cells per parasite are needed to reduce the parasite's VI to 50% of its initial value during the imaging period (~ 4 h), and that the dynamics of VI is better explained by the model in which the number of T cells per parasite steadily increases over time (**Supplemental Figure S5** and **Figure 3**). Analysis of the kinetics of T cell clustering and associated parasite's VI dynamics suggested that for most parasites T cells kill the parasite additively, via mass-action at a relatively low per capita killing rate of $k = 0.031/\text{h}$ (**Figure 4**G) suggesting that a single CD8 T cell will need around 52h to eliminate a liver stage; thus, a single CD8 T cell per liver stage is unlikely to be sufficient for sterilizing protection. There was large heterogeneity in the kinetics of VI decline between individual parasites; the rate of VI decline only weakly correlated with the number of T cells present near the parasite (**Supplemental Figure S10**). VI of some parasites surrounded by several CD8 T cells remained relatively constant during the imaging suggesting extremely small killing rate by the clustered T cells (**Figure 4**H). Indeed, stochastic simulations suggest that variability in T cell killing efficacy require 3 or more T cells to cluster around the liver stage to ensure parasite elimination over the life span of the liver stage (**Figure 4**I). Additional stochastic simulations of the VI dynamics in presence of different numbers of T cells suggested that constancy of the VI over the observation period for some parasites cannot be due to limited duration of imaging (**Figure 5** and **Supplemental Figure S9**) and thus can be due to lack of cytotoxic T cells in the cluster.

Details of how individual CD8 T cells kill their targets in vivo remain poorly understood, in part of difficulty of recording killing events in live animals. Several studies reported that CD8 T cells are able to kill either peptide-pulsed or virus-infected cells in 1-2 hours after initial contact [14, 17]. It may take longer times, about 6 hours, for a CD8 T cell to kill a cancer cell [15] although a recent

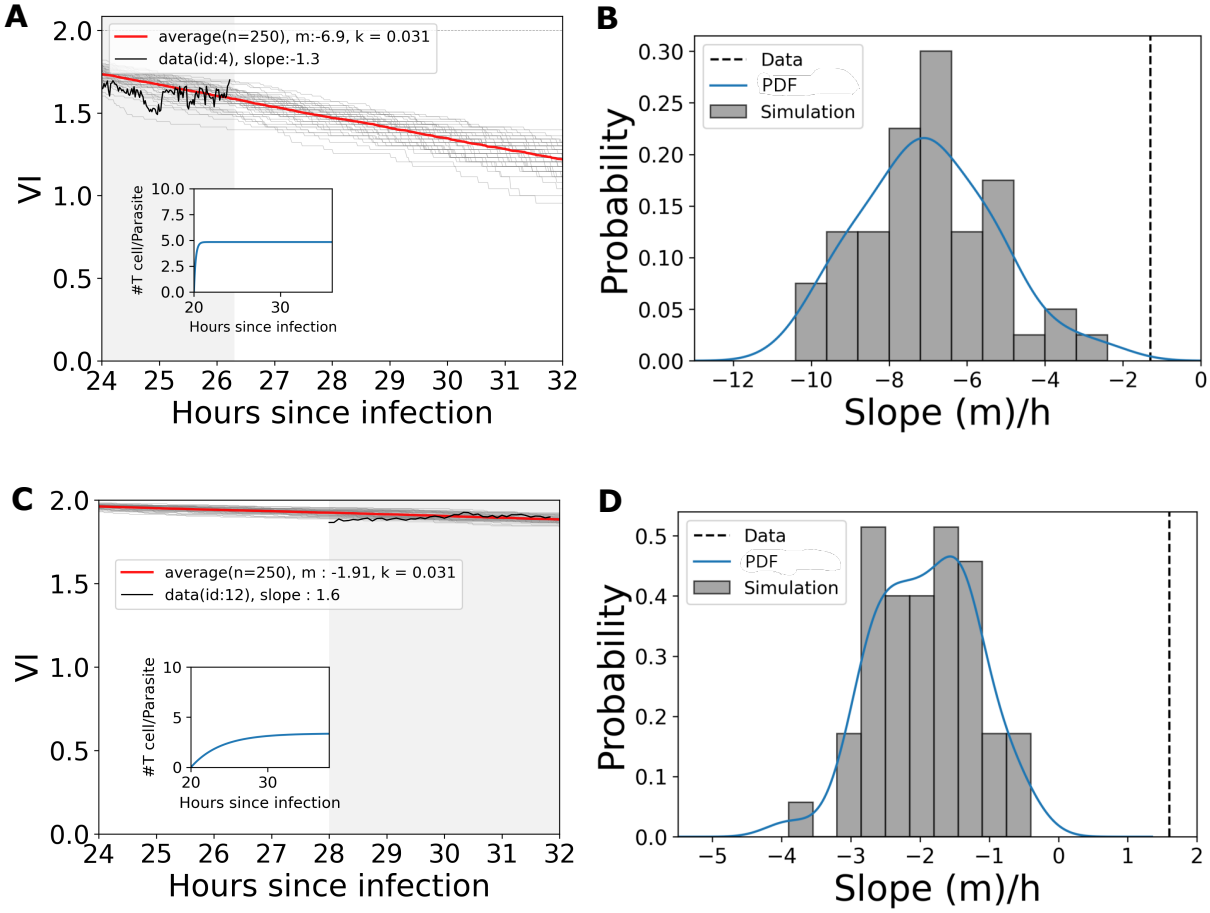


Figure 5: Constancy of parasite's VI is not consistent with stochastic simulations of killing by T cells. We simulated parasite's VI dynamics using Gillespie algorithm for 20 hours with a small growth rate $r = 0.0001/\text{h}$ and then added killing by T cells at a per capita rate $k = 0.031/\text{h}$ with the total kill rate being determined by the number of T cells per parasite increasing with time (see Materials and methods for more detail). **A, C**: We plot trajectory from 250 simulations (gray lines) with the average change (red line) calculated from every time step of 0.02 hour. T cell dynamics was added in the simulations using eqn. (18) with parameters estimated for individual parasites (A-B: ID = 4, C-D: ID = 12). Black lines in panels A&C show the actual change in VI over time as was observed in the data for parasite IDs 4 (A) and 12 (C). **B, D**: For every simulation we calculate the decay rate of the VI and show the distribution of decay rate with probability density function (blue line). The actual decay rate for the VI in the data for these two parasites is shown by horizontal black dotted line. Inserts show the T cell dynamics as assumed by the clustering model. Gray shaded area denote the imaging period which we used to calculate the VI decay rate. Simulations were done using package *gillespy2* with *Tau-Hybrid solver* in python. None of VI slopes in simulations were above the VI slope in the data suggesting $p < 0.01$ for the comparing simulations with the data.

study suggests a larger kill rate of B16 cancer cells by CD8 T cells in vivo [19]. Yet, all these estimates of kill rates are larger than what we found in our study suggesting that the type of target cell (e.g., type of intracellular pathogen) and of the tissue may influence the killing ability of T cells. One previous study found evidence of T cell cooperativity in killing of virus-infected cells [17], although a later re-analysis of the same imaging data suggested additive (mass-action like) killing by T cells [18]. Linear/additive effect of killing was also proposed in another study where delivery of 3 independent lethal hits by the same or different T cells within a short time period (< 1 h) was associated with target cell death [19]. We also did not find any evidence of T cell cooperation at elimination of Plasmodium liver stages but when multiple T cells cluster around the parasite, the probability of the parasite's death during the imaging period was higher (**Figure 2**Ci).

Many studies have estimated the rate at which a population of antigen-specific CD8 T cells kill their targets in vivo, for example, by using in vivo cytotoxicity assay (e.g., [32–35]), with target cell death rates ranging from minutes to days (reviewed in [36]). The exact reasons for this variability have not been fully elucidated but may involve differences in type of target cells used in experiments, how T cell antigens are expressed by the targets (e.g., peptide-pulsed vs infected), and variability in individual T cells in their killing ability. Indeed, several recent reports by tracking individual CD8 T cells suggested great variability of antigen-specific T cells in ability to kill their targets [17, 19]; variability in ability of different T cells to kill targets in vitro has been also well documented [19, 37, 38].

Our study has several limitations. To track viability of the Plasmodium liver stages we imaged a relatively small area around the parasite ($\sim 200 \times 200 \times 50$ μm) and T cells within 40 μm of the parasite were considered to be close to the infected hepatocyte for killing [22]. For the parasites located at the deeper liver areas (with a higher z-coordinate), we may have underestimated the number of clustered T cells. Indeed, artificially increasing the number of clustered T cells improved the model prediction on the VI dynamics supporting the idea that there may have been more clustered T cells than that observed experimentally. To more accurately evaluate how Plasmodium-specific CD8 T cells eliminate the infection our experiments were performed in "reverse": mice were first infected, T cell transferred only 20 hours after the infection and imaging was done several hours after the T cell transfer (**Figure 1**A). In part, this was also done due to low GFP expression by individual Py sporozoites that did not allow imaging of individual parasites from the start of infection. This setup corresponds to cases of adoptive T cell transfer therapy against cancer and not to prophylactic vaccination when activated/memory T cells are typically present prior to infection. Whether killing of Plasmodium liver stages proceeds similarly in cases when T cells are present in mice prior to infection and when sporozoites just invade the liver remains to be investigated.

Our estimates of the T cell killing rates were based on the DDR model predicting kinetics of T cell clustering around individual liver stages (**Supplemental Figure S6**). The typical prediction of this model is that the rate of T cell exit from the cluster is larger than the rate of T cell recruitment into the cluster, $\mu > \lambda_1$. This contradicts the basic idea of the DDR model suggesting amplification of the number of T cells in a cluster via positive feedback loop [16]. We suggested that the parameters of the DDR model are likely to be time-dependent, and with $\lambda_1 > \mu$, the recruitment parameters decline with time since T cell transfer allowing both increase in number of T cells in larger clusters but also stabilizing T cell numbers at later time points [22]. We simulated T cell clustering dynamics with the DDR-alpha model (DDR model with time-dependent parameters, eqn. (17)) and then fitted the DDR model with time-independent parameters (eqn. (18)) to subset of these "simulated data". We found that the DDR model typically overestimates the number of T cells present near the parasite at early time points suggesting that we may have slightly underestimated the T cell killing efficacy

(results not shown).

Several in vitro studies suggested that CD8 T cells are able to serially kill their targets [39–42]. Because we typically followed individual parasites located in different areas of the liver we could not document if T cells in these experiments performed serial killing. In fact, given seemingly random search of most T cells for the liver stages [43], sparcity of infected hepatocytes in the liver even at high infection doses, and relatively long time it takes for T cells to kill the parasite, it is unlikely that serial killing is relevant to CD8 T cell-mediated elimination of Plasmodium liver stages in mice.

Our study opens up directions for future research. Details of T cell clustering around individual liver stages remain incompletely understood. While previously we found a strong support for the DDR model [22] our inability to find evidence of attraction of most T cells towards the infection site is troubling [43]. One recent study also suggested a potential role of recirculating T cells in control of infection with Plasmodium sporozoites [44], and T cells may be following attracting cues via the liver sinusoids rather than via direct, Euclidean distance-based search as we have assumed previously [43]. Developing rigorous frameworks of how T cells search for the infection via the sinusoids is an active area of our research. Several cytokines such as IFNg and chemokine receptors (e.g., CXCR3, CCR5, and others) have been shown to be important in T cell-mediated control of Plasmodium infection [11, 45]. The role of these molecules in the efficiency of T cell search for and elimination of Plasmodium liver stages remains to be investigated. Future studies will need to combine the estimates of times it takes for CD8 T cells to locate and then to kill the liver stage. While several studies have found bias in T cell movement towards an infection site [46, 47], we failed to do so for most T cells in the liver even using a more sensitive metric to detect attraction [43]. In the absence of attracting cues the time to find the infection site may be substantial [11, 43] further reducing a chance that a single T cell is able to eliminate a liver stage and will require even larger T cell clusters for efficient elimination of the liver stage.

Taken together, our analyses indicate that the average ability of CD8 T cells to kill Plasmodium liver stages is rather limited and is not in agreement with the conclusion that activated CD8 T cell act as “rapid” and “serial” killers that destroy hundreds or thousands of targets per day [36]. Deeper understanding of factors that contribute to the ability of T cells to kill their targets – such as the dynamics of CD8 T cell response, cytolytic heterogeneity of CD8 T cells, T cell recirculation/migration kinetics, and specific details of the tissues where T cells encounter their targets [48] – are likely to improve our ability to estimate T cell kill rates and to make more accurate predictions on the number of T cells required to control infections and cancers [49]. Ultimately, better experimental methods, for example those using Ca-flux mice allowing to visualize recognition of antigen by T cells (and thus potentially, the delivery of the lethal hit) [19], will provide more a sophisticated description of how CD8 T cells kill their targets in vivo.

Data availability

The data used in the analysis are provided as a supplement to the paper as well as on github along with computer codes: https://github.com/soumenbera89/Killing-of-Malaria-Parasite-by-CD8-T-cell

Code availability

We performed most of our analyses in python and provided several key codes to ensure reproducibility of our results on github: https://github.com/soumenbera89/Killing-of-Malaria-Parasite-by-CD8-T-cell

Author's contributions

The data for the analyses have been generated in previous study primarily by IAC and RA. RA also contributed previously unpublished changes in the vitality index of Py liver stages in control experiments. VVG and SB designed some of the quantitative analyses including formulation of mathematical models. Different analyses have been performed by SB and VVG. IAC provided feedback on the analyses performed. SB wrote the first draft of the paper which was then finalized by VVG and edited by all authors. All authors contributed to writing the final version of the paper.

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Need for CD8 T cell clusters to eliminate a malaria liver stage arises in part due to heterogeneity in killing efficacy of individual effector T cells

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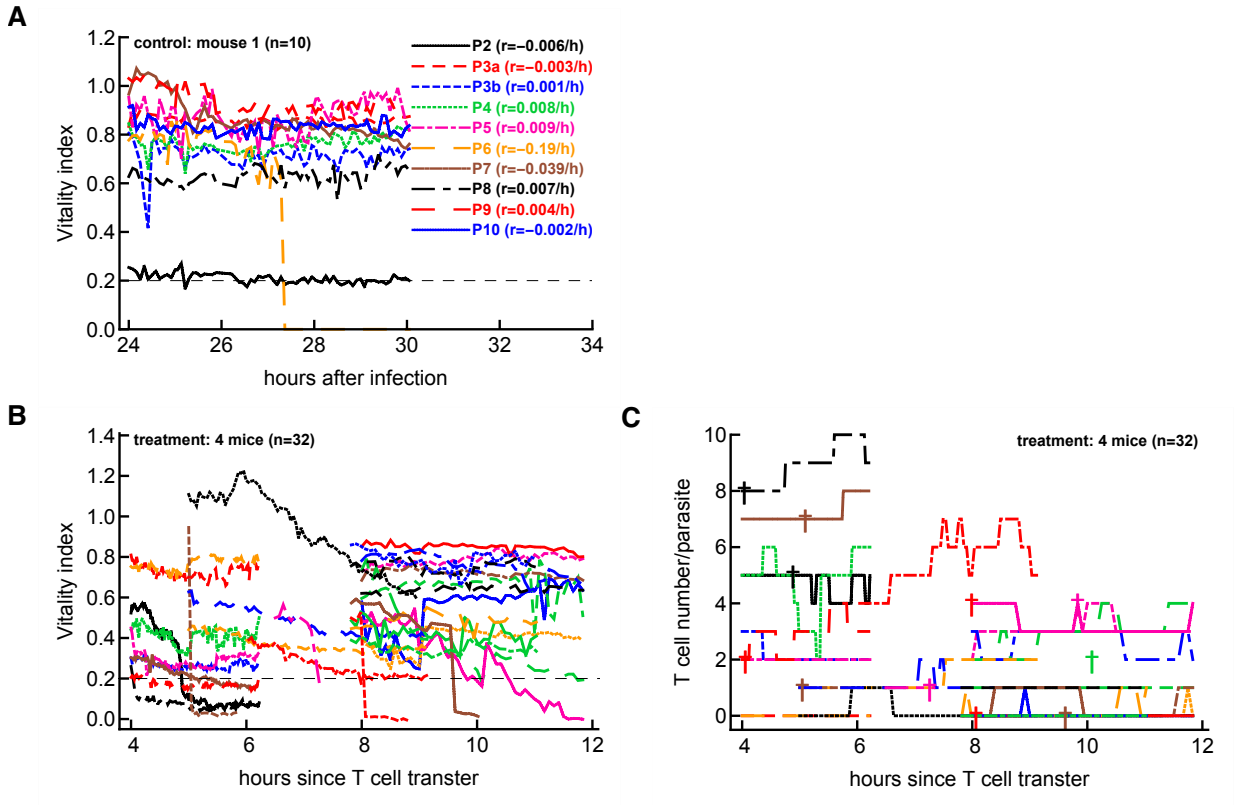
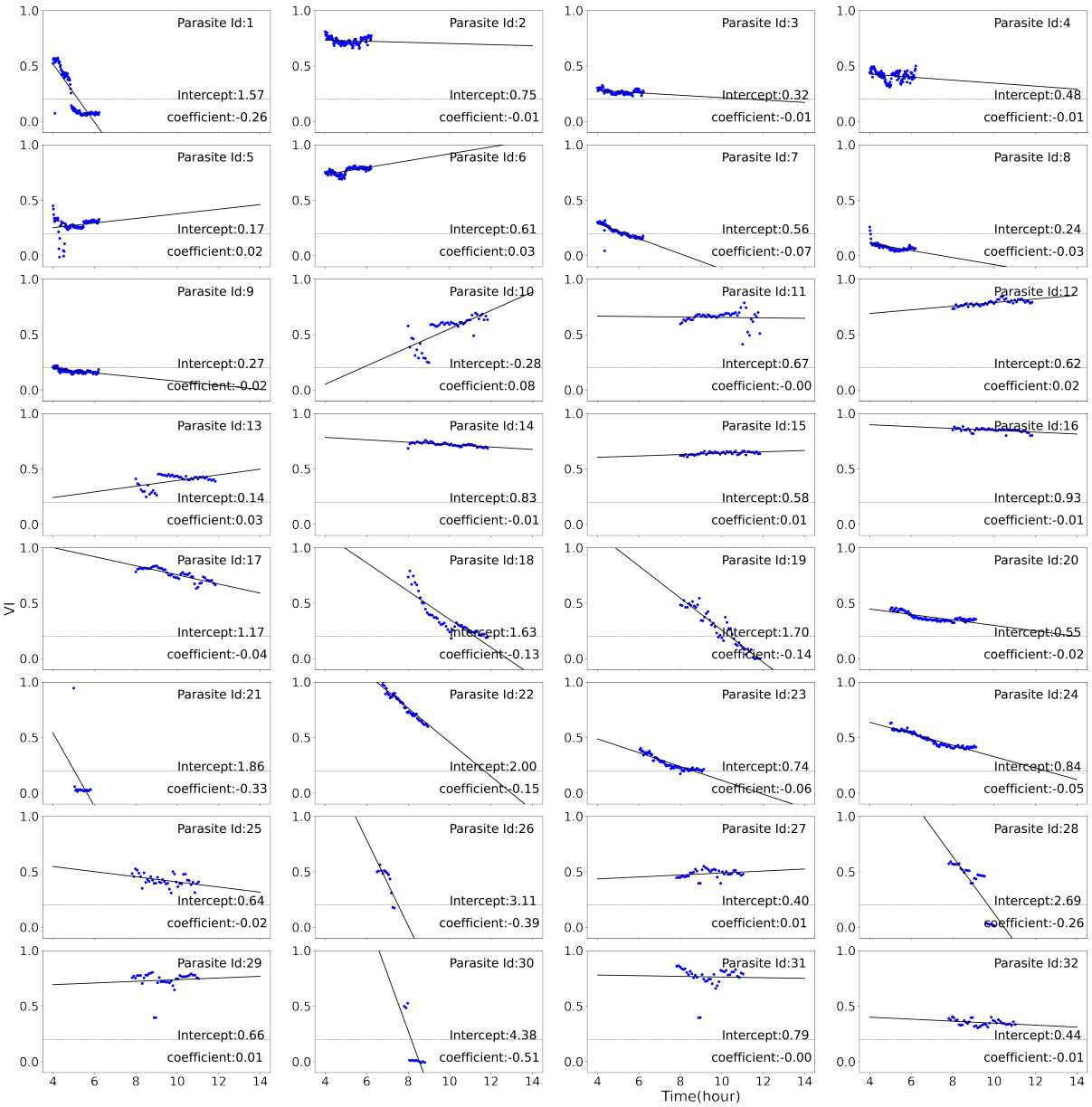
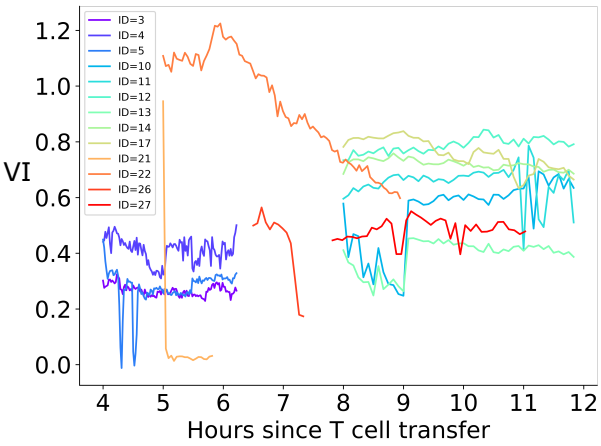
Supplemental Information



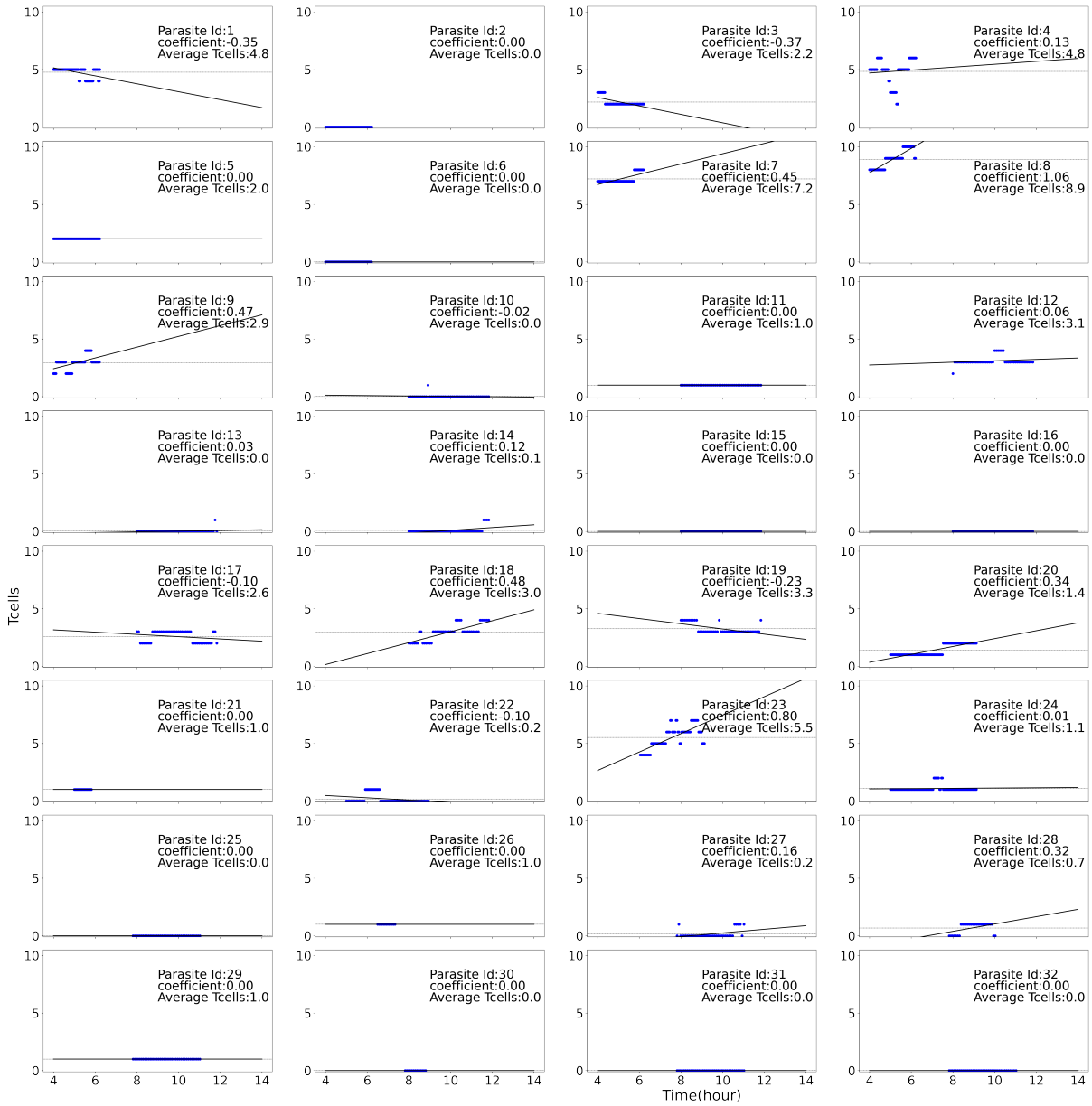
Supplemental Figure S1: Detailed data on dynamics of VI and T cell numbers in control and treatment groups of mice. (A) We plot the dynamics of parasite's VI for a subset of parasites ($n = 10$) in one of the two control mice along with estimated rates of VI change over time r. (B) We plot the dynamics of parasite's VI from 32 parasites in 4 mice in treatment group. (C) We plot the dynamics of T cell numbers located near each of the liver stages in B. Crosses indicate parasites that eventually died during the imaging (VI dropped below 0.2). In panel A&B dashed horizontal line denotes the threshold for a dead parasite (VI = 0.2). Note that in panel A time is in hours since infection and in panels B-C time is in hours since T cell transfer (that occurred 20 hours after the infection, see **Figure 1**A). Data for individual parasites are also shown in **Supplemental Figures S2 and S4**.



Supplemental Figure S2: Variable dynamics of the parasite's VI with time for all 32 parasites in the data. We performed linear regression of VI vs. time and parameters of the regression (slope and intercept) are indicated on individual panels. Regressions were performed using **scipy.stat** python package. Dotted horizontal line represent the VI = 0.2 cutoff for dead parasites.



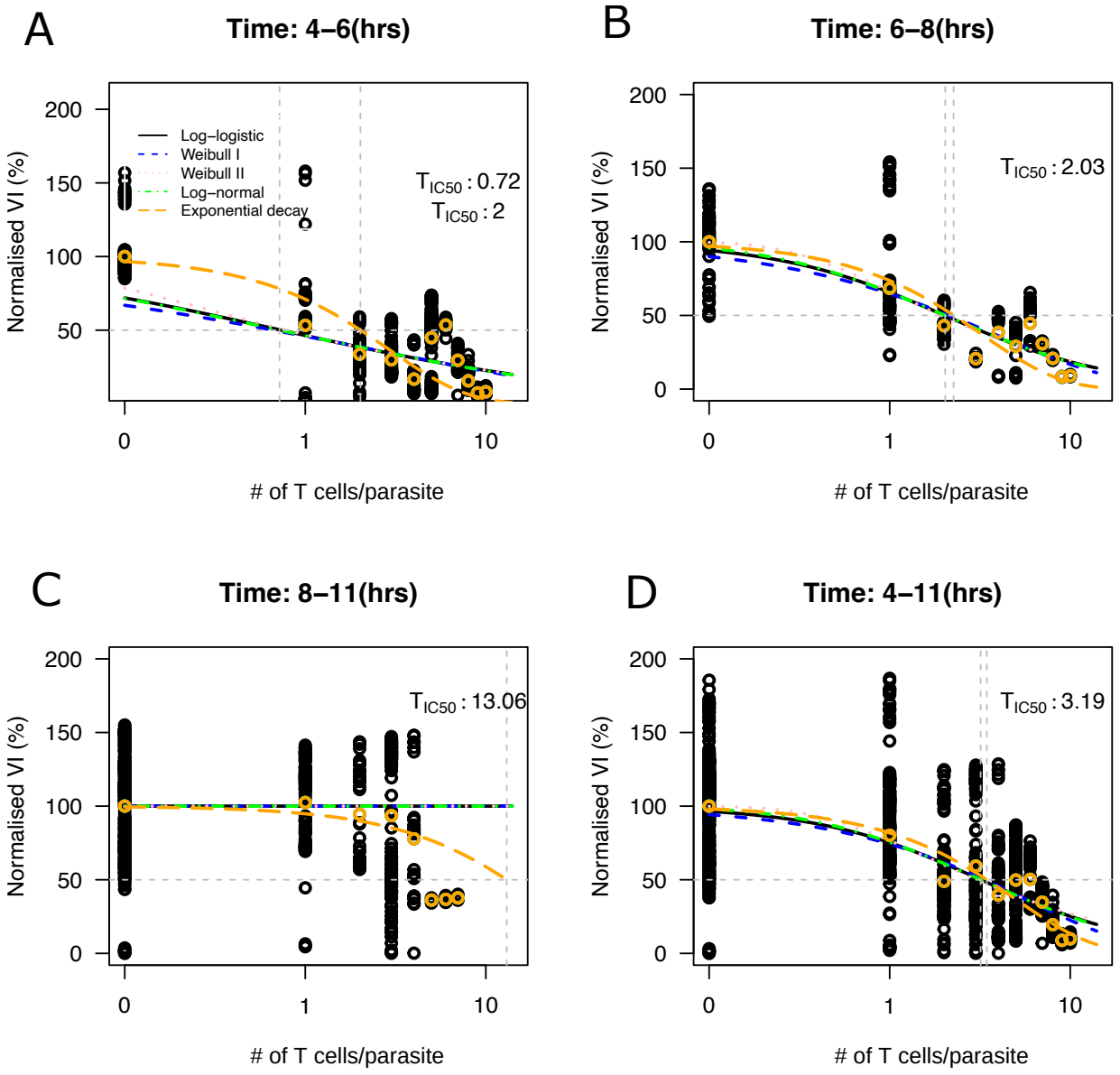
Supplemental Figure S3: Stability in parasite's VI dynamics with time for many parasites with non-zero T cells. We show the dynamics of VI of parasites that had some T cells nearby but did not die during the observation period (i.e., VI remained above 0.2). The correlation between VI and T cell numbers for these parasites is non-negative and thus, these were excluded from some of the analyses. The data are colored from violet to red based on the parasite ID number.



Supplemental Figure S4: Dynamics of T cells near each of 32 parasites. The slope (coefficient) and intercept of the T cell's trajectory was calculated using *scipy.stat* Python package. Dotted horizontal line represent the average number of CD8 T cells per parasite. Parasites with following IDs did not have any T cells nearby during the imaging period: 2, 6, 15, 16, 25, 30, 31, 32.

Model	β_1	β_2	β_3	β_4
	4-11 hours			
Log-logistic	0.9536	0	100	3.2
Weibull I	0.7	0	100	5.66
Weibull II	0.287	0	100	2.386
Lognormal	-0.6	0	100	3.2
Exponential decay	NA	4.99	0	100
	4-6 hours			
Log-logistic	0.47	0	100	0.74
Weibull I	0.29	0	100	2.39
Weibull II	-0.39	0	100	0.31
Lognormal	-0.29	0	100	0.73
Exponential decay	NA	2.92	0	100
	6-8 hours			
Log-logistic	0.92	0	100	2.02
Weibull I	0.61	0	100	3.89
Weibull II	-0.7	0	100	1.14
Lognormal	-0.57	0	100	2.03
Exponential decay	NA	3.27	0	100
	8-11 hours			
Log-logistic	15.77	0	100	143.89
Weibull I	276.2	0	100	7054.2
Weibull II	-2875.7	0	100	7088.4
Lognormal	-749.03	0	100	11301.5
Exponential decay	NA	18.85	0	100

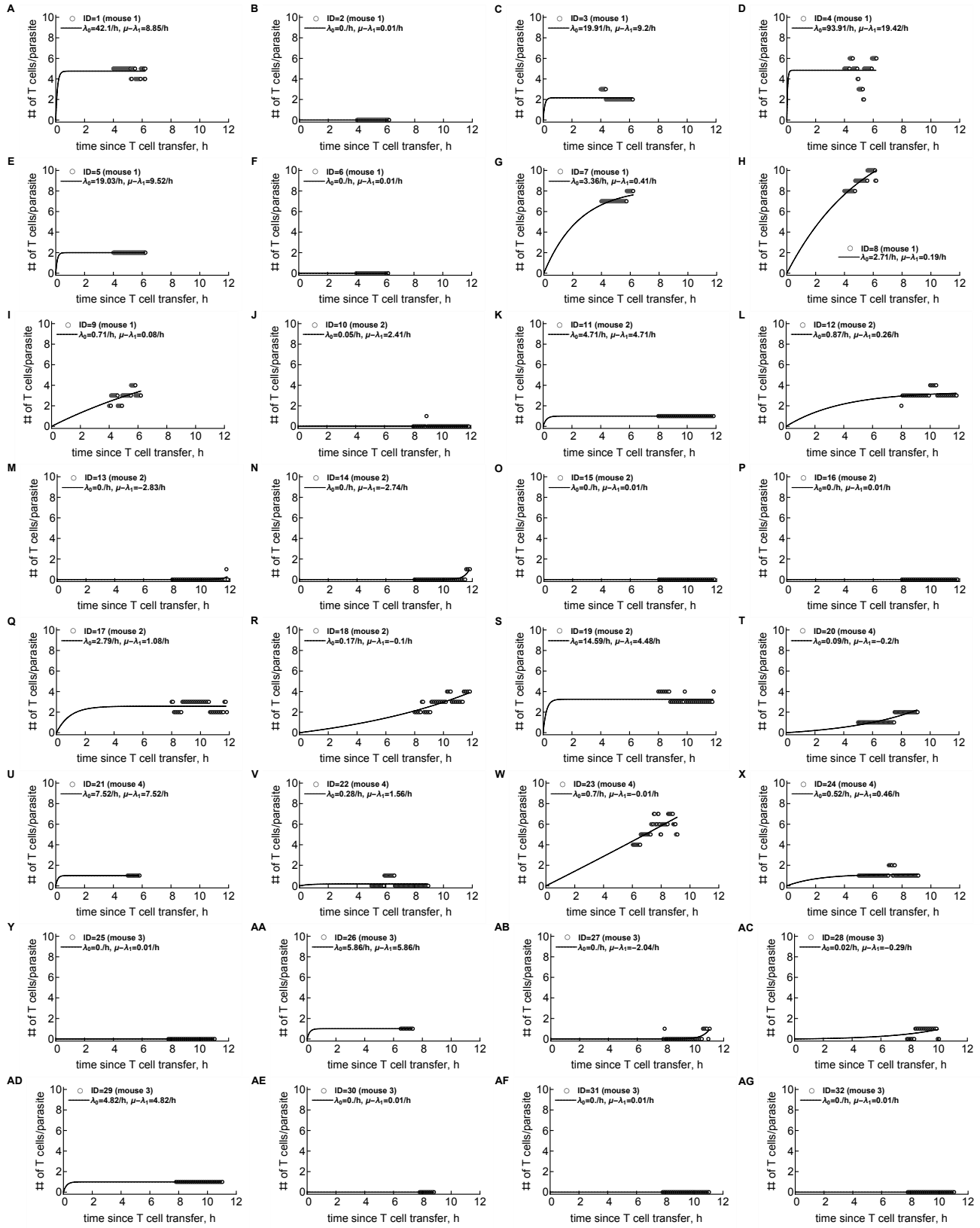
Supplemental Table S1: Estimated parameters of the dose response models. We fitted log-logistics (eqn. (1)), Weibull I (eqn. (2)), Weibull II (eqn. (3)), lognormal (eqn. (4)), and exponential decay (eqn. (5)) models to normalized VI data divided into different time periods (4-8, 6-8, 8-11, and 4-11 hours post T cell transfer, see Materials and methods for more detail). Model fitting was done using `drc` package in R. Estimated parameters are β_1 (slope), β_2 (lower limit), β_3 (upper limit), and β_4 (T_{IC50}), and NA denotes not applicable. Values for lower and upper limits were restricted to 0 and 100, respectively.



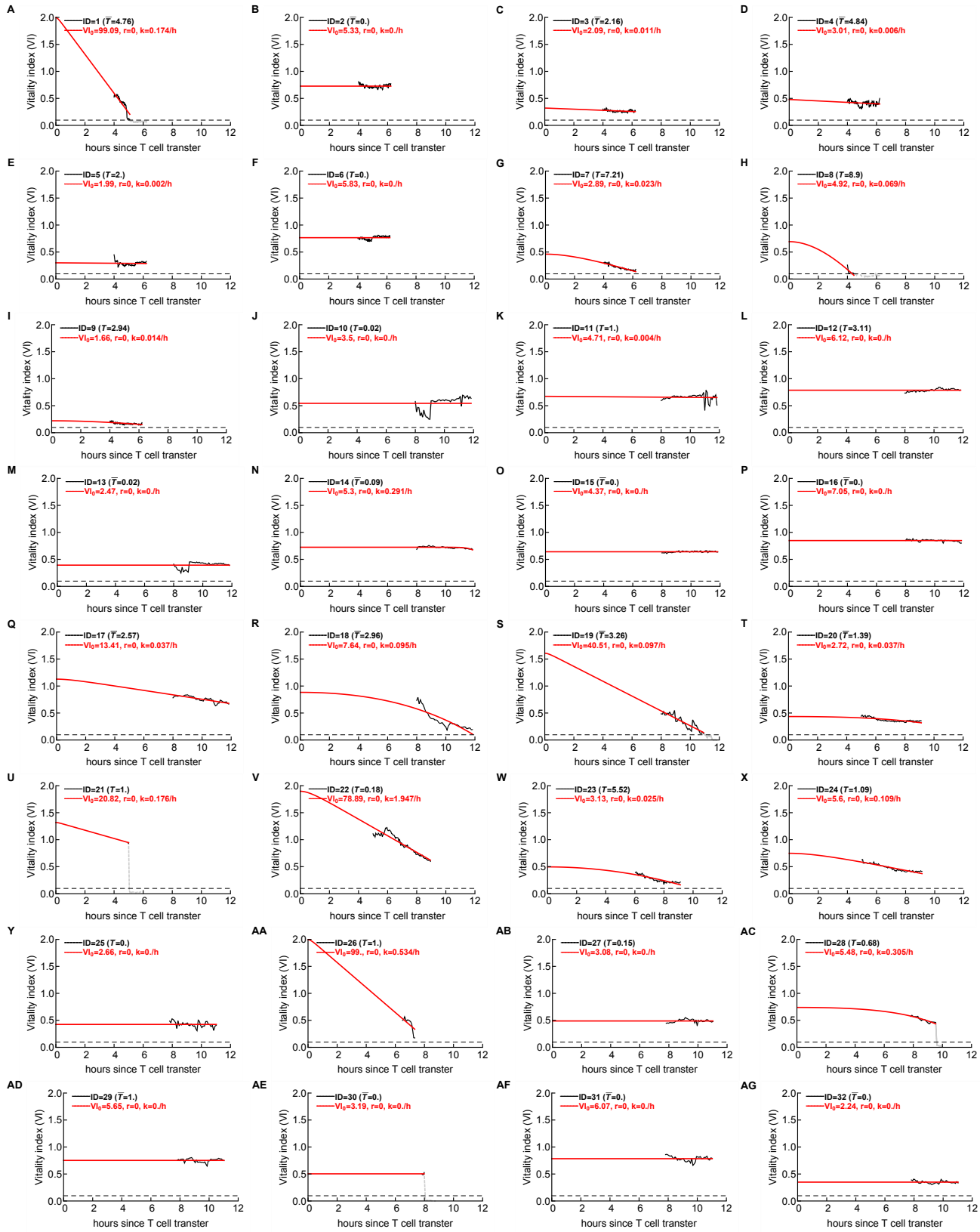
Supplemental Figure S5: Higher numbers of T cells per parasite are needed to reduce parasite's VI by 50% at later times since T cell transfer. We fitted several dose-response functions (eqns. (1)–(5)) to normalized experimental data on VI values for all time points with T cell numbers as a "dose". Data were normalized to their initial value. (A-C) Datasets were partitioned in different time periods (4-6, 6-8, and 8-11 hours after T cell transfer) (D) The models were fitted to all data. A decision-tree based approaches is used to select the best fit model among the candidates using AIC in R package *drc*. The predicted number of T cells at which VI reaches 50% of its initial value (T_{IC50}) is shown on individual panels by the dashed vertical lines. Dashed horizontal lines denote 50% of initial VI. Parameters of the best fit models are given in **Supplemental Table S1**.

Parasite ID	Null Model (no T cell)	Model (with experimental T cells)			Model (increasing T cell/15 mins)			Model (increasing T cell/30 mins)			Model (increasing T cell/60 mins)		
	P, 1/hr	**P, 1/hr**	α	**k, 1/hr**	**P, 1/hr**	α	**k, 1/hr**	**P, 1/hr**	α	**k, 1/hr**	**P, 1/hr**	α	**k, 1/hr**
1	-0.036	0.0877	1.555	0.0381	-0.011	9.332	1.178	0.2443	**1.4139*****	0.0728	0.9628	**1.132*****	0.2206
3	-0.0019	0.0105	9.069	177.7	0.0196	**12.07****	5876	0.0224	**9.616****	389.8	0.0369	**6.55***	15.22
4	-0.0015	0.0355	7.356	1.664	**0.0649***	**7.256****	1.829	**0.055***	**7.154***	1.633	0.06	6.136	0.888
5	-0.0149	-0.179	-0.073	-0.021	**-0.096****	**-0.358****	**-0.0025***	**-0.1167****	**-0.274***	**-0.005***	**-0.127****	-0.257	-0.008
7	-0.016	0.3475	**1.334*****	0.083	0.3224	**1.59*****	0.095	0.3628	**1.638*****	0.121	0.362	**1.6381*****	0.121
8	**-0.049*****	0.2662	**1.4627*****	**0.1055*****	0.2499	**1.548*****	**0.114*****	0.3052	**1.4583*****	**0.1149*****	**0.3052***	**1.4583*****	**0.1149*****
9	-0.0036	**0.0521****	4.152	4.63	**0.0828*****	**7.201*****	882.1	**0.078****	**5.529*****	66.15	**0.072***	**4.283*****	9.265
12	0.0013	0.008	21.14	0.2239	0.0073	27.64	0.26	0.007	29.04	0.556	0.007	28.22	0.7046
13	-0.005	-0.0051	2.25	0.0118	0.006	23.15	2.6e5	0.007	22.44	3.3e5	0.007	22.44	3.3e5
14	-9e-05	0.0012	**145.1*****	4.5e20	**0.0125****	**30.88*****	29.88	**0.0105***	**33.91*****	187.4	**0.0076***	**31.82****	182
17	-0.0035	0.0028	3.0855	0.0042	0.0279	**5.4811***	0.0138	**0.0421***	**6.1223*****	**0.0316***	0.0457	**4.7322*****	0.032
18	-0.0374	0.0419	**1.8391****	0.0586	**0.172***	**2.621*****	**0.1624****	0.0744	**2.4047*****	0.0989	**-0.0265***	63.93	150000
19	-0.0393	**-0.4337***	**0.7558*****	-0.0906	0.1968	**1.9948*****	**0.0868***	**0.3357***	**1.7309*****	**0.1374***	0.3447	**1.466*****	0.1309
20	-0.0031	0.0089	6.6652	2.1162	**0.0351****	**8.7531*****	13.704	**0.0259***	**9.1719*****	24.67	0.0202	**7.6859*****	7.643
22	**-0.0059***	-0.0045	10.14	0.0014	0.0074	**3.068****	**0.0032***	0.0058	**3.55****	**0.006***	0.0197	**2.717*****	**0.015****
23	-0.0126	**0.203***	**1.9964*****	**0.1476****	**0.3146*****	**2.5811*****	**0.353*****	**0.3365*****	**2.2805*****	**0.3202*****	0.1764	**1.8378*****	**0.1182***
24†	**-0.0055***	-0.0036	339.6	2.6E66	-0.0011	**28.34*****	1.6e4	0.0184	**7.6052*****	0.8049	**0.04****	**5.517*****	**0.5883*****
27	-0.0005	0.0023	7.2209	1.803	**0.037***	**13.97***	108.08	0.0304	**13.43***	153.32	0.0125	29.24	1.5e07
28	-0.0455	-0.0105	0.6655	0.0457	0.0309	3.3187	0.1683	0.0183	3.4518	0.3911	-0.0176	11.008	226.7

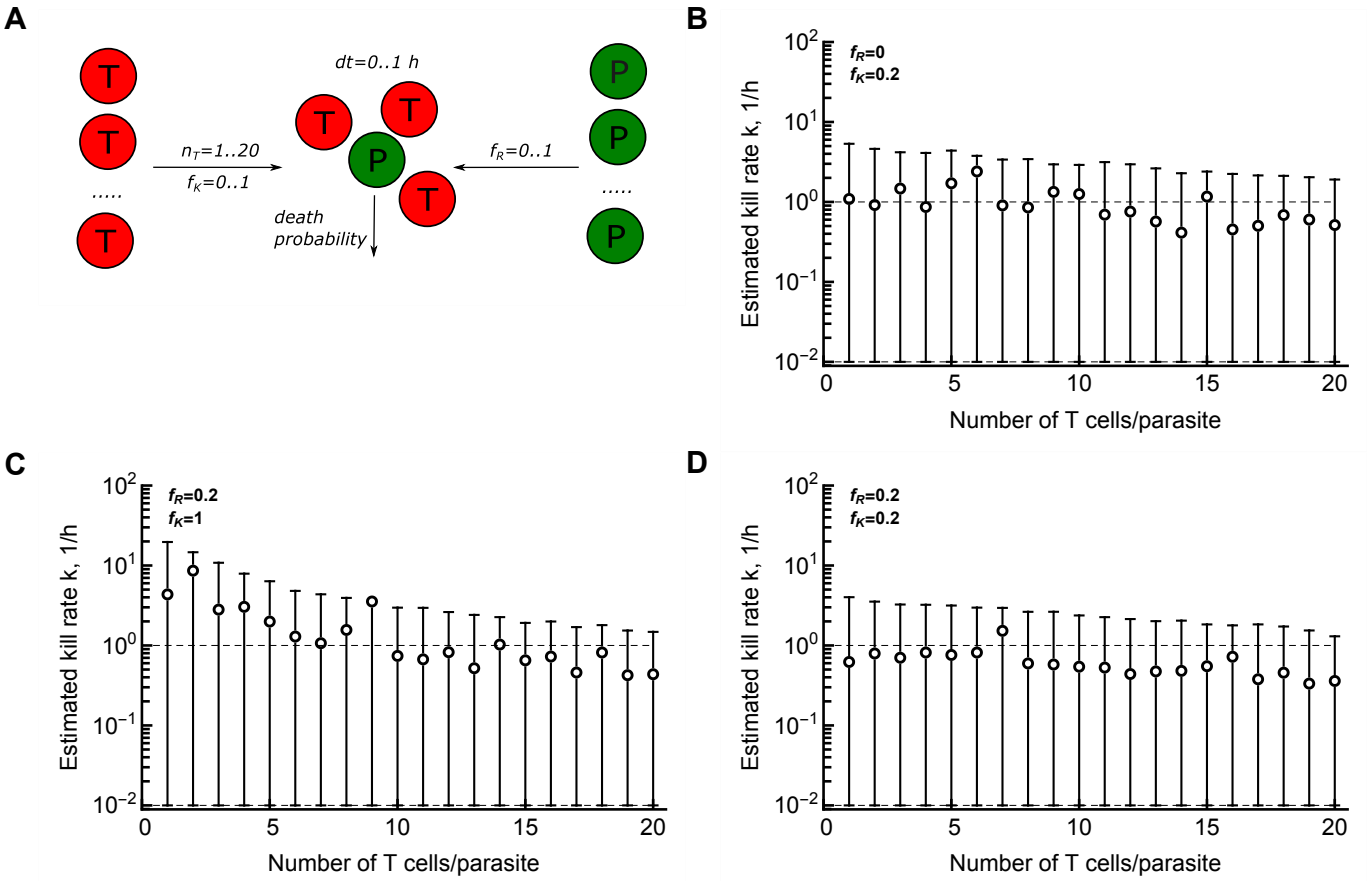
Supplemental Table S2: Estimated parameters of the forecasting model in which the number of T cells per parasite was assumed to increase over time at different time intervals. The null model (without T cell, eqn. (14)), or forecasting model with experimentally measured T cell numbers or when we assumed a steady increase in T cell numbers per parasite (eqn. (15)) were fitted to data. All the forecasting models were compared with the null model using ANOVA. Model fitting was done by R package *minpack.lm*. Statistical significance code shown with bold where '***p'< 0.001, '**p' < 0.01, and '*p' < 0.05. † represent model fitted with data without convergence.



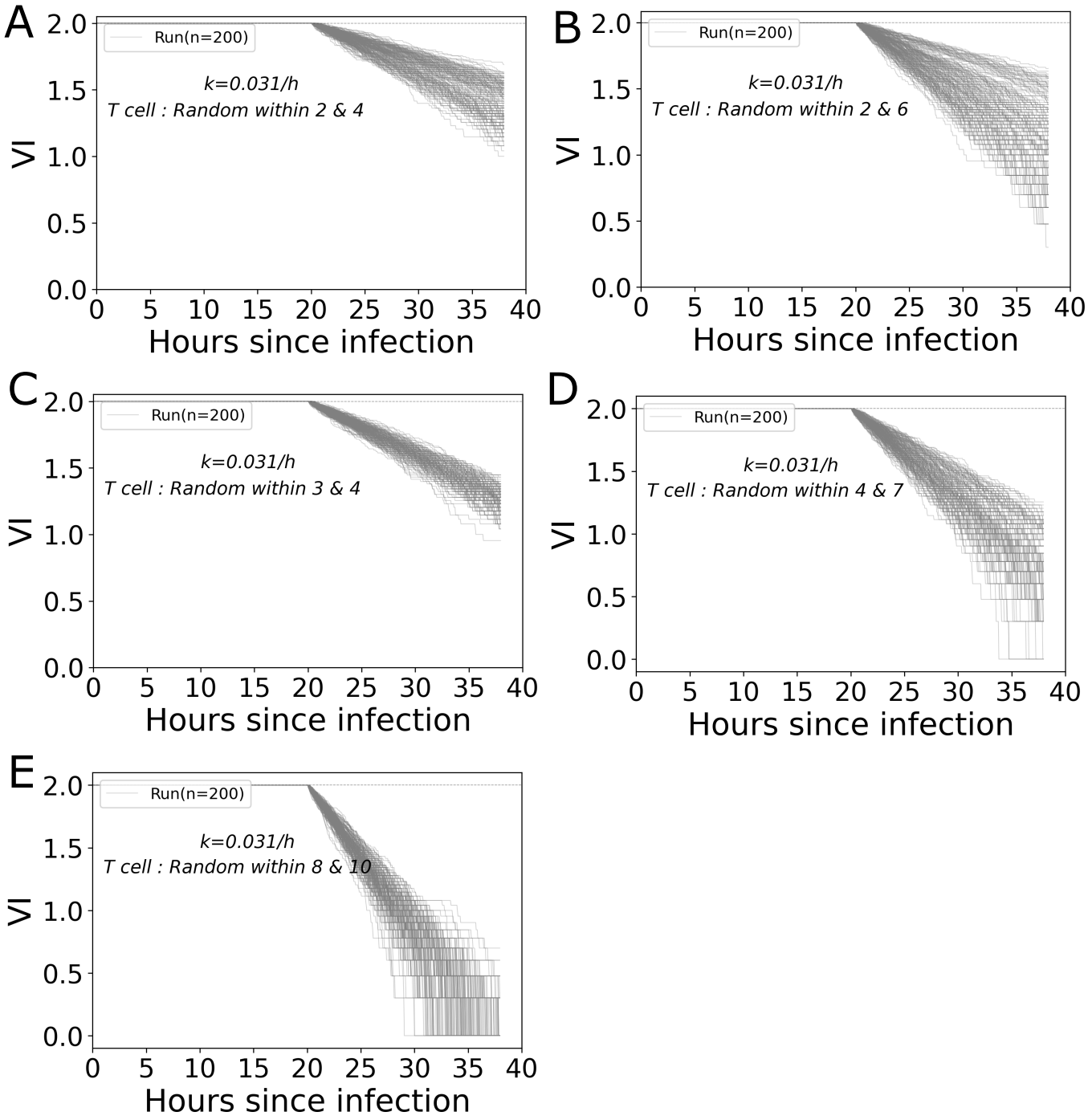
Supplemental Figure S6: Density-dependent recruitment model describes well the change in the number of T cells different parasites. (A-AG): We fitted the DDR model (eqn. (18)) to the change in T cell number found around individual 32 liver stages. The data are shown by markers and predictions of the best fit model by lines. Each panel shows the estimated parameters λ_0 and $\mu - \lambda_1$. Fitting was done using `NonlinearModelFit` routine in Mathematica using nonlinear least squares.



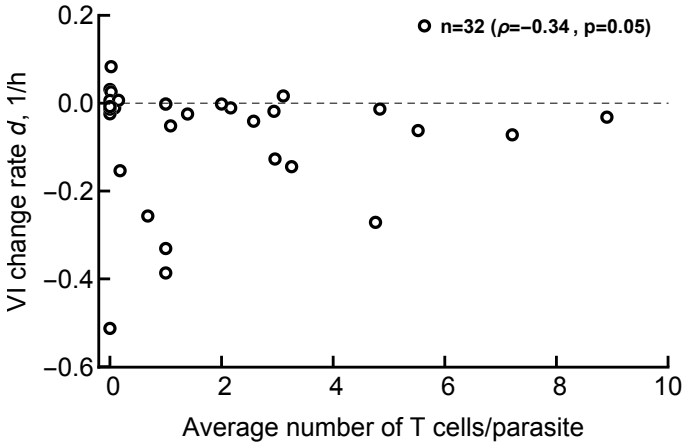
Supplemental Figure S7: The dynamics of VI is well explained by the mass action-like killing of CD8 T cells. We fitted alternative models (eqns. (19)–(20)) to the dynamics of VI for individual liver stages assuming that T cell clustering dynamics following the DDR model (**Supplemental Figure S6**). (A-AG): The data are shown by black lines and predictions of the best fit basic model (eqn. (19)) by red lines. Each panel shows the time average of the number of T cells per parasite and estimated parameters VI_0, r, and k. Horizontal dashed line in all panels denotes a critical VI = 0.1 and we only used the data with VI > 0.1 in model fitting. A slightly lower critical VI was used here to allow for more data in fitting models to the data. Fitting was done using `FindMinimum` routine in Mathematica with nonlinear least squares.



Supplemental Figure S8: Stochastic simulations suggest that both variability in parasite resistance and per capita T cell killing efficiency explain highly variable estimates of kill rates. (A): Schematic representation of stochastic simulations of killing of the liver stages by T cells. In simulations, we varied the number of T cells in the cluster ($n_T = 1 \ldots 20$) assuming that T cells either can kill the liver stage at a rate $k = 1/\text{h}$ or are nonlytic $k = 0$ with a probability f_K while the parasite may be fully resistant to killing with a probability f_R. T cells interact with the parasite for Δt time chosen uniformly from $0 \ldots 1$ h. (B-D): estimated killing efficacy (mean and 95% range) as the function of the number of T cells in the cluster assuming that T cells vary in killing efficacy ($f_K = 0.2$) while parasites are fully susceptive to killing ($f_R = 0$, panel B); all T cells can kill ($f_K = 1$) but some parasites are fully resistant to killing ($f_R = 0.2$, panel C); both T cells vary in killing efficacy ($f_K = 0.2$) and parasites vary in resistance ($f_R = 0.2$, panel D). In panels B-D, in cases when estimated killing efficacy was lower than 10^{-2} it was assigned a value 10^{-2} to plot these values on the log-scale. Simulations were repeated 10,000 times for each parameter combination.



Supplemental Figure S9: Stochastic simulations of VI dynamics are inconsistent with constant VI observed for most parasites. We performed stochastic simulations of VI dynamics assuming the model with mass-action killing ($k = 0.031$/h) using Gillespie algorithm. To mimic our experimental design we simulated the model for 20 hours without any CD8 T cell with a minimal parasite's growth rate. Then we adding a random number of T cells (chosen 200 times from a uniform distribution with limits indicated on individual panels and taken from the actual range observed for individual parasites) and simulated the dynamics for the next 16 hours. Dotted line shown the VI threshold of a death parasite. The simulations were done using Python package *gillespy2* with *TauHybrid Solver* routine.



Supplemental Figure S10: The number of T cells per parasite is a relatively poor predictor of the VI change rate. For every of 32 parasites in our datasets we calculated the rate d of VI change with time using linear regression (see **Supplemental Figure S2**) and for the same parasites we calculated the average number of T cells observed in imaging experiments. Negative values for the change rate imply declining VI. Note that many parasites had only few T cells in their vicinity. Spearman rank correlation coefficient ρ and p value from the test is shown.