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Macrophage transactivation for chemokine production identified as a negative regulator of granulomatous inflammation using agent-based modeling.

Daniel Moyo[1,2], Lynette Beattie[1*], Paul S Andrews[3], John W J Moore[1], Jon Timmis[3], Amy Sawtell[1], Stefan Hoehme[4], Adam T. Sampson[5], Paul M Kaye[1]

[1.] Centre for Immunology and Infection, Department of Biology and Hull York Medical School, University of York, UK.

[2.] Department of Computer Science, University of York, UK.

[3.] Department of Electronics, University of York, UK and SimOmics Ltd, York. U.K.

[4.] Institute for Computer Science, University of Leipzig, Germany

[5.] Division of Computing and Mathematics, Abertay University, Dundee, UK.

*Current address: Doherty Institute, University of Melbourne, Australia.

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Abstract

Cellular activation *in trans* by interferons, cytokines and chemokines is a commonly recognized mechanism to amplify immune effector function and limit pathogen spread. However, an optimal host response also requires that collateral damage associated with inflammation is limited. This may be particularly so in the case of granulomatous inflammation, where an excessive number and / or excessively florid granulomas can have significant pathological consequences. Here, we have combined transcriptomics, agent-based modeling and *in vivo* experimental approaches to study constraints on hepatic granuloma formation in a murine model of experimental leishmaniasis. We demonstrate that chemokine production by non-infected Kupffer cells in the *Leishmania donovani*-infected liver promotes competition with infected KCs for available iNKT cells, ultimately inhibiting the extent of granulomatous inflammation. We propose trans-activation for chemokine production as a novel broadly applicable mechanism that may operate early in infection to limit excessive focal inflammation.

Introduction

Immune responses are commonly initiated by localized infectious insult and multiple mechanisms have evolved to allow spread of host effector responses to meet the challenge of pathogen containment. In the late 1950's, seminal studies by Isaacs and Lindenmann defined how "interferons' amplified local cellular resistance following virus infection [1, 2]. A decade later, Mackaness described cross protective cellular immunity mediated via T cell cytokine-dependent macrophage activation [3]. More recently, cytokine-and chemokine- mediated amplification of host protective immunity has been described across a spectrum of responses driven by both innate lymphoid cells and via conventional T cells [4-9]. Whilst serving to eliminate pathogens more effectively, a potentially undesirable consequence of amplifying immune effector responses is immunopathology, collateral damage induced by an over-zealous drive towards inflammation. Hence, an equally impressive array of "regulatory" or "suppressive" mechanisms have been defined that serve to limit immunopathology, and that suggest an evolutionary balance between pathogen elimination and host survival [10-12].

Granulomatous inflammation represents an extreme form of focal inflammation, often initiated around pathogens or foreign bodies that pose a formidable challenge for immune clearance. Granulomas are a hallmark of the immunopathology of many human infectious diseases including tuberculosis [13, 14], schistosomiasis [15]and leishmaniasis [16]. Whilst granuloma formation may provide means for containment and be host beneficial, excessive granuloma formation, numerically or in terms of individual granuloma size can lead to severe pathological consequences. Hence,

mechanisms for limiting the exuberance of the granulomatous response through late acting regulatory pathways are also well described in the literature [17-20]. However, the question of whether additional regulatory mechanisms operate at the earliest stages of granuloma initiation and prevent or limit over-exuberant granuloma formation has not been previously addressed.

Experimental visceral leishmaniasis, resulting from infection of mice with the Kupffer cell (KC) tropic parasite *Leishmania donovani*, has provided a highly tractable tool to study the initiation of granulomatous pathology in the hepatic microenvironment. Following infection of mice with *L. donovani*, infected KCs transiently release the chemokines CCL1, CCL2 and CXCL10 in a T cell-independent manner, whereas sustained expression of CXCL10 is dependent upon IFNγ production by invariant NKT (iNKT) cells [21]. IFNγ production by iNKT cells is in turn costimulated by ligation of CD47 on NKT cells by signal regulatory protein alpha (SIRPα) expressed on KCs, providing positive feedback for sustained iNKT cell recruitment and KC activation [22]. A similar role for CXC chemokines in recruiting hepatic NKT cells has been observed in other models of liver infection / inflammation [23, 24]. For example, CXCL9 produced by KCs following infection with the bacterium *Borrelia burgdorferi* results in CXCR3-dependent clustering of NKT cells around infected KCs [25] whereas CXCR6 and its ligand CXCL16 regulate NKT cell accumulation in the liver during fibrosis [26]. Hence, early recruitment of "amplifier" cells such as NKT cells is a central and common theme of focal inflammation.

Examination of the kinetics of granulomatous inflammation in this model of visceral leishmaniasis suggests, however, that there may be inherent limitations imposed on the ability of the host to form hepatic granulomas. Notably, granuloma formation proceeds asynchronously, and even many weeks after infection, fully formed granulomas sit side by side with infected KCs that appear to have failed to stimulate an inflammatory focus [16, 27]. Here, we have combined transcriptional profiling and computational modeling to probe possible mechanisms that might underpin the asynchronous development of granulomas in this model. We demonstrate that KC chemokine production, contrary to expectations, is not restricted to infected cells alone, but spreads in trans to include uninfected KCs within the infected liver. Data generated using a novel agent based model (ABM) in which KCs and iNKT cells interact within a spatially constrained sinusoidal network suggest that the spreading of chemokine production to uninfected KCs limits the competitiveness of infected KCs in terms of their ability to attract iNKT cells and initiate granuloma formation. In silico experiments predicted that this competition could be overcome by increasing the number of available NKT cells, a prediction borne out in vivo. Hence, our data identify a new pathway that operates early in infection to limit excessive inflammation by introducing competition for a finite resource (i.e. iNKT cells) that is needed for granuloma initiation.

Materials and Methods

Mice and parasites.

C57BL6 mice were obtained from Charles River (UK). mT/mG [28] and LysMcre [29] mice have been previously described. Mice were bred and housed under specific

106 pathogen-free conditions and used at 6-12 weeks of age. The tandom Tomato
107 fluorescent protein expressing Ethiopian strain of *Leishmania donovani* (tdTom.LV9)
108 [30] were maintained by serial passage in *Rag1*$^{-/-}$ mice. Amastigotes were isolated
109 from infected spleens, and mice were infected with $3x10^7$ *L. donovani* amastigotes
110 intravenously (i.v.) via the tail vein in 200µl of RPMI 1640 (GIBCO, UK). All
111 animal procedures were approved by the University of York Animal Welfare and
112 Ethical Review Board and carried out in accordance with UK Home Office license
113 (PPL 60/4377).

114

115 *Microarray analysis*

116 As previously described [31], Kupffer cells were flow sorted (on the basis of
117 SSC/FSC and expression of CRIg, Gr-1 and F4/80) from naive mice and from
118 infected mice and KCs from infected mice were further sorted (on the basis of
119 TdTomato expression) into those containing amastigotes ("infected") and those that
120 did not ("inflamed"). A total of 64 mice were used in the microarry study, in four
121 independent infection experiments. RNA was isolated, amplified and equal amounts
122 were assayed using Agilent SurePrint G3 Gene Expression 8x60 Microarray chips.
123 Scanned data were normalized (80^{th} percentile) and gene expression data analysed
124 using Genespring v9. Differentially expressed (DE) genes were defined using a false
125 discovery rate (FDR) of 5%. Source data is accessible from EBI Array Express (E-
126 MEXP-3877) and methodology for subsequent data analysis is described in further
127 detail elsewhere [31].

128

Histological Analysis.

Mice were treated with 1μg recombinant IL-15 (BioLegend) intravenously and infected 3 days later. Four days post-infection, mice livers were extracted, weighed then placed into 2% PFA in PBS for 2 hours, then 30% sucrose in PBS overnight. Tissues were then embedded in Optimal Cutting Temperature (OCT)(Sakura) and stored at -70°C until use. 10μm cryosections were fixed and labeled with Alexa647 or Alexa488 conjugated F4/80 (eBioscience) and DAPI (Invitrogen) to visualize KCs and cell nuclei respectively. Images were captured as 0.81μm optical slices using a LSM510 confocal microscope (Zeiss). Blinded slides were imaged to score the percentage of infected foci having formed a distinct inflammatory focus (greater than 15 cells), with imaging fields selected via tdTomato expression.

Flow Cytometry.

Livers were homogenized and mononuclear cells prepared as previously described [30]. Cells were incubated with anti-CD16/32 and then labeled with NK1.1, CD3, B220 and CD1d tetramer (a kind gift from V. Cerundulo) to identify T, NK and NKT cells. Samples were analyzed using a CyAn flow cytometer with Summit software (DAKO). Autofluorescent events and dead cells were excluded from analysis by gating on unused fluorescent channels and LIVE/DEAD fixable dead cell stain (Invitrogen) respectively.

Parameterizing and Calibrating the Simulation.

A full summary of the biological data available that was used to calibrate the simulation is listed in **Table S1**. The entire list of baseline simulation parameters is found in **Tables S3**. Full details of parameterization and calibration of the simulation are provided in the **Supplemental Experimental Procedures**.

Statistical Analysis.

When quantifying granulomas, experimental data are expressed as mean ± SEM for each group of 5 mice from two independent experiments, and statistical analyses performed using two-tailed paired Student t-tests. All tests used 95% confidence intervals. Simulation data non-normality was determined using the D'Agostino and Pearson test, and non-normal simulation data was analyzed using either Wilcoxon signed-rank or Kolmogorov-Smirnov tests where appropriate. Aleatory analysis was used to determine the minimum number of simulation results required to mitigate stochastic uncertainty (see **Figure S4**). Latin-hypercube sensitivity analysis was facilitated by using the Spartan tool for understanding uncertainty in simulations [32].

Results

Chemokine production by KCs in mice infected with L. donovani

Both chemokines and iNKT cells are central to the initiation of granulomatous inflammation following *L. donovani* infection. In order to gain insight into the production of chemokines involved in KC-directed recruitment of NKT cells, we used transcriptional profiling of KCs isolated from mice infected with *L. donovani* as

previously described [31]. Following infection of mice with Td-tomato transgenic *L. donovani*, approx. 20% of the KC population are infected with amastigotes. We isolated KCs from infected mice and sort purified these KCs on the basis of whether they contained intracellular amastigotes ("infected') or not (herein referred to as "inflamed" to denote their exposure to inflammatory signals *in vivo*) [31]. As shown in **Figure 1A**, KCs from infected mice expressed a variety of chemokines when compared to KCs isolated from naïve mice. At 2h post infection (p.i.), enhanced accumulation of mRNAs for *Cxcl1*, *Cxcl2*, *Cxcl3* and *Cxcl5*, as well as *Ccl3* and *Ccl4*, was evident (determined as differentially expressed using a 5% FDR). This transcriptional response was transient, in keeping with previous studies at the level of whole liver tissue [21]. Rapid secretion of chemokines in response to *L. donovani* infection can also be inferred from studies in which G-protein coupled receptor signaling was abrogated by pertussis toxin [22]. A suite of inducible chemokines, including *Cxcl9*, *Cxcl10*, *Ccl8* and *Ccl12* showed enhanced mRNA accumulation at 12h p.i. (at a 5% FDR), again in keeping with data in whole liver and with previously published data indicating the production of IFNγ by iNKT cells during early *L. donovani* infection (e.g. Figure 2 in reference 22). For example, qRT-PCR demonstrated sustained and elevated *Cxcl10* at 24h p.i. [33]. Similarly, transcriptional profiling of the livers of infected BALB/c mice (n=4-5 per time point) indicates sustained elevation of *Cxcl9* (Log_2FC compared to controls of 5.25, 5.14, 5.34 and 4.74 for days 15, 21, 36 and 42 p.i. respectively; FDR 0.05, $p<0.05$) and *Cxcl10* (Log_2FC of 4.84, 4.92, 5.36 and 4.55, respectively; Ashwin et al, manuscript in preparation). Strikingly, there was little difference to discriminate the chemokine response of infected vs. inflamed KCs, although we cannot rule out different degrees of post transcriptional regulation of chemokine secretion in infected vs. inflamed KCs

198 [34]. Collectively, our data suggest that although initiated by infection, production of
199 chemokines rapidly spreads in trans throughout the liver KC network.

200

201 Chemokine induction by infected cells is thought to provide a means for focal
202 inflammation, the recruitment of additional leucocytes in an ordered manner being
203 essential for granuloma formation and the ultimate activation of macrophage host
204 defense mechanisms. However, given this argument, these data appear
205 counterintuitive. In order to try to understand how transactivation for chemokine
206 production might influence the generation of focal inflammation, and given the
207 absence of tools to selectively and directly manipulate chemokine production by
208 infected vs. uninfected KCs *in vivo*, we adopted an *in silico* experimental approach
209 conducive to testing a variety of different hypotheses (**Figure 1B and C**).

210

211 *An agent-based model of the hepatic sinusoidal microenvironment.*

212 Agent based models, where rule-driven "agents" can represent a cell or lower-scale
213 entities of interest, are naturally suited to simulating inflammation in a spatially
214 constrained environment [35-37]. To construct this environment, we used published
215 3D data describing the overall size of lobules, the average non-branched sinusoid
216 length, and the branching angles between sinusoids [38] as the basis for developing a
217 novel algorithm to generate statistically realistic liver lobule sections similar to that
218 reported recently [39]. A range of quasi-2D sinusoidal network structures, where
219 each structure can be considered as a slice through a 3D lobule, was created using a
220 multi-stage generative algorithm augmented with these data [38] (**Figure 2A**, **Movie**

221 **S1**, **Figure S1A-D** and **Table S1** and **Supplementary Experimental Procedures**).
222 The resulting networks **(Figure 2B)**, represented as graphs of nodes connected by
223 edges, serve as discrete spatial simulation environments that mimic the sinusoidal
224 structure observed in live mice imaged by 2-photon intra-vital microscopy in (mT/mG
225 x lysMcre)$_{F1}$, as previously described [30] (**Figure 2A vs. 2C**). Analysis (by Pearson
226 correlation coefficients and Kolmogorov-Smirnov tests) using 10 independently
227 generated structures indicated that variance in structure *per se* had minimal impact on
228 the results of subsequent simulations (see below).

229

230 We defined where and how cellular interactions were allowed to occur within our
231 simulation environment based on 3 different types of network node: periportal nodes,
232 located at the peripheries of the structure allow NKT cells to enter and exit the
233 simulated lobule section; regular-nodes, capable of holding a single KC and any
234 number of NKT cells; and a single centrilobular-node, representing the central vein
235 where NKT cells could exit the structure. Only NKT cells were capable of movement
236 within the structure. KCs remain immobile, as reported in early stages of infection
237 with *B. bugdorferi* [25], BCG [40] and *L. donovani* [30]. Our KC placement
238 algorithm distributes KCs in periportal, midzonal and centrilobular locations in a ratio
239 of 4:3:3, based on [41, 42]. As centrilobular KCs have reduced phagocytic capability
240 compared to periportal KCs [41], the distribution of infected KCs in our simulation is
241 65% periportal, 25% midzonal and 10% centrilobular for the purposes of
242 experimentation.

243

A detailed description of the model and key assumptions is provided in the **Supplemental Experimental Procedures and Tables S2 and S3**. State diagrams written in the Unified Modeling Language that illustrate the behaviour associated with KCs and NKT cells are provided in **Figure S2**. Briefly, mechanisms of cellular attraction and retention were modeled generically, since the precise function, functional overlap, and interaction between distinct chemokines has yet to be fully elucidated. For the purposes of the current abstraction, we refer to the chemokines as attractive and retentive, being independent and quantitatively distinct and with discrete areas of influence. The simulation was constructed to allow both a minimum and a maximum diffusion distance to be parameterized for all chemo-attractants produced by KCs. NKT cells traverse the sinusoidal network at 10-20μm/min with a random walk behavior [25], with no enforcement of directionality unless under the attractive influence of KC-derived chemokines. Strength of attraction is modeled as a function of distance from the source KC. Upon interaction with infected KCs, NKT cells produce IFNγ (as a representation of all macrophage-activating cytokines) following cognate receptor engagement [22], facilitating KC activation and NKT cell arrest [25, 43]. Our previous data on SIRPα-CD47 has suggested that cognate receptor-ligand interactions also regulate NKT cell retention on infected KCs, with the induced expression of SIRPα after infection being preferentially but not exclusively observed on infected KCs [22]. In our model, this interaction is used to represent a cognate retention signal, but this reflects an abstraction of what may be potentially much more complex interactions. The amplification of KC derived attractive chemokines through this process can lead to the accumulation of multiple NKT cells at a given KC (referred to here as "inflammatory foci"). It is assumed that through the sum of all KC-NKT cell interactions within an inflammatory focus, a

threshold for granuloma formation and the subsequent recruitment of additional leucocytes associated with maturing granulomas (including B cells, T cells, monocytes and NK cells) is reached, but these cells and processes are not explicitly modeled. We have also not modeled the ultimate microbicidal activity of these granulomas.

Parasite Induced Activation of Infected KCs with/without Bystander Chemokine production by Uninfected KCs.

Two experimental scenarios were devised to investigate the influence of varying both infected and inflamed KC function. Scenario 1 (**Figure 1B**) was constructed to restrict chemokine production to infected KCs only, and scenario 2 (**Figure 1C**) to investigate the impact of transactivation of KC for chemokine production. As KC activation of NKT cells is optimal in the presence of cognate interactions [22], our model assumes these are a requirement for retention; hence only infected KCs can generate stable inflammatory foci, and these foci, for the purposes of the model, are composed only of NKT cells and KCs. In contrast, inflamed KCs in scenario 2 might act as potential competitors for available NKT cells, being able to attract but not retain them. Although this model can be used to probe a variety of different potential questions related to the initiation of granuloma formation (see Discussion), we focus here on a factorial analysis that involved simultaneously modifying the simulation parameters related to chemokine diffusion distance, time required to activate KCs, and time for KCs to reach maximal chemokine production.

Firstly, we quantified the influence of distance from effect on attraction. Factorial analysis, modifying the maximum diffusion distance of chemokine, showed that greater chemokine diffusion distance leads to increased percentages of infected KCs forming inflammatory foci in both scenarios (**Figure 1B** and **C**), whether those foci were qualified as containing 4, 6 or 8 NKT cells. However, our simulation predicted diminishing returns when increasing maximum diffusion past ~120μm (**Figure S1E**). Thus, significant differences ($P=\leq 0.001$) were observed when comparing the frequency of inflammatory foci that resulted from each increase in diffusion distance against the previous distance (e.g. 20μm-30μm: $P=0.001216$, 30μm-40μm: $P=0.000019$). However, when increasing from 120μm-130μm and beyond, the increase in inflammatory foci was not significant ($P=0.312$). Interestingly, this tipping point is close to the ~100μm reported as the distance of a functional chemokine gradient *in vivo* [44]. These results suggest that if it were possible to selectively increase chemokine diffusion via increased production (or other means) by infected KCs compared to inflamed KCs, or conversely decrease chemokine diffusion by inflamed KCs, infected KCs would gain competitive advantage in terms of attracting NKT cells.

We next compared our two experimental scenarios in terms of total stimulation time (i.e. a measure of activation) received by the entire infected KC population, and the frequency of inflammatory foci formed associated with that population. **Figure 3A** illustrates a response curve for scenario 1 showing the total stimulation time received by all infected KCs, across a range of the two main parameters that determine KC activation dynamics – the time required to activate KCs and the duration KCs remain

316 activated. When comparing this response landscape of scenario 1 with that generated
317 in scenario 2 (**Figure 3C**), there was a marked reduction in stimulation time received
318 overall by infected KCs in scenario 2 compared to scenario 1. This trend is also
319 observable when comparing the percentage of inflammatory foci, whether qualified at
320 8 NKT cells (**Figure 3B** for scenario 1 and **Figure 3D** for scenario 2) or at 4 or 6
321 NKT cells (data not shown).

322

323 Together, these results demonstrate that in comparison to chemokine production
324 restricted to infected KCs, additional chemokine production by inflamed KC
325 generates a less focused inflammatory response, measured either by frequency of
326 infected KC that form inflammatory foci, or by stimulation time received by infected
327 KCs. This result most likely reflects the liver lobule becoming saturated with
328 attractive chemokines derived from both inflamed and infected KCs in scenario 2,
329 reducing the competitiveness of infected KCs to selectively recruit NKT cells. In
330 other words, chemokine production by inflamed KC acts in a negative immune
331 regulatory manner, limiting the extent of the inflammatory response around infected
332 KCs.

333

334 *Increasing NKT Cell Numbers Overcomes Bystander Regulation.*

335 We then investigated how modifying the target of this competition affected the
336 quantity and quality of inflammatory foci generated. We hypothesized that altering
337 NKT cell frequency might result in either i) similarly abundant foci, but with each
338 being more substantive in terms of NKT cellularity, or ii) increased numbers of

339 inflammatory foci, thus overcoming the competitive effect of bystander chemokine
340 production by inflamed KCs (**Figure 4A**). Our simulation results showed that
341 increasing NKT cell numbers above the calibrated value lead to significant increases
342 in the frequency of inflammatory foci in scenario 1, a result that would be expected.
343 Strikingly, an increase in frequency of inflammatory foci was also observed to be the
344 case for scenario 2, regardless of how we qualified focus size (**Figure 4B**). For
345 example, with an increase in NKT cell availability of 2-fold, the number of
346 inflammatory foci increased 1.5-fold, whereas increasing NKT cells by 3-fold
347 doubled the frequency of inflammatory foci.

348

349 To test whether this predictive *in silico* data was also borne out *in vivo*, we treated
350 mice for 3 days with recombinant IL-15 to induce increased NKT cell proliferation
351 and survival [45] and then infected these mice with *L. donovani* and scored early
352 granuloma formation. In uninfected mice, IL-15 treatment resulted in increased
353 numbers of NKT cells (including CD1d restricted NKT cells), NK cells, and T cells
354 (**Figure 4C-E** and **Figure S3A-D**). In infected mice, all cell types were already
355 increased in number compared to naïve mice, and the effect of IL-15 pre-treatment
356 was limited to an increase in the number of NKT cells (**Figure 4C**). Similarly, IL-15
357 pre-treatment had no effect on the relative frequency of NK cells and T cells (**Figure**
358 **S3B-C**) but resulted in an increase in the relative frequency of NKT cells (from 15.0
359 ± 0.1% to 17.36 ± 0.8%; n=10; P=0.0043; **Figure S3E**).

360

361 To ensure that we were scoring a biologically relevant histopathological response,
362 whilst minimizing potential longer terms effects of rIL-15 treatment, we chose to

score the granulomas early in their development (day 4 p.i.) and define these as accumulations of 15 or more cells formed around an infected KC (not discriminating between NKT cells or other mononuclear cells). Although there was significant heterogeneity in size of these granulomas (**Figure 4G-H**), we found that the frequency of infected KCs that formed distinct granulomas was increased ~1.5 fold in mice pre-treated with IL-15 and which had a higher number of NKT cells in the liver at the time of infection (P=0.0038; **Figure 4F**). Thus, treatment of mice with rIL-15, even under conditions where the increase in NKT cell number is relatively modest, leads to a significant enhancement in the frequency of infected KCs that can provide a nidus for granuloma formation.

Discussion

Granulomas represent a specialized form of inflammation that allows for the focal delivery of host effector responses and / or containment of pathogen products. Whilst generally considered host beneficial, excessive granuloma formation may have significant pathological consequences. Here, we provide evidence that chemokine-dependent competition between infected and uninfected KCs for iNKT cells in the hepatic microenvironment acts as a natural attenuator of granuloma formation.

In models of experimental visceral leishmaniasis, granuloma formation is asynchronous, limiting the extent of hepatic inflammation, but also delaying parasite clearance [16, 27]. A variety of different models could explain why isolated infected KCs can be found at times when other infected KCs are engaged in a fully mature

386 granulomatous response. In a model of *Mycobacterium marinarum*-induced
387 granulomas in zebrafish, macrophage migration out of the granuloma has been
388 observed [14, 46], and it is possible that infected KCs leave granulomas in mice
389 infected with *L. donovani*. However, in both *L. donovani*-induced granulomas [30]
390 and BCG-induced granulomas [40, 47] in immunocompetent mice, KCs appear to
391 retain their characteristic lack of motility. Alternatively, there may be heterogeneity
392 in KCs, a subset being more efficient in promoting granulomatous inflammation.
393 Although we had previously modeled this possibility using an early version of our
394 ABM [48], our recent studies evaluating differences between yolk-sac derived and
395 bone marrow-derived KC indicate that both are competent to form granulomas and
396 participate effectively in this response [49]. A further possibility is that granuloma
397 formation is rate limited by the availability of key amplifier cells. Experimental data
398 to date indicates that iNKT cells play this role in experimental visceral leishmaniasis
399 [22, 33, 50, 51], though we do not discount a role for other more recently identified
400 innate lymphoid cells [52, 53].

401

402 Through transcriptional profiling, we demonstrated that both inflamed and infected
403 KCs produce a variety of inducible chemokines able to attract NKT cells, suggesting
404 the possibility that uninfected as well as infected KCs could compete for this
405 resource. However, as neither the mechanisms that regulate this transactivation nor
406 experimental means to selectively regulate chemokine production by KCs are
407 currently available, we adopted a computational approach to further explore this
408 hypothesis. ABMs are well-suited towards studying tissue and cellular level
409 inflammation [35-37]. In constructing our ABM, we developed a novel algorithm for

410 creating virtual sinusoidal networks that are visually representative of liver lobule
411 sections, being defined by published statistics that captured the length between central
412 vein and portal triad, average lengths of non-branched sinusoids and sinusoid branch
413 angles [38]. This represents an improvement on similar work [39]. Our algorithm was
414 not intended to produce a fully realistic whole lobule structure, but rather we were
415 interested only in developing suitable quasi-2D vascular networks within liver lobules
416 to provide an environment for the cellular and chemokine "agents" contained in the
417 model. Similarly, whilst our ABM contained only three cellular agents (infected and
418 inflamed KCs and NKT), this abstraction was nevertheless sufficient to probe
419 previously inaccessible aspects of the underlying biology.

420

421 Our *in silico* results predicted that chemokine diffusion plays an important role in
422 regulating the formation of inflammatory foci around infected KCs, though there are
423 diminishing returns as a result of increased competition when lobules become flooded
424 with chemokines. Subsequently, our model predicted an intuitive, but nonetheless
425 previously unreported mechanism by which the production of NKT cell-attractive
426 chemokines by inflamed KCs dampens the overall inflammatory response in the liver
427 microenvironment, reducing the activation received by infected KCs. Our *in silico*
428 data also predicted that this competition could be overcome by increasing the
429 availability of NKT cells, and we were able to confirm that granuloma frequency can
430 indeed be increased *in vivo* by increasing NKT cell numbers using rIL-15. The
431 relationship between availability of NKT cells and an increase in the frequency of
432 infected KCs generating granulomas has not previously been demonstrated.

433

Natural killer T (NKT) cells represent a potent therapeutic target in a variety of clinical settings, due to their immune adjuvant function and production of various effector cytokines [54-57]. Protective immunity associated with NKT cell activation has been reported in several disease settings. For example, Vα14 NKT cells activated by α-galactosylceramide (α-GalCer) have been shown to inhibit the development of malaria parasites in mice [58]. Similarly, in a murine model of *Mycobacterium tuberculosis* infection, α-GalCer induced activation of NKT cells was associated with reduced bacterial loads, tissue injury, and improved mouse survival [59]. Conversely, NKT cells have been implicated as key drivers of liver inflammation such as chronic liver injury [26]. Although our results suggest that in leishmaniasis the initiation of granulomatous inflammation can be enhanced by increasing the availability of NKT cells, further long-term studies would be required to determine whether the host protective advantages of this intervention outweigh any possible pathological consequences.

It is important to recognize that our model has been developed to address early events in granuloma formation and does not take into account the potential for diversity in granuloma form and function, including variations in microbicidal activity. These may be regulated via other aspects of the immune response that develop over time, and more complex models have been developed to address some of these issues [60]. Redundancy of immune regulatory pathways is a common finding and it is possible that other mechanisms come into play at later stages of granuloma evolution that affects the ability of Kupffer cells to recruit inflammatory cells and initiate granuloma formation. The kinetics of chemokine production is also likely to be highly dynamic,

458 though in respect of CXCL9 and CXCL10, long term transcriptomic profiling
459 indicates that expression of these IFNγ-inducible chemokines is sustained for at least
460 45 days post infection (Ashwin et. al., unpublished).

461 In summary, our data argue that chemokine production by uninfected trans-activated
462 KCs provides an example of a novel negative regulatory mechanism to limit the
463 impact of over-zealous inflammatory responses that might otherwise lead to excess
464 tissue pathology. Further studies to evaluate this hypothesis in a broader context of
465 inflammation are clearly warranted.

466

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472

473 **Author conflict of interest statement**

474 JT is Director of SimOmics Ltd; PSA is employed by SimOmics Ltd; all other authors
475 declare no conflict of interest.

476

477 **Author Contributions**

478 DM, PSA, JT, LB and PMK designed the simulation model. DM implemented the
479 simulation model. LB and PMK designed the experimental study. DM, JWM, LB and
480 AS performed experimental studies. SH provided data and input on model

development. PSA and ATS designed and implemented the algorithm for the generation of the artificial sinusoid structures. DM, LB, PSA, JT and PMK analyzed the data and wrote the manuscript.

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734 **Figure Legends**

735 **Figure 1. *L. donovani* infection induces transactivation of Kupffer cells for**
736 **chemokine production**

737 (**A**) Heat map showing chemokine mRNA abundance in flow sorted Kupffer cells
738 from naïve mice (control) and from KCs isolated from infected mice and separated
739 into those containing parasites ("infected") and those that do not contain parasites
740 ("inflamed"). KC isolation was performed at 2h and 12h post infection, with matched
741 controls. Lanes numbered 1-4 indicates separate sorts. The gating strategy for
742 separating "infected" from "inflamed" KCs is provided in Figure 3 of reference 31. (**B**
743 and **C**) Two modeling scenarios were generated. In scenario 1 (panel B), only
744 infected KCs produce sufficient chemokine to attract and retain NKT cells. In
745 scenario 2 (panel C) both infected and inflamed KCs produce chemokines to attract
746 NKT cells, although only infected KCs have the ability to retain these through
747 cognate interactions.
748

749 **Figure 2. Overview of the liver agent based model**

750 (**A**) A simulated sinusoidal network was constructed in quasi-2D space using a
751 sinusoidal structure generation algorithm (see **Supplemental Experimental**
752 **Procedures**). A drain node representing the portal vein (black) is placed in the centre
753 of a 2D space with six surrounding entry nodes representing the portal triads (green),
754 forming an irregular hexagon layout (i). Sinusoids (red) are grown from entry nodes
755 to the drain node (ii). Additional entry nodes created around original entry nodes
756 conceptual form a portal triad (iii), allow additional sinusoids to be grown (iv).
757 Additional sinusoid branches are added between existing sinusoids (v).
758 Execution of the algorithm is shown in **Movie S1.** (**B**) Node structure of the model

underlying KC placement and chemokine diffusion. Nodes are populated or not with a single KC, and may attract NKT cells to that node. Chemokines exert their effect by "diffusing" across nodes. For further details, see text and **Supplementary Experimental Procedures**. (**C**) Snapshot of 2-photon image of liver from (mT/mG x lysMcre)$_{F1}$ mice, showing sinusoids (red) and KCs (green).

Figure 3. Response landscapes for parasite-induced KC activation with and without KC activation in trans.

(**A-D**) Two-at-a-time (TAT) parameter analysis showing the effect on total KC stimulation time (A, C) and on % inflammatory foci (B and D) of modifying either cumulative time to activate KCs and parasite-induced activation time (A and B) or cumulative time to activate KCs and bystander activation time (C and D). For further details, see **Supplementary Experimental Procedures**.

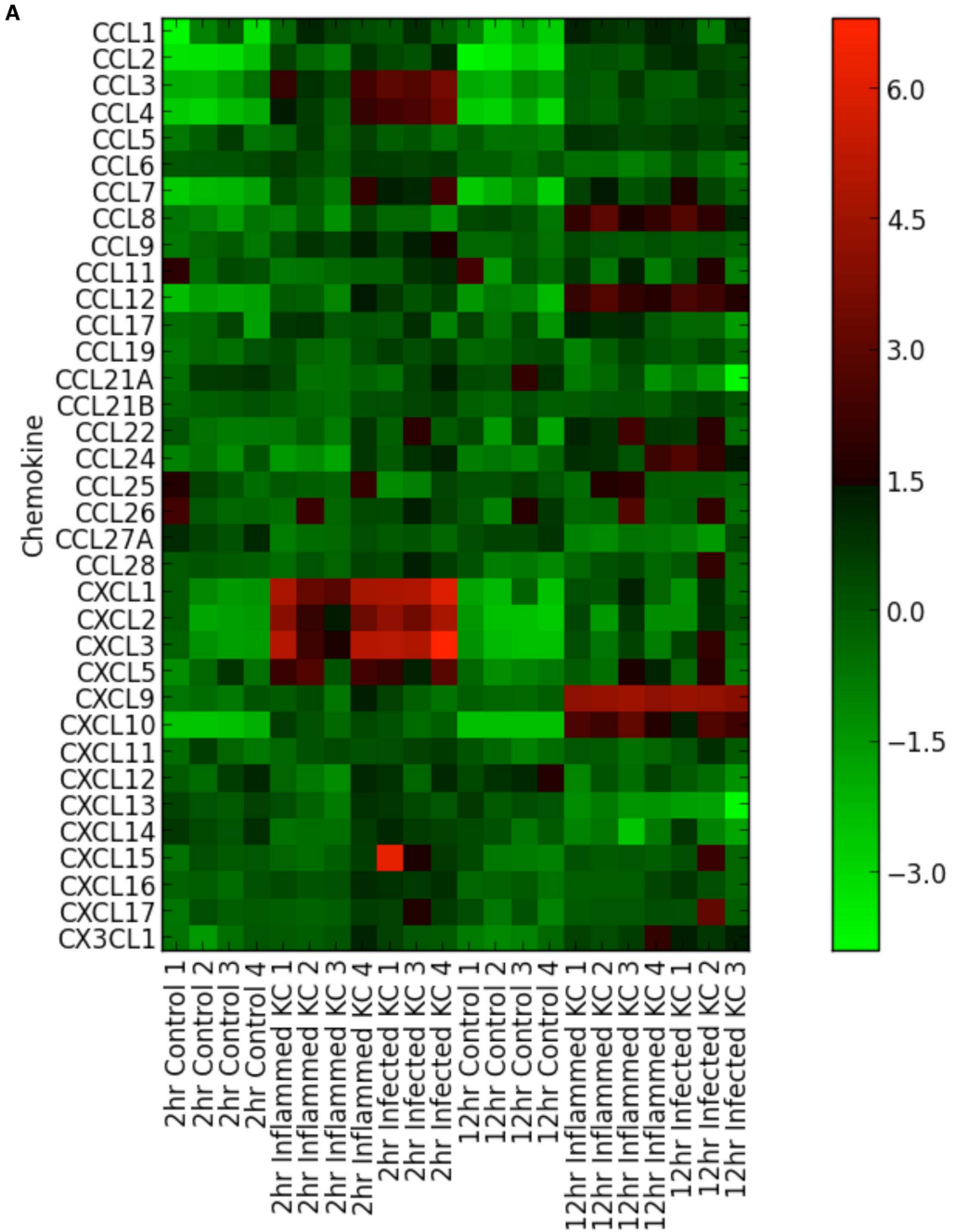
Figure 4. Expansion of NKT Cells promotes granuloma formation

(**A**) Alternate hypotheses for impact of increasing NKT cell number. (**B**) Increasing NKT cells in silico leads to greater percentages of KCs that form an inflammatory focus, when qualified at 4, 6 and 8 cells. (**C - E**) Absolute numbers of NKT (C), NK (D) and T cells (E) in naïve and infected mice with or without administration of rIL-15. Results are pooled from two independent experiments and represent mean±SEM (n=10 mice per group). *P<0.05, **P<0.01, ***P<0.001, by paired Students t-test. (**F**) Percentage of infected KCs with surrounding granuloma in control and rIL-15-treated infected mice. **P<0.01 (n=10 mice). (**G** and **H**) Heterogeneity of granulomas comparing infected (G) and rIL-15-treated (H) mice infected with

784 TdTomato-*L. donovani* (red). Sections were stained using F4/80 (green) and

785 counterstained with DAPI (blue).

786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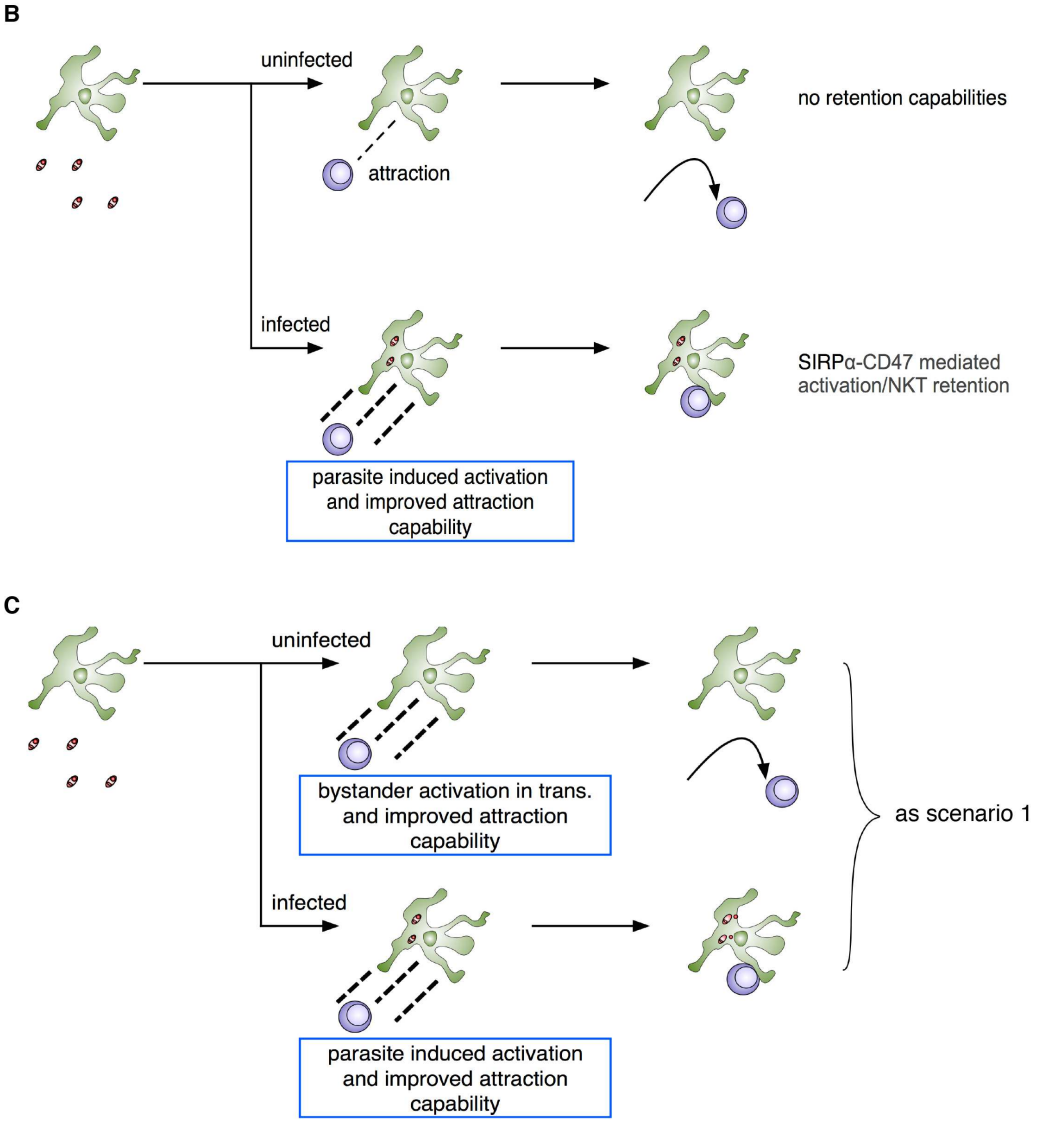
B
uninfected
attraction
no retention capabilities
infected
SIRPα-CD47 mediated
activation/NKT retention
parasite induced activation
and improved attraction
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C
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and improved attraction
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infected
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and improved attraction
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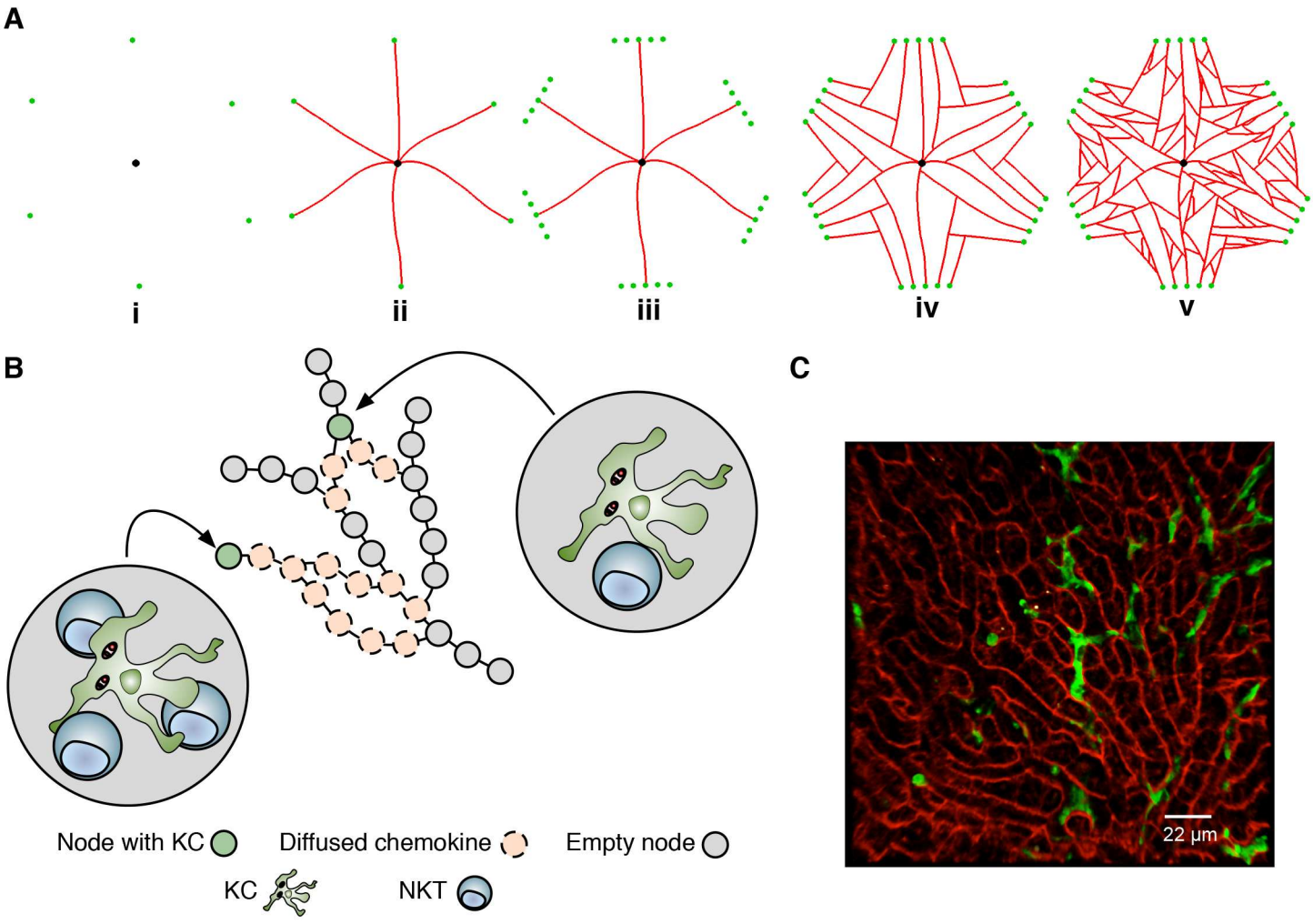
A
i
ii
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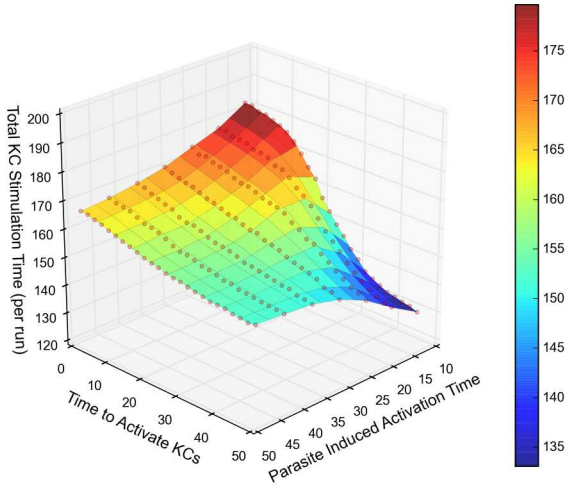
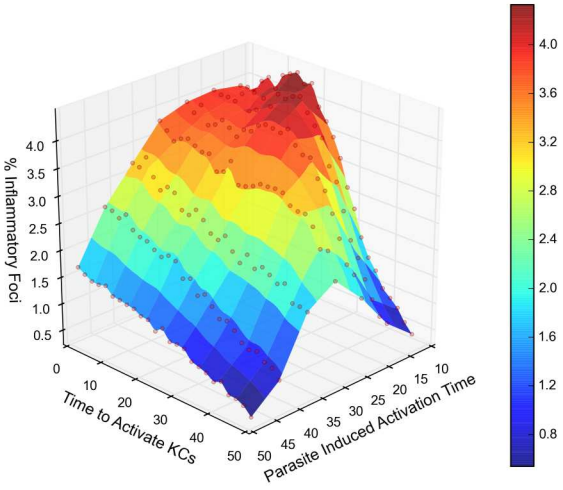
B
Node with KC
Diffused chemokine
Empty node
KC
NKT
C
22 µm

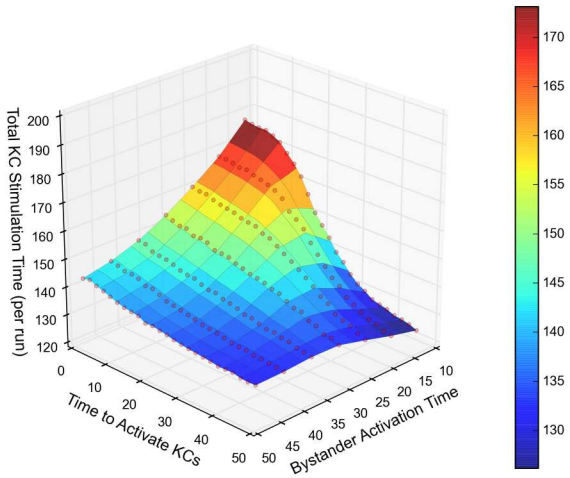
A


Total KC Stimulation Time (per run)
Time to Activate KCs
Parasite Induced Activation Time

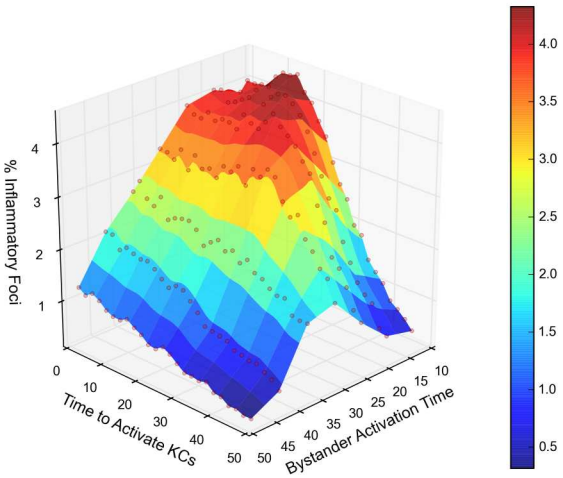
B

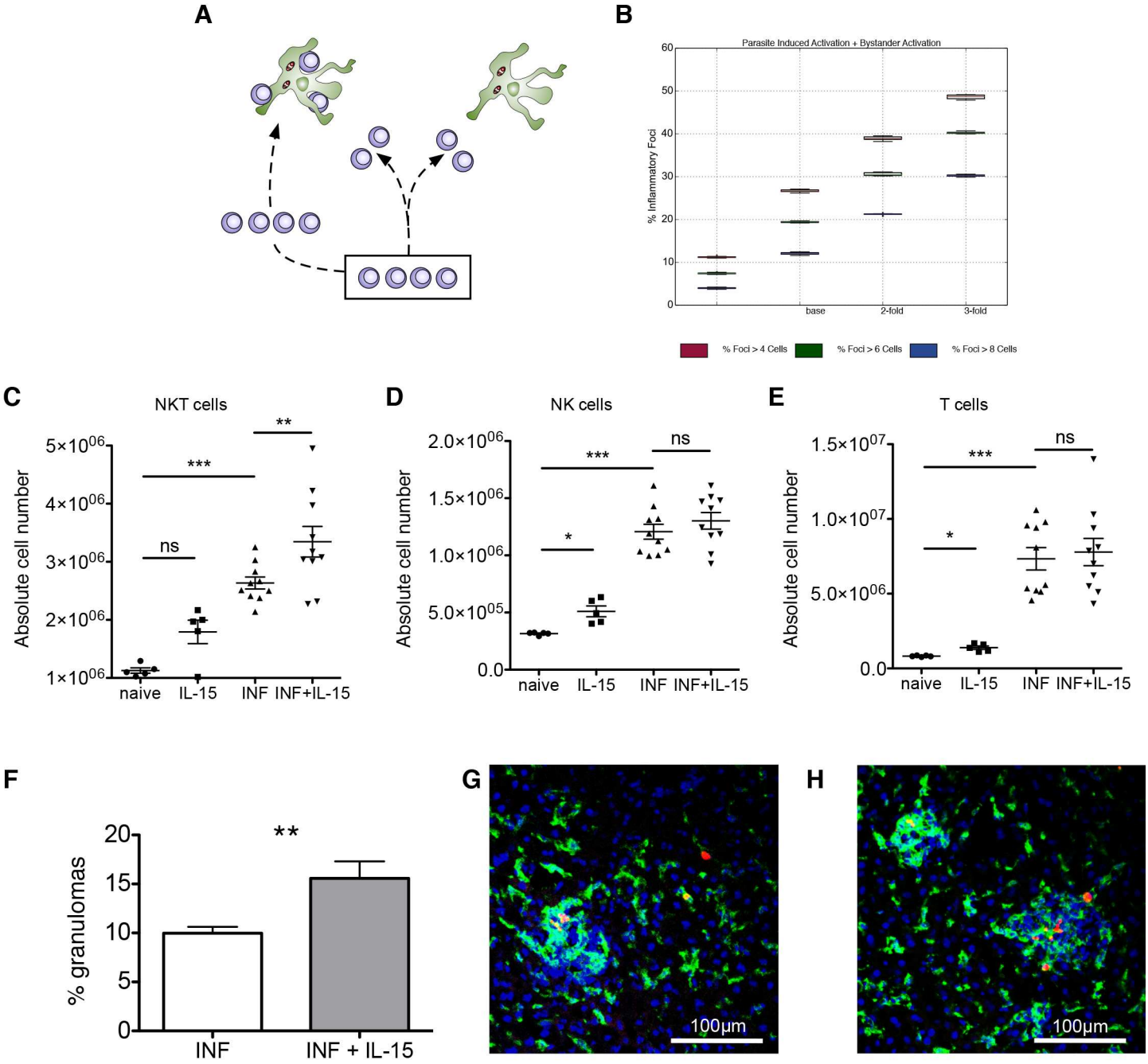

% Inflammatory Foci
Time to Activate KCs
Parasite Induced Activation Time

C


Total KC Stimulation Time (per run)
Time to Activate KCs
Bystander Activation Time

D


% Inflammatory Foci
Time to Activate KCs
Bystander Activation Time

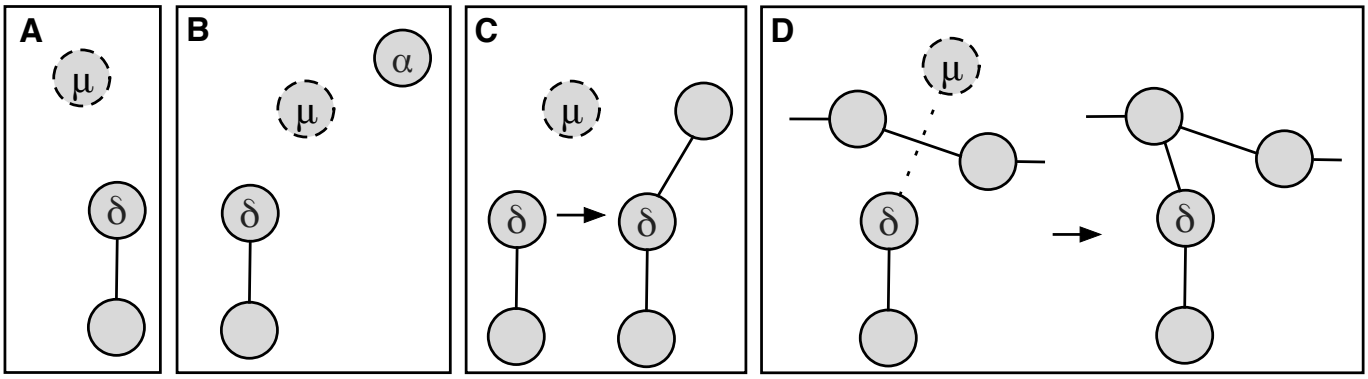

A
B
Parasite Induced Activation + Bystander Activation
% Inflammatory Foci
base
2-fold
3-fold
% Foci > 4 Cells
% Foci > 6 Cells
% Foci > 8 Cells
C
NKT cells
Absolute cell number
naive
IL-15
INF
INF+IL-15
D
NK cells
E
T cells
F
% granulomas
INF
INF + IL-15
G
H
100µm

Supplemental Information

Macrophage transactivation for chemokine production negatively regulates granulomatous inflammation.

Daniel Moyo[1,2], Lynette Beattie[1*], Paul S Andrews[3], John W J Moore[1], Jon Timmis[3], Amy Sawtell[1], Stefan Hoehme[4], Adam T. Sampson[5], Paul M Kaye[1]

Supplemental Figures



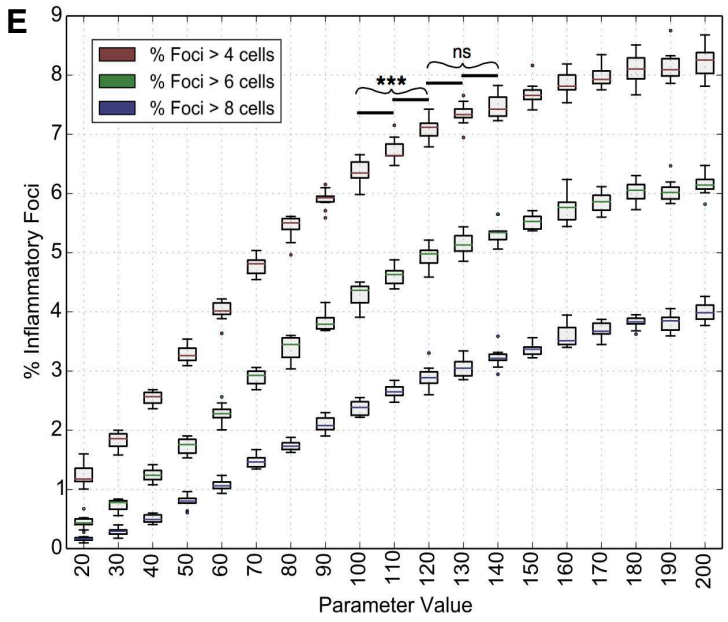


Figure S1. Related to Figure 2. Generation of Nodes and Edges of a Sinusoid Network.
(A-D) See Algorithm 1 in Supplemental Experimental Procedures. (E) Effect on percentage inflammatory foci qualified at 4, 6 and 8 cells, when modifying maximum chemokine diffusion distance.

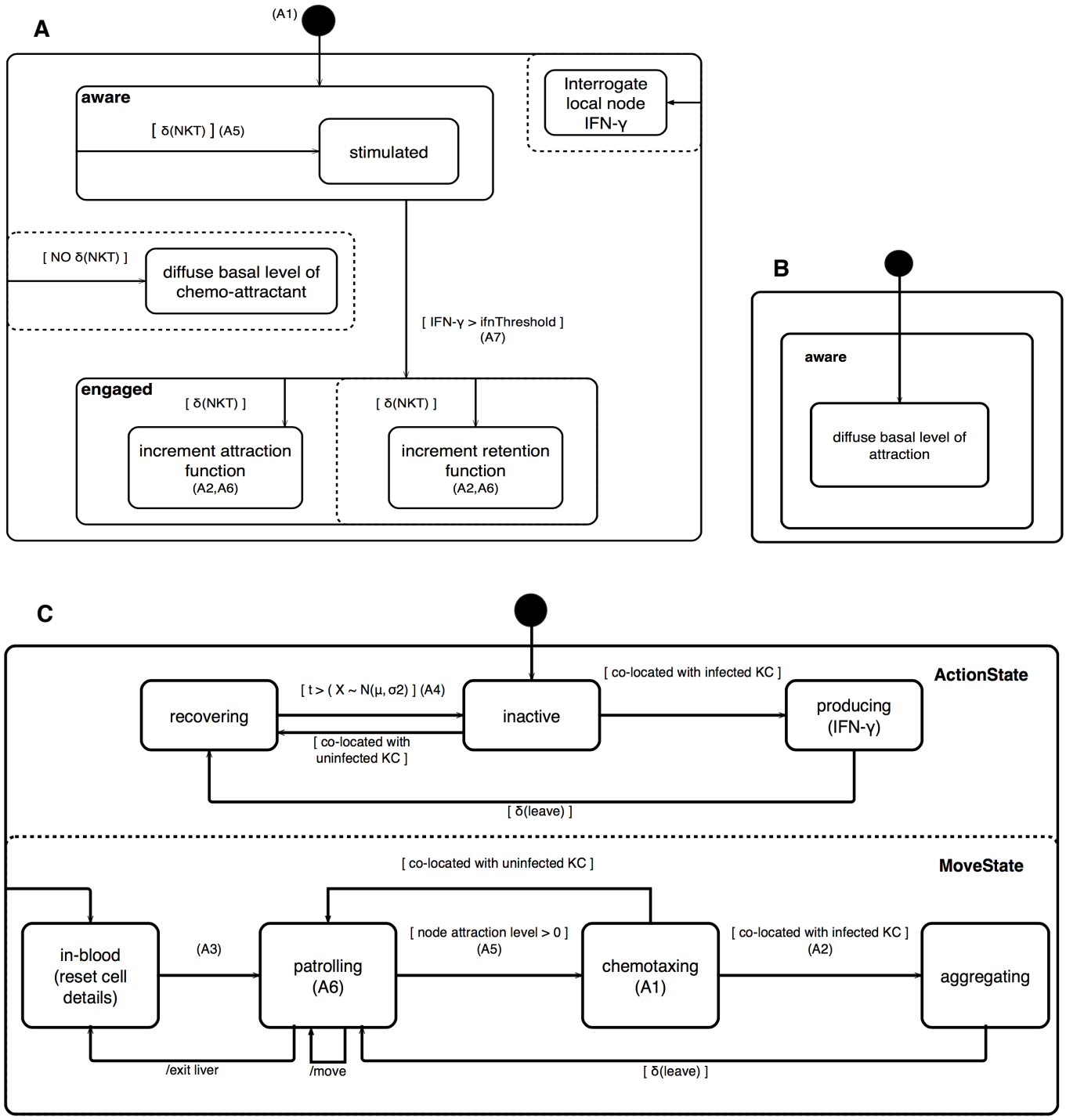


Figure S2. Related to Figure 2. State-diagrams for Kupffer cell and NKT cell behaviors.
(A) Infected Kupffer Cell; (B) uninfected Kupffer Cell; (C) NKT cell. See State Transition Diagrams in Supplemental Experimental Procedures.

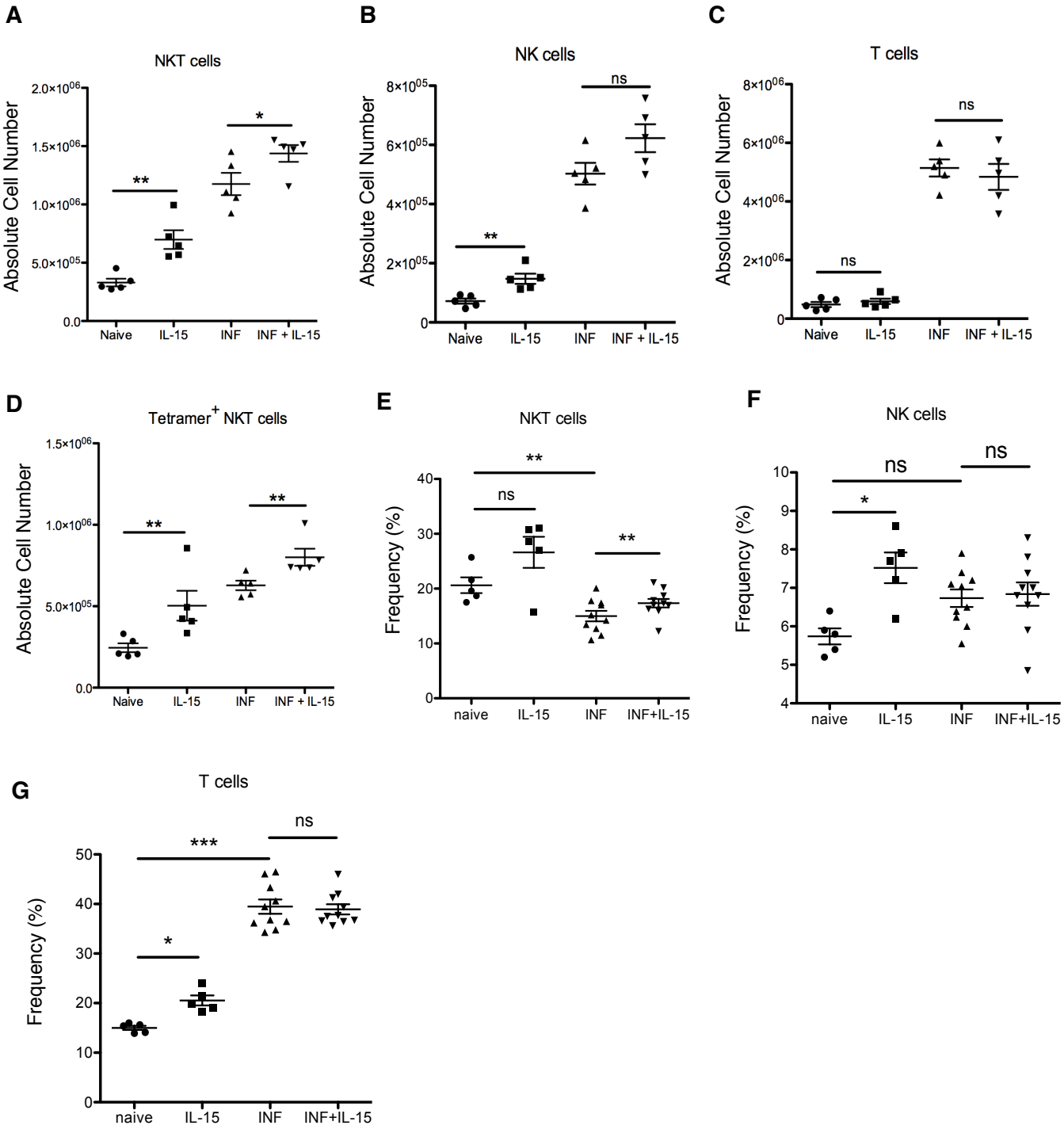


Figure S3. Related to Figure 4. IL-15 Promotes NKT Cell Expansion.

(A) Absolute cell numbers for NKT, (B) NK and (C) T cells, and (D) CD1d tetramer+ NKT cells for naïve, IL-15 treated naïve (IL-15), infected (INF) and IL-15 pre-treated infected (INF+IL-15) mice. (E) Relative frequency of NKT, (F) NK and (G) T cells for naïve, IL-15 treated naïve (IL-15), infected (INF) and IL-15 pre-treated infected (INF+IL-15) mice. Results are depicted as mean ± SEM of 5 mice per group. *P≤0.05, **P≤0.01 paired Students t-test.

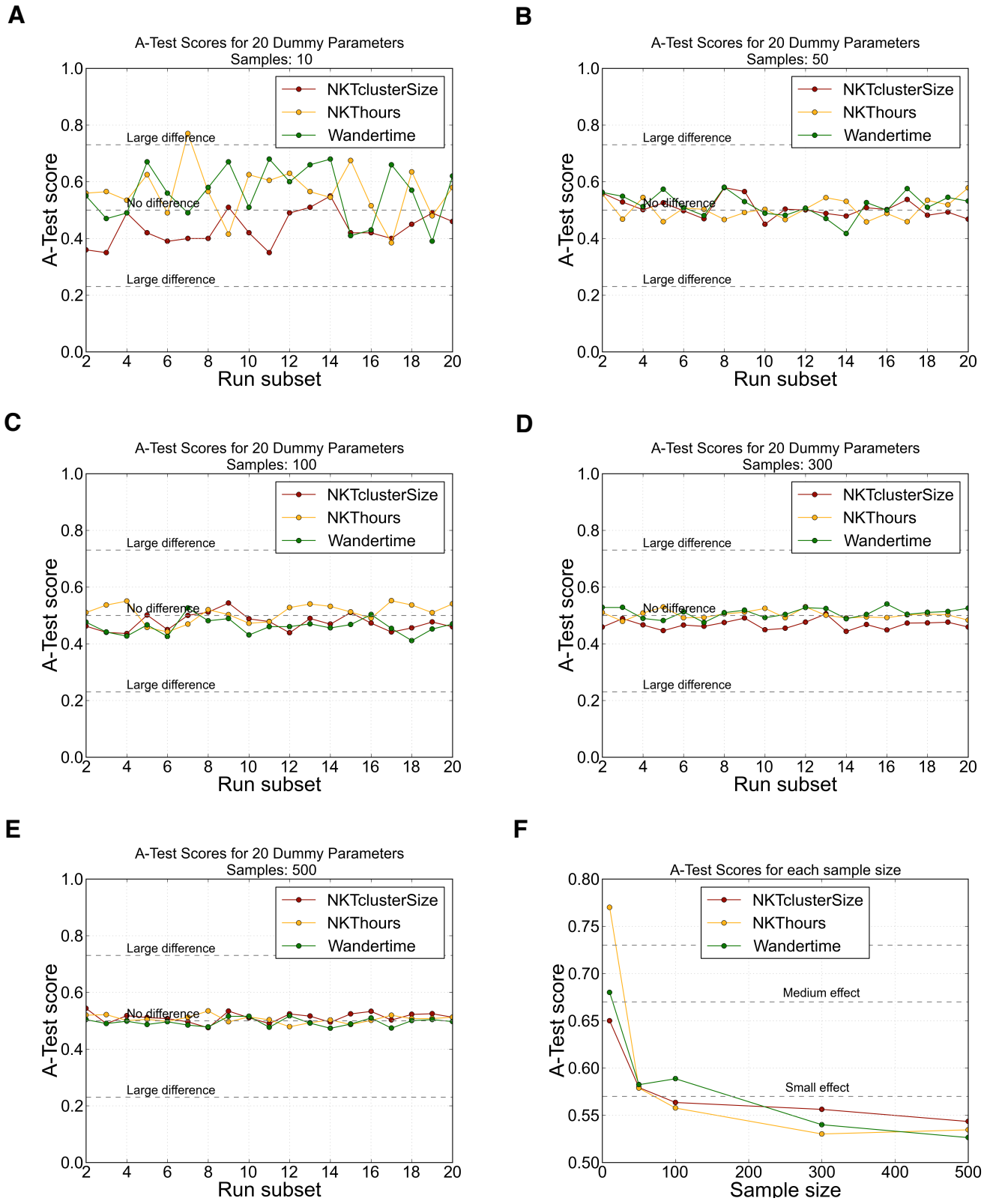


Figure S4. Related to Figure 2. Aleatory Analysis Determines a Minimum of 300 Simulation Runs per Experiment.
A-test (Vargha and Delaney, 2000) scores for three simulation output measures across sample sizes of (A) 10, (B) 50, (C) 100, (D) 300 and (E) 500, illustrating that greater than 300 simulation runs are needed to capture the variation in output results and mitigate uncertainty, summarized in (F).

Supplemental Tables

Biological Parameters	**Value**	**Source**
NKT cell velocity in the sinusoids	10-20μm/minute	(Geissmann et al., 2005)
NKT cell numbers in a section of mouse liver lobule	$\sim$49($\sim$1:3 ratio with KCs)	Derived from (Lee et al., 2010) and unpublished data
Kupffer cell numbers per gram	14-20 x 10^{6}/g	(Bouwens et al., 1986)
Infected KCs at 2 hours	$\sim$23%	Unpublished data
KCs per lobule section	$\sim$146	Unpublished data
Non-branched segment length	43.1 $\pm$ 2.25 μm	(Höhme et al., 2010)
Mean branching angles of sinusoids	32.5° $\pm$ 11.2°	(Höhme et al., 2010)
KC spatial distribution	Percentages: Periportal (PP) - 43 Midzonal (MZ) - 28 Centrilobular (CV) - 29 Ratios: 4(PP), 3(MZ), 2(CV)	(Bouwens et al., 1986; Sleyster and Knook, 1982)

Table S1. Related to Figure 2. Table of biological parameters used for calibration.

	Domain	Platform	Justification
KC_A1		Infected KCs are infected at initiation of the simulation, t(0).	KCs rapidly phagocytose parasites. We are not investigating conditions pre-infection.
KC_A2		Infected KCs can recruit and retain cells.	Unpublished data.
KC_A3		Uninfected KCs can only recruit cells.	Unpublished data.
KC_A4	KCs are immobile	KCs have no movement rules	(Lee et al., 2010)
KC_A5	KC retention of NKT cells is probabilistic, mediated by SIRP-a - CD47 interactions and local IFN-g concentration.	Cognate interactions occur when two cells are co-located on the same node and are not modeled explicitly. Retention is modeled probabilistically using a function modified by local IFN-g level	(Beattie et al., 2010; Svensson et al., 2005)
KC_A6	NKT produced IFN-g affects KC attractive chemokine production.	Retentive chemokine level increases in-line with local IFN-g level and increases the diffusion distance of attractive chemokine linearly. Retentive chemokine diffusion distance can decay.	Simplification, no experimental data available.
KC_A7	There is a threshold level of stimulation required to activate a KC.	KCs will not transition to an engaged state until a threshold level of IFN-g is reached.	To facilitate implementation, no experimental data available.
NKT_A1	NKT cells respond to chemo- attractant	NKT cells under chemotaxis, when presented with two or more attraction gradients, will choose a direction based on attractive chemokine strength.	To facilitate implementation, no experimental data available.
NKT_A2	NKT cells interact with KCs	NKT cells will interact with the first infected KC they encounter whilst in chemotaxis.	To facilitate implementation, no experimental data available.
NKT_A3		The NKT cell population of the lobule section remains constant; cells exiting the environment will enter as new cells via an entry point.	
NKT_A4	NKT cells are capable of becoming anergic	NKT cells are refractive to stimulation and take a period of time to recover after stimulating and leaving a KC.	(Iyoda et al., 2010)
NKT_A5		NKT cells will respond immediately to a chemokine signal.	To facilitate implementation, no experimental data available.
NKT_A6	NKT cells can walk the sinusoids and switch direction probabilistically NKT cells perform a random walk of the tree- node structure, and a probability governs their	NKT cells perform a random walk of the tree-node structure, and a probability governs their ability to turn in the sinusoids at random.	(Geissmann et al., 2005)
C_A1	Attractive chemokines flow in the same direction as blood would.	Attraction diffuses downstream of infected KCs towards the central vein.	Chemotaxis in 3D environments is poorly understood (Haessler et al., 2011)
C_A2		Strength of attractive chemokine is a function of distance from source, calculated using a simplified Ficks Law of diffusion.	To facilitate implementation.
C_A3		Chemokine growth is calculated using a sigmoid function.	To facilitate implementation, no experimental data available.

Table S2. Related to Figure 2. Modelling Assumptions. Statement of assumptions made regarding the underlying biological domain (domain) and how we have abstracted this information in the engineered simulation (platform). Assumptions labeled KC_ relate to Kupffer Cells, NKT_ to NKT Cells, and C_ to chemokines. Assumptions make it possible to model when data is limited or there is a gap in understanding or the literature.

Parameter		Value	Units	Description	Source
Simulation	p_numInfectedKCs	33	cells	Number of infected kupffer cells in a π*(284μm)^2 sectional area of sinusoid.	Calibrated to unpublished data
	p_numUninfected	113	cells	Number of uninfected kupffer cells in a π*(284μm)^2 sectional area of sinusoid.	
	p_numNKTs	49	cells	Number of NKT cells in a π*(284μm)^2 sectional area of sinusoid.	Calibrated to unpublished data and (Lee et al., 2010)·(Geissmann et al., 2005)
Chemokine	p_chemoAttract	43200	iterations	Stimulation time required to reach maximum attractive chemokine concentration.	No biological equivalent; explored and chosen through parameter sensitivity analysis
	p_chemoRetain	172800	iterations	Interaction time required to reach maximum retentive chemokine concentration.	
	p_chemoIFN	172800	iterations	Interaction time required to reach activate infected KCs.	

Parameter		Value	Units	Description	Source
NKT cell	p_turnProb	0.005	probability	Probability that an NKT cell will reverse direction in the sinusoids.	No biological equivalent; explored and chosen through parameter sensitivity analysis.
	p_moveMin	3	iterations	Value given to link simulation iterations to NKT cell velocity.	Calibrated to published NKT cell speeds from (Geissmann et al., 2005)
	p_moveMax	6			
	p_anergicItns	3600	iterations	Time in iterations for an NKT cell to remain unable to stimulate a KC.	No biological equivalent; explored and chosen through parameter sensitivity analysis.
	p_escapeItns	600	iterations	Time in iterations for an NKT cell to escape the influence of KC produced chemo-attractant.	
	p_leaveProb	0.000265306	probability	The probability of an interacting NKT cell leaving the location of an infected KC.	
	p_minLeaveProb	0.00005	probability	To guard against the probabilistic tipping point whereby retention causes cells to never leave.	
	p_chemoIFN	172800	iterations	Interaction time required to reach maximum attractive chemokine concentration.	
Kupffer cell	p_chemoDist	20	distance(nodes)	Starting diffusion distance for attractive chemokine.	No biological equivalent; explored and chosen through parameter sensitivity analysis.
	p_ratioCV	0.1	percentage	Ratio of infected cells in the CV region of the lobule section	Bouwens et al., 1986. Sleyster et al., 1982.
	p_ratioMZ	0.25	percentage	Ratio of infected cells in the MZ region of the lobule section	
	p_ratioPP	0.65	percentage	Ratio of infected cells in the PP region of the lobule section	
	p_maxDist	200	distance(nodes)	Maximum diffusion distance for attractive chemokine.	Calibrated to twice reported max(Weber et al., 2013)
	p_ifnThreshold	0.999	threshold	Threshold value of IFN-γ required to activate a KC. Chemokine function f(x)→1, therefore a threshold is required.	No biological equivalent

Table S3. Related to Figure 2. Simulation Parameters. Summary of the simulation parameters, descriptions of their purpose, values and any data sources for parameters relating to cell numbers and chemokine functions. All estimated values are based on a comprehensive sensitivity analysis for parameters that have unknown or no clear biological value.

Supplemental Movies

Movie S1. Related to Figure2. Sinusoid structure generation algorithm. Execution of the sinusoid structure generation algorithm at 8x speed. Drain node (cyan), entry nodes (green) and sinusoids (red).

Supplemental Experimental Procedures

We assume that our sinusoid network exists in a quasi-2D space (we can consider this as a slice through a 3D lobule). We also assume that the lobule structure is roughly hexagonal with a single central vein in the centre and six portal triad areas placed at roughly regular intervals around the central vein. The flow of blood borne cells is assumed to be from portal triads to the central vein, so in the algorithmic description below the central vein is termed a drain node, and the portal triad regions deemed entry nodes.

Algorithm 1 describes how the nodes and edges of the sinusoid network are generated, whilst Algorithm 2 describes how the overall sinusoid network (the lobule) is generated using Algorithm 1. Höhme et al. (2010) provide us with the following statistics that guide Algorithm 2:

- Average length between central vein and portal triad = 284μm;
- Average length of a non-branched sinusoid = 43.1μm;
- Average angle between branching sinusoids = 32.5°.

Algorithm 1: Sinusoid branch generation

1. A potential new node (μ) is generated 1μm from the current node (δ)
   (a) If we are within range of an attracting node (α) then μ is generated in the direction of α (see Figure S4(B)).
   (b) Otherwise μ is generated based on our current direction with a small random adjustment (see Figure S4(A)).
2. Create a new edge between δ and another node:
   (a) If the line between δ and μ intersects another edge in the sinusoid network, then connect δ to the closest existing node (see Figure S4(D)).
   (b) Otherwise connect δ and μ (see Figure S4(C)).
3. Repeat Steps 1 and 2 until an intersection is detected.

Algorithm 2: Sinusoid network (lobule) generation

1. A drain node (representing the central vein) is placed in the centre of the 2D space, surrounded by six entry nodes (representing the locations of portal triads) in an irregular hexagon formation (see Figure 2(Ai)). The exact location of the entry nodes is determined stochastically.
2. For each of the six entry nodes a sinusoid branch is grown (see algorithm 1) from the entry node towards the attracting drain node (see Figure 2(Aii)).
3. An additional set of entry nodes is created for each original entry node and aligned with the original node. These additional nodes represent additional sources of blood supply coming out of the portal triad (see Figure 2(Aiii)).
4. For each of the new entry nodes a sinusoid branch is grown (see algorithm 1) from the entry node towards the existing sinusoid structure (see Figure 2(Aiv)).
5. Additional sinusoids are created to connect existing sinusoids (see Figure 2(Av)).
   - Select the longest sinusoid in the structure
   - Select a node in the longest sinusoid and grow a sinusoid (see algorithm 1) to either the left or right at an angle drawn from a normal distribution with a mean of 32.5°.
   - Repeat until the mean sinusoid length of the entire structure reaches 43.1μm.

Cell Attraction Dynamics

If we assume an infected KC diffuses chemokine to a downstream node α, chemokine strength at α is a function of distance:

$$\lambda/\delta$$

Where:

λ is the chemokine strength at the infected node.
δ is the distance in nodes between the KC and α.

Uninfected KCs are unable to modify their attraction diffusion distance from the parameterized minimum (Scenario A only), whereas infected-KC attractive chemokine diffusion distance is variable between a minimum and maximum distance. That distance is calculated as a function of the current level of attractive chemokine at the source KC location:

$$\delta = | \lambda \cdot (\delta\text{max} - \delta\text{min}) |$$

Where:

λ is the chemokine strength at the infected node.
δmax is the maximum parameterized diffusion distance.
δmin is the minimum parameterized diffusion distance

The function is floored to the nearest integer and that is used as the updated diffusion distance.

Cell Retention Dynamics

The equation governing NKT cell retention is:

$$\delta\text{nktleave} = \delta\text{leave} \ \ (\phi \cdot \delta\text{leave})$$

Where:

δnktleave is the probability of an NKT cell leaving an infection site.
δleave is the maximum parameterized retention probability.
ϕ is the level of retentive chemokine at the infected node.

As the calculated probability will approach zero given suitable conditions, a minimum retention probability is parameterized to ensure that KCs do not become so retentive that NKT cells are then incapable of leaving.

State-Transition Diagrams

Figure S2 depicts state-transition diagrams using the Unified Modelling Language (UML). These diagrams are the engineering specific (platform) ones used to create the simulator. To improve clarity, various annotations are added to convey information relevant to our modelling context. Arrows denote transitions between states. Square brackets ([]) denote guards for a transition, conditions that must be met before a transition can occur. Dashed lines denote states or behaviours that occur concurrently. Where an assumption number is stated on a diagram, denoted by (An), refer to the relevant cell assumption table. The $\delta()$ notation denotes an interaction that might occur probabilistically, for example a cell-cell interaction.

- **Infected Kupffer Cells** (Figure S2(A)): begin in an aware state and have a minimum level of attractive chemokine and minimum diffusion distance of attraction. If the level of cell-local interferon-gamma produced by NKT cells reaches a threshold (ifnThreshold), infected KCs become engaged. When infected KCs are engaged, if there is sustained interaction with NKTs, indicated by δ(NKT), they will increase their level of attraction and retention.
- **Uninfected Kupffer Cells** (Figure S2(B)): always in an aware state and only diffuse the minimum level of attractive chemokine. They do not interact with NKTs by any other means.
- **NKT cells** (Figure S2(C)): have two state types, ActionStates and MoveStates. The initial ActionState is inactive. If an infected KC is encountered the NKT will begin producing interferon- until probabilistically leaving mediated by the retention level of the KC. If NKT cells encounter uninfected KCs, they will transition to the recovering state. NKTs leave the recovering state after a time sampled from a normal distribution, this time is significantly shorter for NKTs that previously left uninfected KCs, and hence havent been in the producing state. The default NKT cell MoveState is patrolling. Upon sensing a level of attraction, NKT cells will transition to a chemotaxing state. Interaction with an infected KC will cause the NKT to switch to an aggregating state; alternatively an uninfected KC encounter will lead back to a patrolling state. Aggregating NKT cells can transition to patrolling behavior probabilistically. Should NKT cells exit the liver environment, if the entry condition is satisfied, they will emerge from an environment entry point, effectively as another cell.

Parameterizing and Calibrating the Simulation

A full summary of the biological data available that was used to calibrate the simulation is listed in Table S1, though these are merely the domain specific parameters, and a number of implementation specific parameters are required in order to abstract domain behaviors into executable computer code. A good example of an implementation specific parameter relates to NKT cell speed. NKT cells traverse the sinusoids at 10-20m/minute. In the simulation, this corresponds to 10-20 nodes/minute. Our simulation iterations are in seconds, so for a cell to travel at a maximum speed of 20 nodes/minute it would have to move every 3 simulation iterations (p_moveMin), and a minimum speed of 10 nodes/minute every 6 simulation iterations (p_moveMax). Rather than have individual cell speed remain constant, we allow it to be dynamic within the published biological range. We calculate, probabilistically between p_moveMin and p_moveMax, the number of iterations a cell will remain stationary before its next move. This allows individual cells to speed up and slow down dynamically, yet maintains a normal distribution of cell speeds across the population and within the biologically specified range. The entire list of baseline simulation parameters can be viewed in Table S3. Several parameters have no biological equivalent though are fundamental for the implementation of many behaviors. We performed parameter sensitivity analysis (SA) in order to determine which parameters the simulation is extremely sensitive to, and to establish baseline parameter values. Finally SA allows us to ensure we are always interpreting our results with the knowledge that particular extreme parameter combinations might influence those results.

Each simulated experiment is run across 10 separate structures in order to approximate variance across the set. For each parameter value investigated (or combination of parameter values) per experiment, 500 simulation runs are performed, this number chosen after performing aleatory uncertainty analysis on the simulator. Aleatory analysis can be used to determine the minimum number of replicates runs required to both mitigate the effects of stochasticity on simulation output, and to generate results that cover a representative spectrum of possible system behaviours (Alden et al., 2013). Fig. S3f shows that 300 simulation runs per parameter combination are sufficient to have acceptable uncertainty (small variance between identical sample sizes), though we perform 500 in order to strike a balance between further reducing A-test effect size (Vargha and Delaney, 2000) and maintaining tractable simulated-experiment execution times.

Supplemental References

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