

Spatially explicit model of the lymphocyte diaspora in influenza-infected lung quantifies constraints of chemokine directed migration

Drew Levin^{1,*}, Stephanie Forrest¹, Soumya Banerjee¹ Candice Clay², Melanie Moses¹, Frederick Koster²,

1 Department of Computer Science, University of New Mexico, Albuquerque, NM, USA

2 Lovelace Respiratory Research Institute, Albuquerque, NM, USA

*** E-mail: Corresponding drew@cs.unm.edu**

Abstract

During the primary immune response, clearance of influenza in the lung requires the homing of activated CD8 T cells during the lymphocyte diaspora from regional lymph nodes to small infected foci comprising a tiny fraction of the total lung. T-cell navigation to the infected region is enabled by local cytokine and chemokine production from infected epithelial cells. Avian H5N1, seasonal H1N1, and 2009 pandemic influenza strains were used separately to induce chemokine production *in vitro*. Of the eight chemokines tested, only CXCL10 (IP-10) and CCL5 (RANTES) were secreted in tissue (results only) with IP-10 always dominating the affected T-cell migration direction. A delayed differential equation model was fit to the empirical data, revealing per cell chemokine production rates for each strain. These values were coupled with known biological constants to calibrate a spatially explicit agent-based model to explore the effects of inter-strain variation of chemokine production on T-cell recruitment and infection control. T cells appear to be sufficiently sensitive to chemokine to function as well as they possibly can. The modeled immune response is unable to clear the pandemic strain due to its high rate of viral production and large plaque size. The spatial nature of the model reveals unique challenges to T-cell recruitment and motility not visible in spatially homogeneous ODE models. Expanding plaque sizes isolate infected cells, impeding T-cell discovery and subsequent clearance of the infection over time.

Author Summary

Introduction

The adaptive immune response induced during acute influenza A infection is a complex web of defense mechanisms that controls all but the most virulent strains. Understanding its components and their interactions are relevant to improving vaccines and strategies to control immunopathology. Elegant studies in the mouse model have described the induction and effector phases of the adaptive immune response, including functional capabilities of the innate interferon-directed response, macrophages, specific antibody, and cytotoxic effector lymphocytes [1–3]. CD8+ T cells are necessary for the resolution of pneumonia and complete clearance of mouse-adapted influenza strains [1–4], but gaps remain in our understanding of the behavior of activated T cells in infected tissue.

The generally held view of the sequence of CD8+ T cell events during a primary immune response to influenza in the lung involves the following steps: dendritic cells bearing specific antigen migrate from the lung to the draining lymph node where naive T and B cell precursors are activated in specialized architecture [5–10]. T cells proliferate in the lymph node and are released into the bloodstream, appearing simultaneously in the lung, spleen and other organs 4–5 days post-infection, a whole-body distribution known as the lymphocyte diaspora [11]. In the lung, extravasation from capillaries is signaled by inflammatory cytokine-mediated integrin-activation on endothelial cells. Once in the tissue, T cells follow a chemokine gradient to the infected epithelial cells secreting the chemokine.

Mathematical models have used detailed mouse data to characterize the evolution of the immune response and predict its impact on viral kinetics [12–16]. Such whole-response modeling has considerable potential to inform strategies of vaccination and therapy, thus avoiding subsequent expensive animal and human trials. Models using ordinary differential equations to predict temporal events, however, do not account for spatial constraints, and must make assumptions about the efficiency of the spread and interaction of populations.

Here we study the time and physical constraints of the lymphocyte diaspora using an agent-based model (ABM). To develop a model with tractable simulations, some components of host defense are abstracted and the model therefore does not aim to predict the true outcome for each strain examined. We ask how very small foci of infected tissue can attract limited numbers of activated CD8 T cells

after release into the systemic vascular system. The circulating blood supply services non-infected tissue orders of magnitude larger than the target infected tissue, necessitating an efficient mechanism to focus cell migration. A host of cytokines and chemokines secreted by infected cells are critical in directing immune cells to sites of infection [4, 17, 18]. While each chemokine has been studied in detail for receptor specificity and function in knockout models, the details of chemokine function and efficiency have not been examined in a virus-infected whole animal model.

To characterize the local chemokine-secretion environment in which T cells migrate, we used data on viral secretion and chemokine secretion patterns from human epithelial cells infected in vitro by three different influenza virus strains of avian, seasonal and pandemic origins [19]. We selected in vitro chemokine data as a tissue environment surrogate, because it may be more accurate than published chemokine levels in mouse blood and bronchial alveolar fluid, and it allowed us to represent sustained chemokine gradients within the model lung. Extensive literature on mouse model data of infections with mouse-adapted strains PR8 and HK-31 were used to calibrate the ABM model. [REF]

The standard hypothesis posits that the marked strain-specific differences in replication efficiency and tissue spread previously reported [19] would largely determine the outcome of infection as eradication or lack of control. Our model confirms this hypothesis, but we also observed three interesting characteristics of chemokine-directed migration not revealed by earlier data. First, of the only two chemokines stimulated by all three strains, the influence of IP-10 consistently dominated the effect of RANTES, regardless of strain. Second, each chemokine exhibited a clear threshold to direct migration, with lesser impact at increasing concentrations above the threshold. Finally, when the target (infection focus) was large, T cell search became inefficient due to the disappearance of the chemokine gradient, possibly contributing to the loss of control of the pandemic strain.

Models

Computational Modeling

Computational modeling used CyCells [20], a modeling platform for two- or three-dimensional agent-based simulations of the immune response. A simplified model of T-cell activation and recirculation was implemented in CyCells (Fig. 2), and simulations measured efficiency of infection clearance under different environmental conditions. The lung was represented as a two-dimensional sheet of healthy epithelial cells.

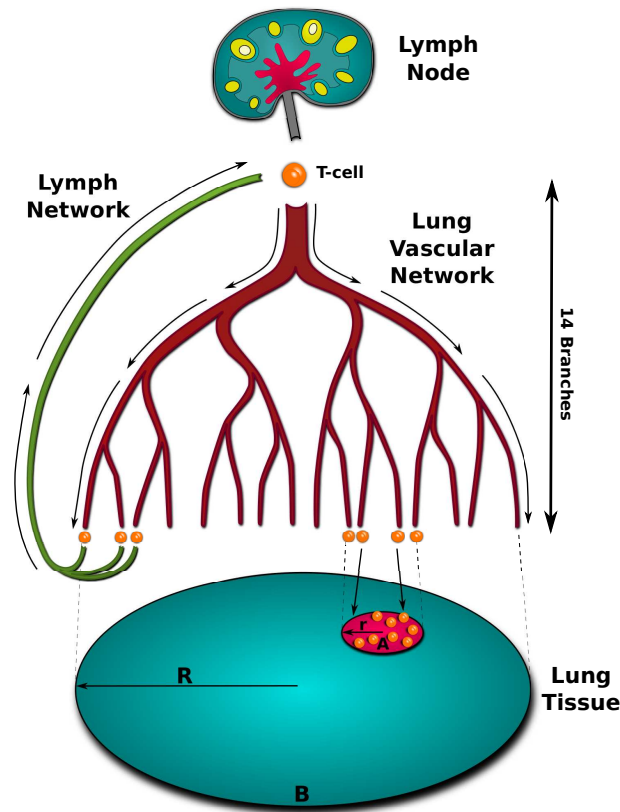


Figure 1. Model of T cell search. Activated T cells originate in the lymph node and enter the bloodstream after which they randomly navigate through the 14 layers of the branching bronchial network. Upon reaching a capillary, T cells exit into tissue if cytokine signal is present. In the absence of signal, the T cell recirculates either through the lymph network or through the pulmonary vein back to the top of the network.

Vasculature was represented as a binary tree with fourteen branches originating at a single lymph node. Activated T cells descend through the vascular tree until cytokine signal is detected, at which point they exit the vasculature and follow the chemotactic gradient to the site of infection. T cells that do not encounter cytokine recirculate to the lymph node. At the site of infection when a T cell encounters an infected epithelial cell it induces apoptosis.

The simulation begins when a single cell in the center of the tissue is infected. After the eclipse phase (incubation), the infected cell begins secreting virus and chemokine. Virus diffuses locally, infecting nearby cells, and continuing the cycle. Chemokine diffuses from secreting cells, creating a ball of stimulation around the infected region. After a five day delay to simulate lymph node stimulation and T cell proliferation, activated T cells exit the lymph node and circulate through the vasculature to the

tissue. Because T cells cannot choose their path through the branching network, we assume they arrive in tissue at random locations.

Model Definition

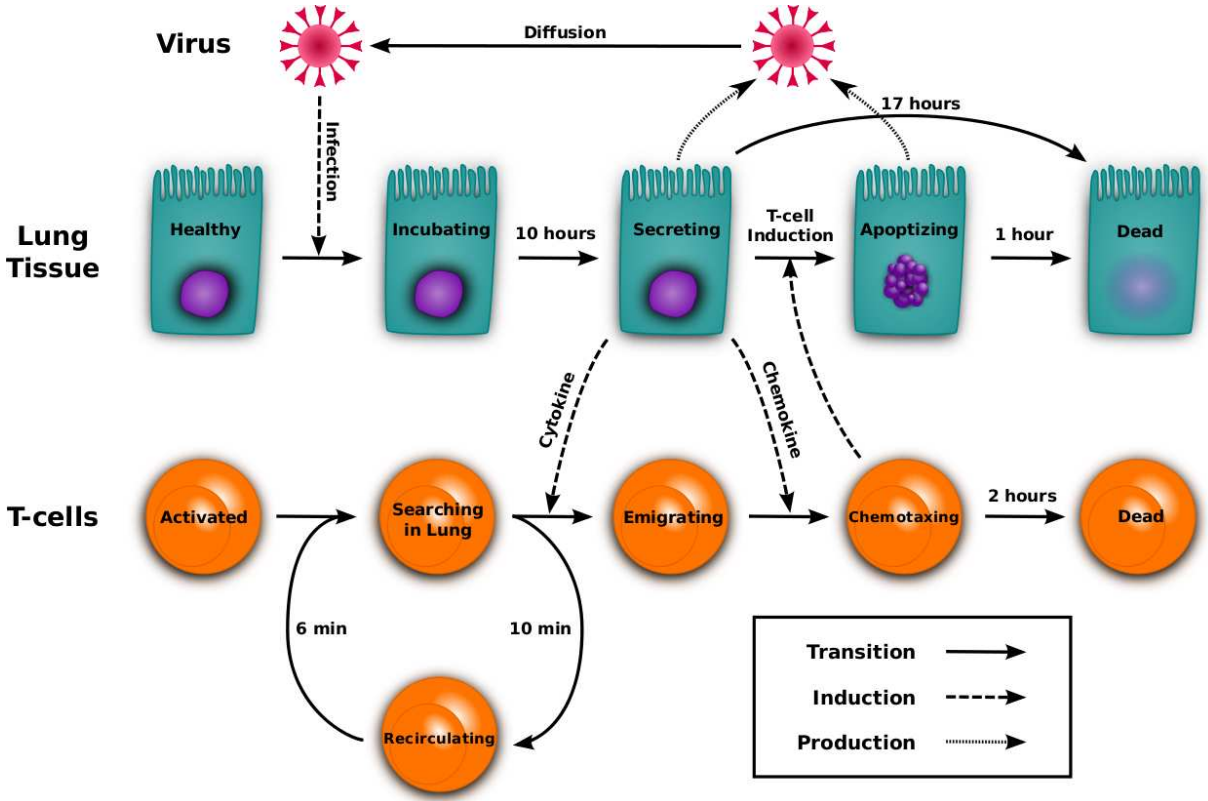


Figure 2. Visual representation of the model. Healthy epithelial cells infected by virus begin secreting virus after the incubation delay. Activated T cells traverse the bronchial vascular network and may be recruited by inflammatory cytokine. Chemotaxing T cells climb the chemokine gradient and induce apoptosis in infected cells. Solid arrows represent a cell state transition from one behavior to another. Dashed arrows display the mechanism used to induce a transition. Dotted arrows indicate the production of new virus.

In the model, epithelial cells are stationary and can be in one of five different states: *healthy*, *virus-incubating*, *virus-expressing*, *apoptotic*, and *dead*. *Healthy* cells remain unchanged unless infected by virus. Once infected, the cell transitions from incubating to *expressing*. *Expressing* cells secrete virus and chemokine for 17 hours and then die. *Expressing* cells become *apoptotic* if they encounter activated T-cells. Apoptotic cells continue to secrete virus until they die one hour after their transition. *Dead* cells

remain inert and do not regenerate over the course of an infection.

T-cells have three states. *Searching* T-Cells begin emerging from the lymph node at five days post infection. *Searching* T-Cells arrive at a random location on the lung’s surface, wander randomly in the tissue for 10 minutes, and transition to *circulating* in the absence of chemokine. *Circulating* cells spend six minutes recirculating to the lymph node, transition to *searching* and are reintroduced to a new random location in the lung. When a *searching* T-Cell encounters chemokine, it converts to *chemotaxing* and begins following the chemotactic gradient to the source of infection. *Chemotaxing* T-Cells move continuously up the gradient, inducing apoptosis if they encounter *expressing* epithelial cells. *Chemotaxing* cells decay exponentially with an average lifespan of two hours.

The model contains two kinds of particles: virus and chemokine. Both are produced at constant rates by *expressing* epithelial cells. Virus diffuses through the lung tissue, infecting healthy cells probabilistically according to the local virus concentration. Chemokine diffuses across the tissue but has no direct effect beyond activating T-Cells. Both particle types decay exponentially.

Parameters that are consistent between every model are shown in Table 1. Strain-specific values are shown in Table 2.

Materials

Chemokine secretion: Epithelial cell culture and supernatant collection was performed as described [19]. Briefly, undifferentiated human tracheal epithelial cells (University of Miami) were cultured for 4 weeks to achieve fully differentiated confluent monolayers on collagen-coated transwell inserts, or commercial differentiated human bronchial epithelial cells (EpiAirway Tissue, MatTek Corp., Ashland, MA) used immediately upon receipt, were infected at an MOI of 0.01 with either seasonal H1N1 virus A/New Caledonia/20/99 (sH1N1), the 2009 H1N1 pandemic strain A/California/04/09 (pH1N1), or avian H5N1 virus A/Hong Kong/483/97 (aH5N1) derived from a fatal human infection. Apical fluid for viral secretion, and basal media for chemokine secretion collected before treatment of the monolayer with protease, was collected from previously undisturbed triplicate or quadruplicate wells at 0, 6, 10, 12, 16, 20, 24, 30, 36, 42, 48, and 72 hours after infection, and stored at -80C until assay. Quantitative viral culture was performed by standard plaque assay. Quantitative chemokine levels were performed in 30 l aliquots for a panel of 17 chemokines and cytokines (Luminex Assay, Luminex Corp.) and reported as ng/mL basal

| Paramter | Value | Source |
|---------------------------|-------------------------------|------------------|
| Viral Diffusion | .0318 | [21] |
| Viral Decay | 1/ <i>day</i> | Phenomenological |
| Chemokine Diffusion | .318 $\mu\text{m}^2/\text{s}$ | [21] |
| Chemokine Decay | 3.8508e-4/ <i>s</i> | 30m half-life |
| Infection Sensitivity | 2 <i>h/virion</i> | Phenomenological |
| Incubation Time | 10 <i>h</i> | [19] |
| Expression Time | 16.7 <i>h</i> | [19] |
| Apoptosis Time | 1 <i>h</i> | Phenomenological |
| T-Cell Production Rate | 777/ <i>h</i> | [4] |
| Circulation Time | 6 <i>m</i> | [22] |
| Search Time | 10 <i>m</i> | [22] |
| T-Cell Speed (Search) | 30 $\mu\text{m}/\text{s}$ | [23] |
| T-Cell Speed (Activated) | 3 $\mu\text{m}/\text{s}$ | [23] |
| T-Cell Sensitivity | 1 <i>ng/mL</i> | [24] |
| T-Cell Expected Kill Rate | 10 <i>m</i> | [REF] |
| Cell Radius | 25 μm | Phenomenological |
| T-Cell Age (at FOI) | 2 <i>h</i> | [REF] |
| T-Cell Age (Other) | 3 <i>d</i> | [REF] |
| T-Cell Ramp Up Time | 5 <i>d</i> | [25] |
| IgM Strength | Viral decay of 3/ <i>day</i> | Phenomenological |

Table 1. Model parameters

| Strain | IP-10 Production (pg/s·cell) | RANTES Production (pg/s·cell) | Viral Production (PFU/s·cell) |
|---------------|---------------------------------|----------------------------------|----------------------------------|
| Avian H5N1 | 2.0e-4 8.4e-5 — 4.2e-4 | 1.3e-5 7.9e-6 — 1.9e-5 | 5.4e-5 |
| Seasonal H1N1 | 1.8e-4 1.2e-4 — 3.0e-4 | 8.9e-7 4.8e-7 — 1.6e-6 | 3.8e-4 |
| Pandemic H1N1 | 8.7e-5 1.7e-5 — 7.1e-4 | 4.3e-6 5.0e-7 — 3.5e-5 | 5.1e-3 |

Table 2. Strain-specific model parameters. Small text values show 95% confidence intervals resulting from 1,000 bootstrapping runs for each parameter [26]. Viral production values are taken from [19].

media sampled from a total volume of 4 mL.

Results

Chemokine production

Chemokine data were collected from epithelial monolayers infected with influenza strains, as described in [19] (Fig. 3). IP-10 concentration increases were observed by 8h post-infection (p.i.), and RANTES by 16h p.i.. To estimate per-cell production rates, we extended the ODE model of Ref. [19] to represent chemokine production from infected cells (Supplemental Methods). Model fits, (Table 2), were computed for three strains (Fig. 3) using Matlab's `nlinfit` function (Levenberg-Marquardt algorithm). Best-fit expression rates were similar for all strains except for significantly higher RANTES production in aH5N1. There is no positive correlation between viral production and induced chemokine production across the three strains.

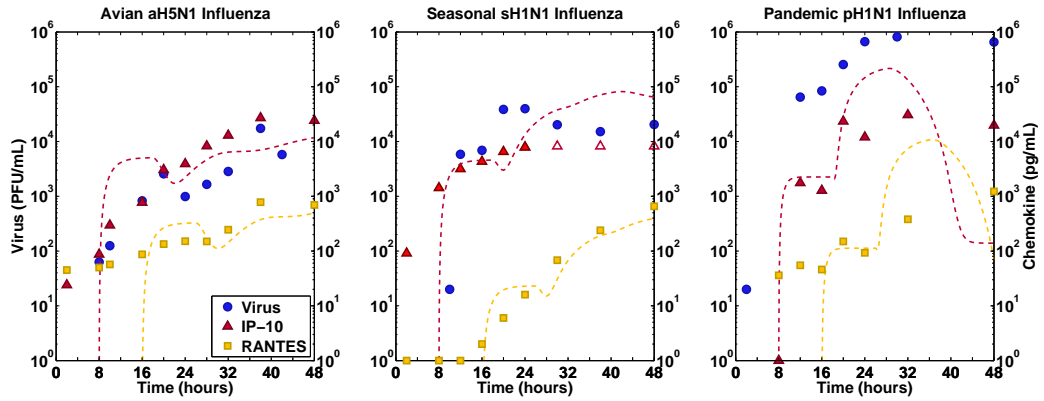


Figure 3. Empirical viral and cytokine titers for three strains of influenza: Avian H5N1, Seasonal sH1N1, and Pandemic pH1N1. Viral titer (blue circles) is in PFU/mL, and IP-10 (red triangle) and RANTES (green square) are shown in ng/mL. sH1N1 IP-10 registered three values, not included in model fitting, above the measurement threshold of 8,500 pg/mL (empty red triangles). Dashed lines show model fits to IP-10 and RANTES data.

T-cell sensitivity to chemokine

The model uses chemokine gradient as a surrogate for the inflammatory cytokines required for extravasation. Figure 5 shows chemokine concentrated around virus secreting cells. However, T-cell sensitivity

determines how strong the aggregate chemokine signal must be.

We simulated T cell sensitivity levels ranging over seven orders of magnitude and found a threshold (Fig. 4) between concentrations of $1 \mu\text{g/ml}$ and 100 ng/ml (100 ng/ml and 10 ng/ml in aH5N1), below which there is no discernible effect on T cell movement. Because multiple T-cells in the same area do not enhance control of infection, we hypothesize more T cells are not better above a critical threshold. We set the sensitivity to 10 ng/mL (1 nM concentration assuming a chemokine molecular weight of 10 kDa) [24]. Single runs were used due to computational limitations. Model variance is discussed in the Supplemental Results.

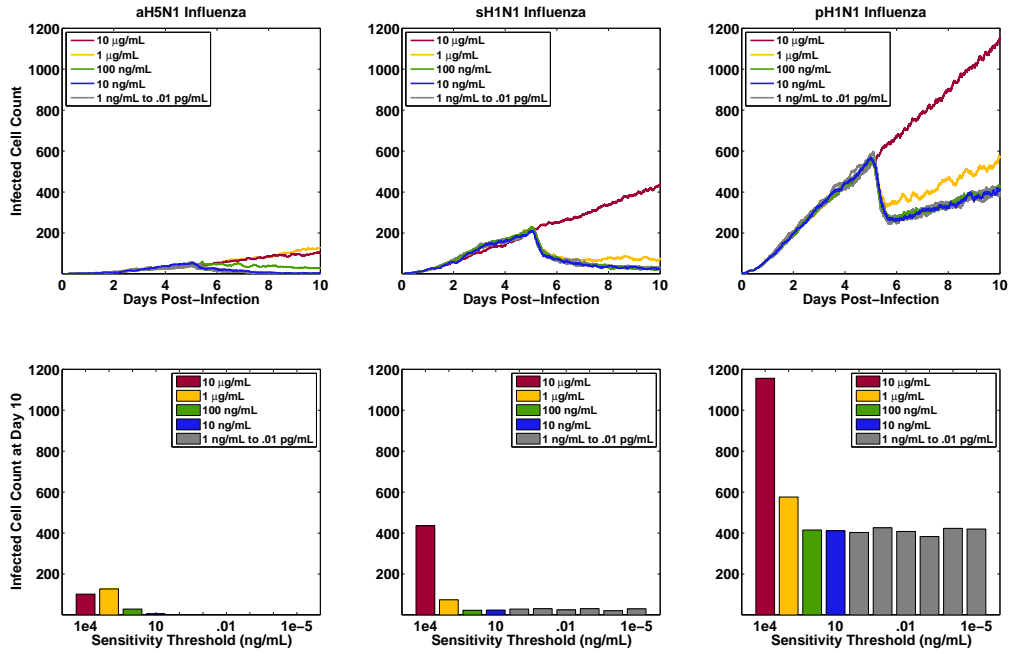


Figure 4. Varying T-cell sensitivity to chemokine: H5N1 model results use RANTES only, and sH1N1 and pH1N1 use both IP-10 and RANTES. Total number of infected, expressing and apoptotic cells are plotted for each infection. The sensitivity value specifies the minimum level of chemokine concentration required for T-cells to detect it.

Spatial effects

Spatial effects of viral and chemokine diffusion play an important role in both the spreading and clearing of infections. Free virus particles diffuse from virus secreting cells and infect healthy cells. Chemokine

produced by infected cells attracts T-cells to the infected cells. Although virus is produced at a higher rate than chemokine, its larger size diffuses much more slowly, while chemokine decays more quickly. These countervailing effects result in similar spatial profiles for the two particle types (Fig. 5). Until day 4 the plaque is dominated by active (incubating and secreting) cells, and dead cells are rare. Over time, cells in the plaque's interior die, and active cells form a decreasing proportion of the plaque. T-cells arrive at day 5 and begin killing the virus-secreting cells. By day 6 many expressing cells have been eliminated and the plaque is dominated by dead cells. In aH5N1, the plaque is dense, allowing T-cells to find secreting cells easily, and infection is eliminated. However, in both H1N1 simulations secreting cells were not eliminated. Secreting cells accounted for at most 10% of the active cell population and less than 1% of the total plaque at 6 days p.i.. T cells still accumulate, but they arrive more slowly than the plaque is growing, leading to lower average T cell killing rate. Further, the regions of concentrated chemokine lag behind the cell and virus spatial layout. It takes time for newly secreting cells to produce chemokine while pockets of high chemokine density are slow to decay. Thus, T-cells can fail to detect cellular changes in the plaque. Taken together, the delayed response and low proportion of virus secreting cells prevent T-cells from completely clearing the infection.

T-cells are unable to kill cells that have not yet presented antigen. At day 5.5, the ratio of secreting cells to the total plaque size is high (Fig. 5-6). By day 7, this ratio is approximately 1:100 for both the pH1N1 and sH1N1 strains. The high replication rate of pH1N1 enhances this effect (Fig. 6C) and the T-cells can control (but not eliminate) the sH1N1 infection.

A cell infected with pH1N1 produces new virus at the rate of 5.08×10^{-3} PFU/s [19]. That is, in each secreting cell a new viral particle is produced approximately every 200 seconds. Assuming that secretion continues for one hour after apoptosis is initiated, the best a T-Cell could do is limit production to 18 new viral particles. Thus, T-Cells alone cannot contain the pH1N1 infection. In contrast, a sH1N1 virus-secreting cell produces a new virus particle every 2,643 seconds, allowing T-cells to limit a single infected cell to 1.3 viral particles in the one-hour window. Avian H5N1 virus-secreting cells produce only 0.2 viral particles in the interval after induced apoptosis.

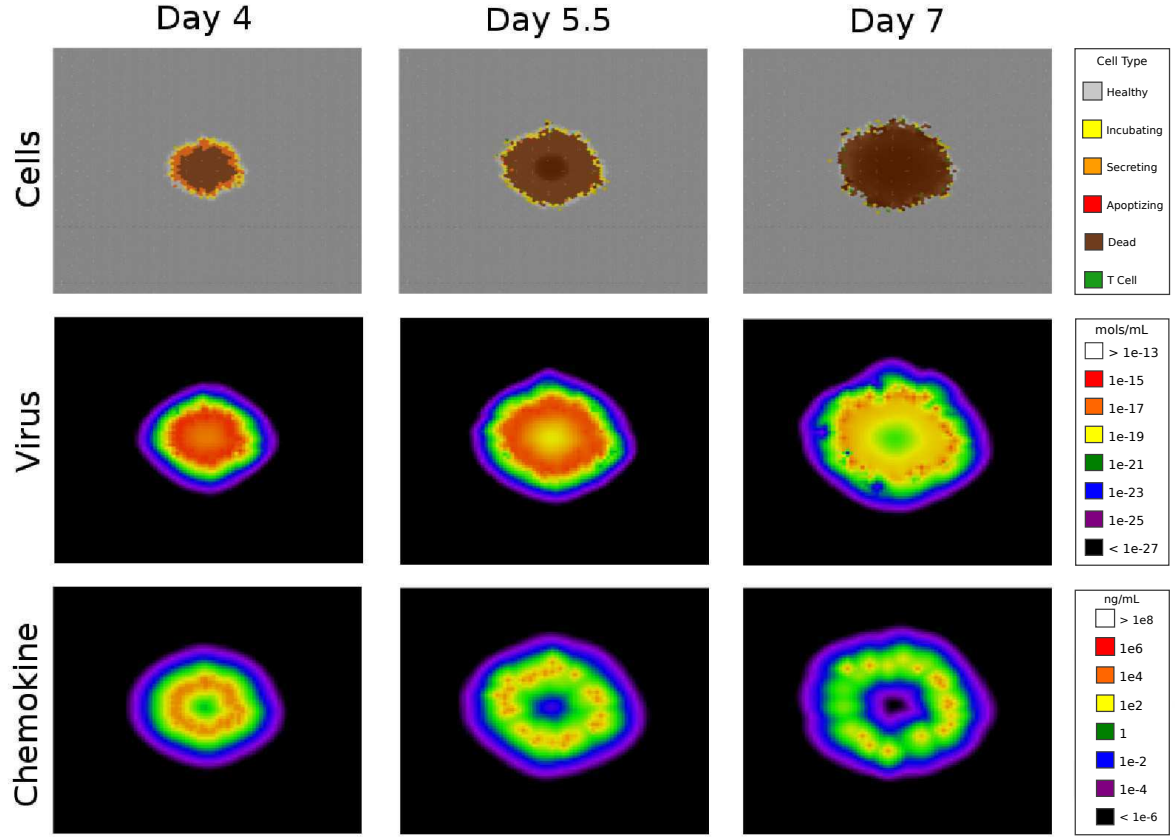


Figure 5. Simulated sH1N1 infection. Screenshots from day 4, day 5.5, and day 7. The top row shows the spreading focus of infection through the color coding of individual cells: healthy cells in uninfected tissue (gray), virus-incubating cells (yellow), virus-secreting cells (orange), apoptotic cells (red), dead cells (brown), and T-cells arriving at day 5 (green). Free virus and chemokine particles are represented by compartmentalized concentrations of mols/mL and ng/mL (see the legend in the bottom right).

Discussion

Caveats

Parameters are estimated to the best of our knowledge when values could not be found in literature. We choose to ignore most aspects of the innate immune response to avoid over-parameterizing the model. The unbounded growth of pH1N1 can partially be attributed to the lack of many innate mechanisms. T cells are assumed to have the same level of sensitivity to both IP-10 and RANTES. Furthermore, T cells climb chemokine gradient in straight lines as our experiments with biased random walks showed no effect

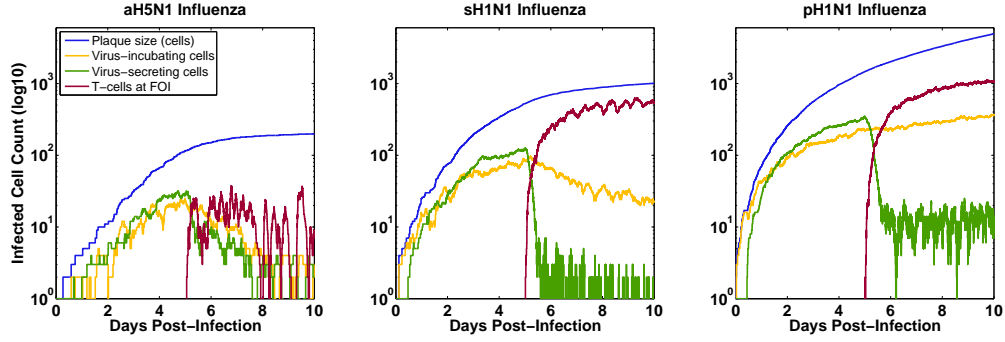


Figure 6. Comparison of total plaque size (blue), number of virus incubating cells (yellow), number of virus secreting cells (green), and T cells (red) for the simulated infections of aH5N1, sH1N1, and pH1N1. T cells are able to clear both secreting and incubating cells in aH5N1, are unable to contain incubating cells in sH1N1, and are unable to contain either type of infected cell in pH1N1.

on model behavior.

Chemokine Directed T-cell Search

Hypercytokinemia is a characteristic of virulent influenza strains [27], but bloodstream levels of cytokines and chemokines may not reflect local concentrations or dynamics critical in guiding T cells to infected epithelial cells. We elected to use our data on in vitro secretion of chemokines by human bronchial epithelial (NHBE) cells obtained from the same cultures of the three virus strains previously reported [19]. In this study the replication kinetics and productivity of the three virus strains were markedly different, but monolayer infection was initiated with a low MOI of 0.01 or 0.001, mimicking the natural initial infection. The levels of the chemokines CCL5 and CXCL10 in the basal media induced by the 3 strains were approximately equivalent at 24h p.i.. When the productivity per cell was calculated, the avian H5N1 strain induced higher secretion of CCL5 (RANTES) than the seasonal or pandemic strains. Greater CCL5 secretion by H5N1 strains has been noted in in vitro NHBE cultures when a relatively high MOI is used compared to seasonal strains [28–30] and pandemic strains [30]. MOI and degree of differentiation of NHBE are critical determinants of cyto/chemokine secretion [29]. However, in spite of the attenuated type 1 interferon response induced by H5N1 strains [31], the chemokine secretion is not attenuated.

Chemokines with a clear role directing T cell traffic include CXCL10 [32], CCL5 [33] and CCL3 [33]. The chemokine receptor CCR5, binding CCL5 and other chemokines, is crucial to accelerated recruitment of CD8+ T cells to lung airways [34]. Other chemokines likely play a role in T cell trafficking. Although we

did not detect significant levels of other chemokines in our cultures, the neutrophil- and T cell-attractant CXCL8/IL-8 is secreted into seasonal influenza-infected NHBE cultures [35, 36]. In the intact animal, immigrant inflammatory cells particularly macrophages augment the multiple chemokine signals [37]. Finally, antigen-specific CD8+ T cell recognition of its target induces lung injury mediated by TNF α and triggers additional alveolar epithelial cell chemokine secretion [17]. Thus our model represents only a portion of the complete chemokine signal complex operating in the infected animal.

A key determinant in the efficiency of chemokine-directed T cell migration towards virus-secreting epithelial cells is the communication distance, defined by the threshold of sufficient chemokine signal required to induce directed motion of the cell up the chemical gradient [11]. The diameter of this cloud generated by a single cell is a function of production rate, decay rate, protein diffusion and the sensitivity threshold. For the threshold of 10 pg/mL and maximal levels of concentration in tissue of 10,000 pg/mL, we calculated the effective communication distance as approximately 250 microns in our model. This calculation agrees with the distance calculated for generic cytokines secreted by a suspended solitary cell [38].

Immune Response Modeling

The adaptive immune response to influenza in the mouse is a complex network of molecular and cellular elements, and incorporation of all of these into a comprehensive predictive model is not yet achieved. Recent whole-animal models using a data-fitting approach, and extensive databases have enhanced our global understanding of response metrics that are difficult or impossible to measure. We have focused exclusively on the problem of search by activated CTL for infected foci in the lung, and as in other models have made a number of assumptions and simplifications to permit tractable simulations. Antigen presentation and peripheral lymphoid tissue amplification of the T cell clonal response is represented solely by the constant rate of emigration of activated T cells from regional lymph nodes. Virus-specific strain replication rates are represented as constant rates, and virus clearance is also constant. The contribution of IgM antibody clearing free virus is represented at a constant rate, and the class switch to higher affinity antibody mediated by CD4+ T cells is not represented. All of these rates may in fact be time-variable as indicated by superior data-fitting models [39]. Immigration and contributions of virus-nonspecific immune cells such as macrophages are not represented in our model. Finally, the proliferation of activated T cells in lung tissue is not represented, but is thought to be crucial in the control of lung

infection [4]. Thus, our model is not intended to predict clearance of virus from the lung. Rather our goal was to examine the features of the response that permitted T cells to sense and contact infected target cells.

ABM Advantages

The use of an ABM has certain advantages over a spatially homogeneous ODE model. An ODE model assumes that any virus particle is capable of infecting any healthy cell. Figure 5 shows that this is clearly not the case. In fact, most free virus exists on top of infected cells that are no longer candidates for viral binding and fusion. ODE models account for this discrepancy by lowering rates of infection by a constant amount, but this assumes that the proportion of unsuitable virions will always be the same. This is limiting as can be seen in Figure 5 where the early infection has a higher proportion of virus overlapping healthy cells.

Our ABM renders the model in OpenGL (Fig. 5). Seeing the model in action reveals spatial dynamics that are absent in ODEs and difficult or impossible to observe in *in vitro* and *in vivo* systems, for example, the spatial dynamics discussed earlier. First, because T-cells find infected cells by climbing a gradient, we see T-cell clustering at local maxima of chemokine concentration, a possible explanation for why T-cells do not increase in effectiveness as their numbers increase. Second, T-cell clustering persists after all virus-secreting cells have been eliminated. The local chemokine maxima takes time to diffuse and decay so that T-cells can climb the gradient to a new maximum. Finally, we can see that infected cells are more disperse as infection size grows. Because T-cells are clustered they cannot cover the increasing plaque effectively. These spatial observations provide explanations for the pH1N1 resurgence that would be obscured without the visualization tools provided by the ABM.

Acknowledgments

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KEY: Gao2003

ANNOTATION: CCL5 (RANTES) and CXCL10 (IP-10) concentrations inducing T cell chemotaxis (adhesion)

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Figure Legends

Tables