

ABSTRACT

Background

- Granulomas are hallmark of *Mycobacterium tuberculosis* (Mtb) infection
- Collections of host immune cells (macrophages and T cells)
- Contain and eliminate the infection
- Expect to be enriched substantially in Mtb-responsive T cells (cells producing cytokines in response to Mtb)
- However, low frequency of Mtb-responsive T cells (~ 10%) in granulomas have been observed
- Important to determine why the frequency of functional T cells in granulomas is so low
- Hypothesis: T cells are being down-regulated directly by Mtb

Methods

- Use a multi-scale modeling (MSM) approach
- Agent based model (ABM), known as GranSim tracks bacteria and individual immune cells as agents
- System of ODEs captures Mtb-mediated down-regulation of MHC II presentation of peptides in macrophages
- Combine ABM and ODEs in MSM that spans intracellular to tissue scales

Results

- Mid range down regulation of MHC II transcription most advantageous for Mtb
- Down regulation of MHC II maturation lowered T cell response

Discussion

- Can provide insights into mechanisms that could be either enhanced or inhibited to therapeutically increase frequencies of Mtb-responsive T cells
- Help to understand what mechanisms may be contributing to the extremely low levels of responsiveness

T CELLS IN MTB

- Tuberculosis (TB): Infectious disease caused by *Mycobacterium tuberculosis* (Mtb). One-third of the world's population is infected with Mtb, 2 million deaths/year¹
- Host immune cells (macrophages and T cells) form granulomas to contain the infection
- Only ~8% T cells in granulomas respond to Mtb²
- It's unknown why T cell response at site of infection is low

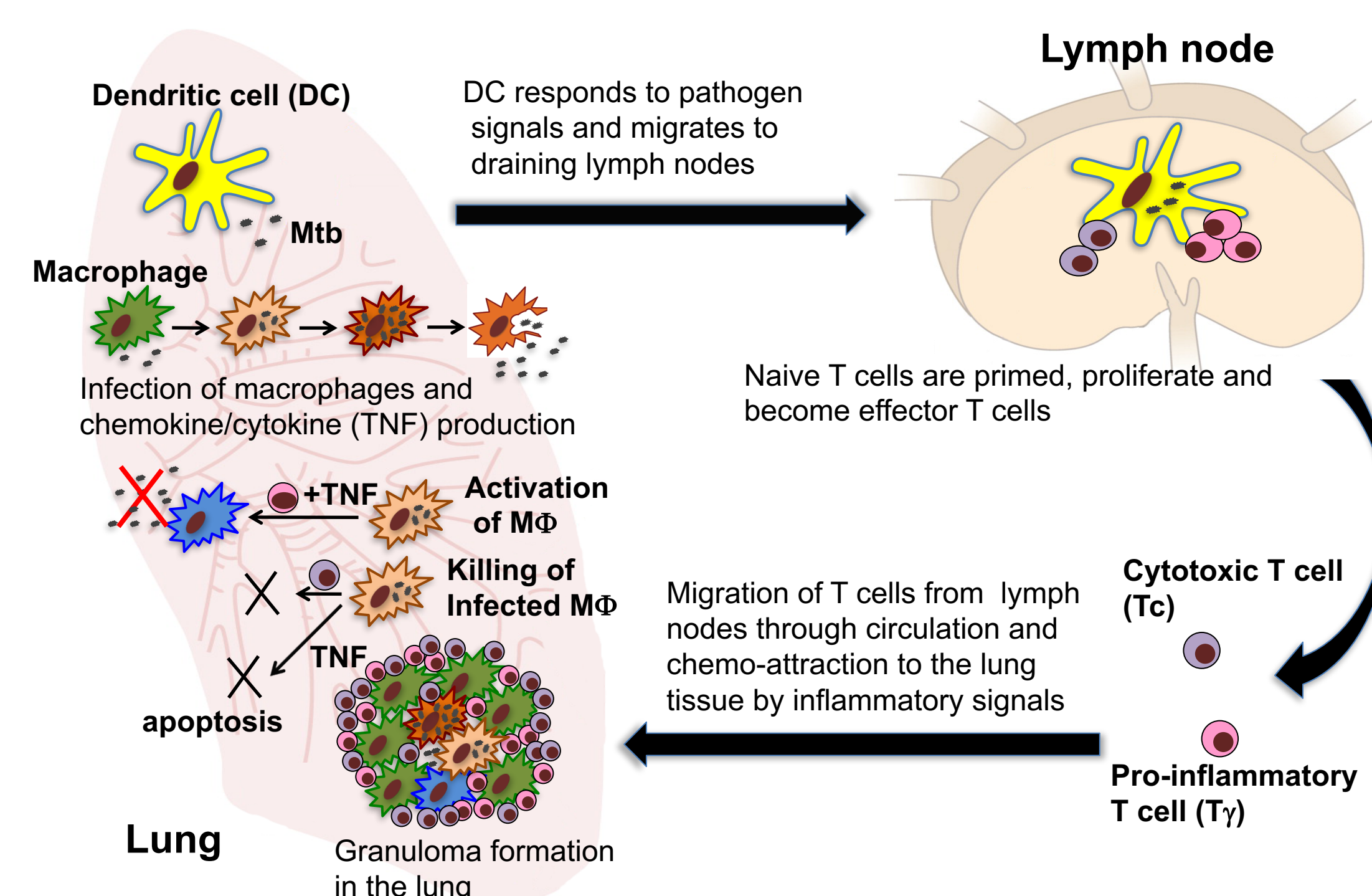


Figure 1: Mtb infection process.

GOALS OF THE STUDY

- Use model to predict how Mtb interferes with T cells at the molecular level (antigen presentation) and cellular/tissue level (T cell, macrophage movement, interaction)
- Combine molecular and cellular/tissue level models to explore how they interact, look for emergent behavior

MULTI-SCALE MODELING

Tissue/Cellular Model

- GranSim^{3,4} captures discrete cellular dynamics between immune cells and Mtb leading to tissue scale outcomes
- Comprised of decision-making heuristics via a set of well-described interactions, calibrated using experimental data, and implemented in C++ code with Boost and FFTw libraries.

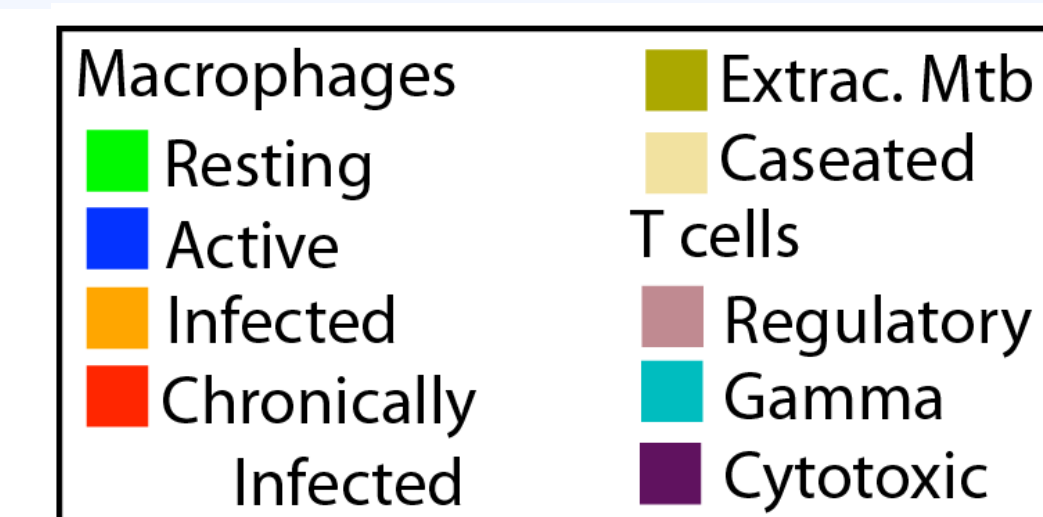
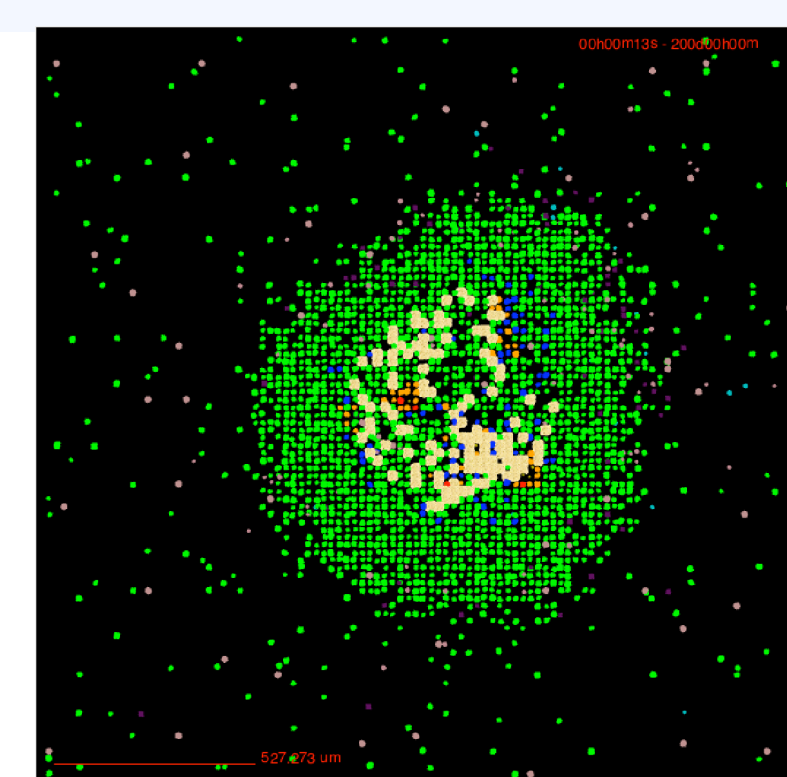


Figure 2: Example time point in GranSim and different types of agents on the grid.

Intracellular Model

- Chang *et al* 2005⁵ ODE model captures Mtb-mediated down-regulation of MHC II presentation of peptides in macrophages
- GranSim has the ability to insert ODEs into individual agents, creating a multi-scale hybrid agent based model that is stochastic and discrete in nature
- Allows observation of interaction between tissue, cellular, & molecular scales

Integrated Multi-Scale Model

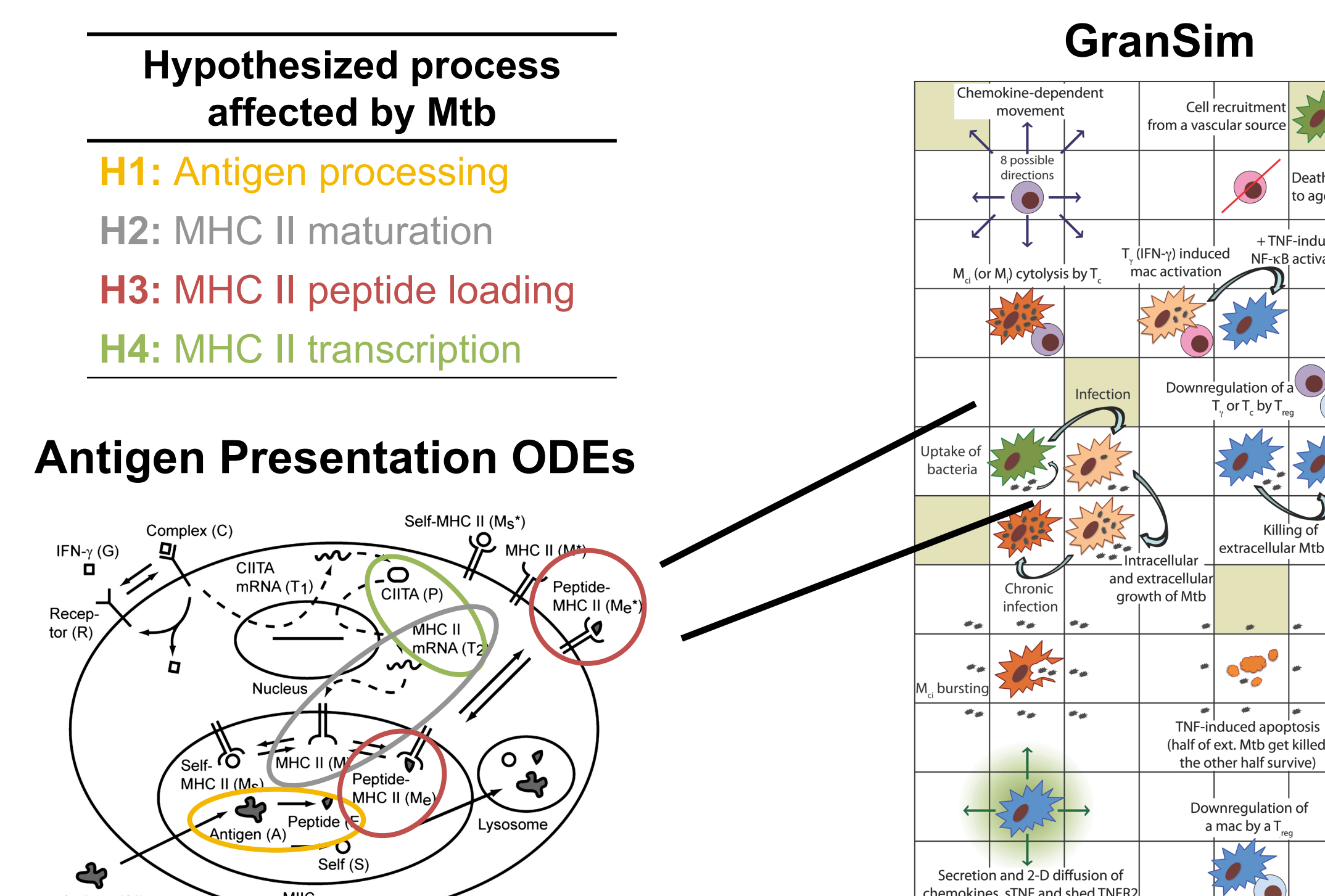
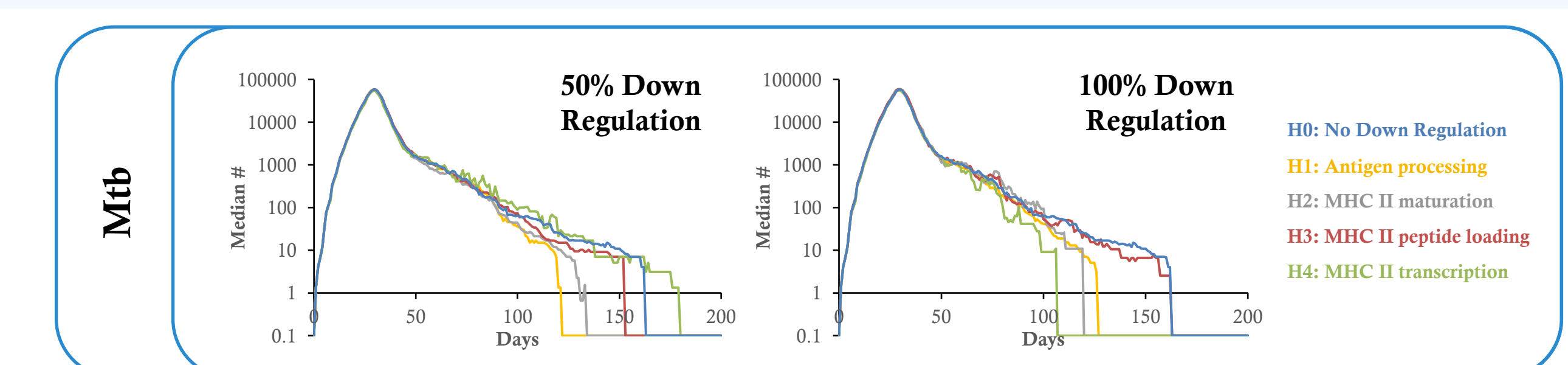


Figure 3: Model schematics of GranSim and ODEs and how they relate to each other as a multi-scale model. Colored circles represent different processes hypothesized to effect antigen presentation by Mtb.

RESULTS

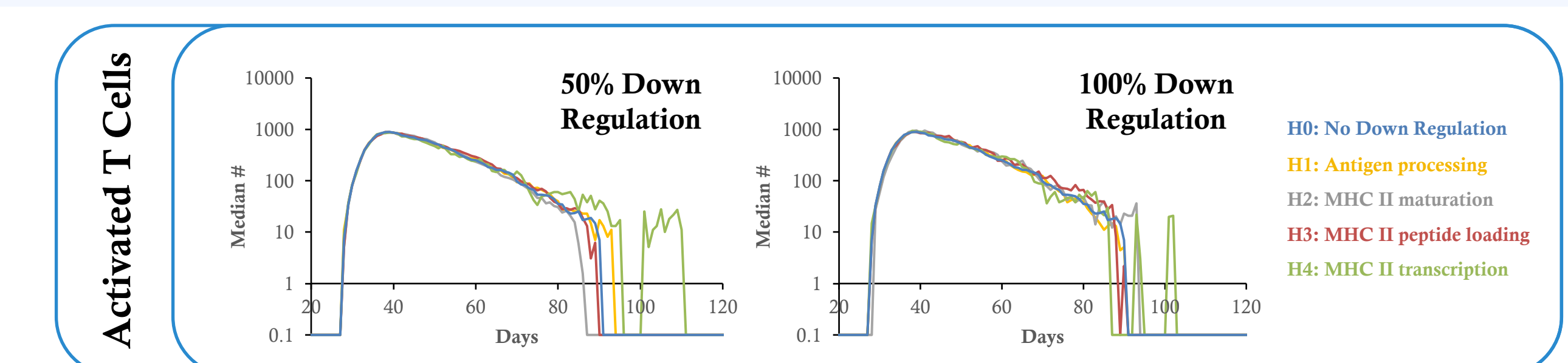
1. Mid range down regulation of MHC II transcription most advantageous for Mtb

- 50% down regulation of MHC II transcription allows Mtb infection to persist longer, along with increased MHC II
- 100% down regulation has the opposite effect



2. Mid range down regulation of MHC II maturation reduces activated T cell response

- 50% down regulation of MHC II maturation stops the activated T cell response about 5 days earlier
- 100% down regulation allows it to continue for a few more days



DISCUSSION / CONCLUSIONS

- Mid range MHC II transcription reduction may reduce MHC II complex recycling, more chance of presenting self peptide vs Mtb
- Mid range MHC II maturation reduction results in less MHC II complexes, likely leading to less activated T cells
- In both cases, there was a “goldilocks zone” where too much down regulation was detrimental to Mtb
- With this in mind, intervention in Mtb infection could possibly consist of blocking these MHC II processing steps in macrophages within granulomas

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