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The basic in-host model for Tuberculosis(TB)

Tuberculosis (TB) is the number one cause of death due to infectious disease today, with over one-third of the world population infected with *M. tuberculosis* and almost 2 million TB-related deaths every year. With the HIV epidemic and the appearance of multidrug-resistant TB, TB is becoming even more deadly. TB infection results in clearance, latent infection or active disease (slow or fast progression). Only $5 - 10\%$ of infected individuals developing active disease in the first 5 years postinfection. Thus, studying the dynamics of immune response in TB infection is crucial to developing predictors of disease outcome. Mathematical models have been used to provide some insight into this, however, such models have been very complicated with very high dimensions (i.e. > 10 equations). This does not compare to the simple and very powerful basic model of virus dynamics (only 3-dimension) that has been used to give great insight into the pathogenesis of various viral infections (i.e. HIV, HCV). We develop a simple 4-dimension mathematical model of TB infection in-host. The model includes macrophages, T lymphocytes, bacteria and their interactions, and captures all disease outcomes. Uncertainty and sensitivity analysis and numerical simulations have given very interesting results, including identification of key parameters that determine disease outcome, as well as model conditions which can produce a backward bifurcation. The model also provides a sound foundation for future studies on the pathogenesis of drug resistant TB and HIV/TB coinfection.