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We mathematically examine what key aspects of the humoral immune response should be elicited to create an effective vaccine against the bacteria Shigella. Shigella, a member of the same family as E. coli, causes one million deaths every year. No vaccine exists for Shigella despite decades of experimental research and clinical trials, in part because the multiple immune components responsible for conferring immunity against Shigella are not known.

I will describe how we are using ordinary differential equation models to search for promising Shigella vaccine targets. We have developed an ODE model of the antibody and B-cell immune response against Shigella, and we parameterize our model using clinical trial vaccine data. We use Latin hypercube sampling and Monte Carlo parameter estimation with this clinical data to identify realistic, biologically grounded parameter value combinations. Subsequent sensitivity analysis enables us to predict which crucial parameters and parameter ranges correlate with disease prevention and clearance. The long-term goal of this collaborative research is to identify which key immune-bacterial interactions should be targeted by a vaccine to successfully protect against Shigella infection. (Received September 11, 2014)