A Mathematical Model for a *Salmonella* Bacteriophage

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In USA, food borne diseases have been estimated to cause 6 million to 81 million illnesses and up to 9,000 deaths each year. The Centers for Disease Control and Prevention (CDC) estimates that Salmonella are responsible for 20% to 40% of those diseases.

The increase number of food borne diseases and the restrictions to the use of antibiotics due to the rising of antibiotic resistant bacteria lead to the investigation of alternative methods in the control of pathogenic bacteria. Phage therapy appears as a promising method.

Mathematical models have been used for studying the dynamics of bacteriophage and, more recently, to evaluate its applicability in phage therapy. The kinetics of active phage therapy is based on the population dynamics of ecological predator-prey models and epidemiological host-parasite models. The utility of simple models is to identify, in a quantitative way, the dominant factors that contribute to the population dynamics and to the evolution of the interactions between bacteria and phage.

The goal of this work was the development of a population dynamic model that predicts the interaction between a Salmonella phage and its respective host. Simulated data generated by the model was compared with the values obtained experimentally allowing to assess the suitability of the model. The model is being used to predict the amount of phage obtained in the production process. Additionally, the developed model is expected to be useful in the optimization of phage production and on the design of experimental studies.

Keywords: Bacteriophage, Model, Phage Therapy.