

COLLOQUIUM

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Modeling gastrointestinal pathway of *Listeria monocytogenes* and mechanistic understanding of dose-response relationships

Abstract

Foodborne infection is a major public health concern. According to WHO, every year 10% of people suffer from foodborne illnesses worldwide. A dose-response relationship measures an infection risk of a pathogen and it is widely used in quantitative microbial risk assessment (QMRA). While many descriptive models (e.g. exponential and log-normal) can demonstrate the dose-response relationship of an outbreak they suffer from the lack of a mechanistic basis. To account for the within-host interaction of a pathogen and to measure its infection potential, we develop several mathematical models. These models mimic the gastrointestinal pathway of a food pathogen and demonstrate the critical steps for the pathogen and host when exposure may turn into an infection. Due to the frequent outbreaks of *Listeria monocytogenes* and its severe impact on public health and economy we consider this bacterium as the model pathogen. These models can be used as complementary tools to assess the pathogen survival in a host and to build the dose-response relationships.

Tuesday, January 28, 2020
12:00 – 12:50 P.M.
372 Mathematics and Science Center (MSC)

(Refreshments at 11:30-12:00 PM in the kitchen area adjacent to 368 MSC)