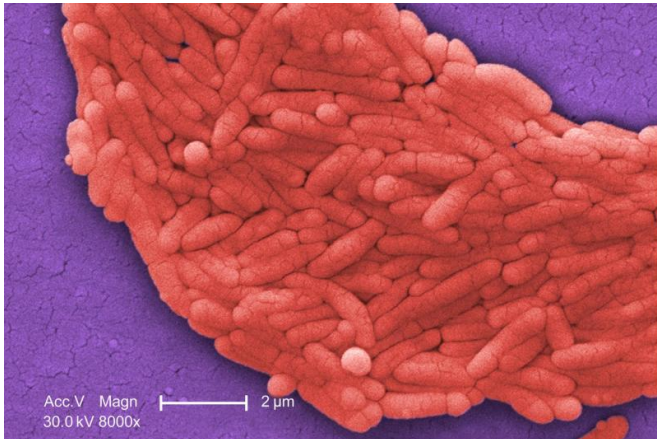


# Researchers map links between salmonella and sepsis

16 September 2016, by Zhenzhen Shi



Salmonella forms a biofilm. Credit: CDC

Research by industrial engineering and biology researchers at Kansas State University marks a significant milestone in the battle against sepsis, the second highest cause of death in intensive care units in the U.S.

The study, "An Agent-Based Model of a Hepatic Inflammatory Response to Salmonella: A Computational Study under a Large Set of Experimental Data," was recently published in the peer-reviewed scientific journal *PLOS ONE*.

Zhenzhen Shi, a December 2015 industrial engineering doctoral graduate and first author; faculty researchers David Ben-Arieh, professor, and John Wu, associate professor, both of [industrial engineering](#); and Stephen Chapes, professor of biology, studied the biological processes that lead to and result from [sepsis](#), a hepatic—or liver-related—inflammatory response.

The research team developed an integrated mathematical and multi-agent-based model to simulate hepatic inflammatory response caused by salmonella. Rapid response is critical to successful

treatment, but because of the unpredictable nature of hepatic [inflammatory response](#), sepsis and septic shock are difficult to identify in individual patients.

"Previous research used a simplified mathematical model to represent the progression of a sepsis episode," Ben-Arieh said. "Such a model was not able to capture the full complexity of this health risk."

The new model allows the researchers to more accurately map interactions among cells, tissues and cytokines, which are small proteins important in cell signaling.

"The strength of the current model is the integration of the complex mathematical and biological description with a simulation engine that can model this phenomenon," Wu said.

By modeling the progression of the sepsis episode, Ben-Arieh and Wu said clinicians can provide the most appropriate and timely care to the patient. Future research in this area will incorporate more biological pathways for increasingly accurate simulations.

"Sepsis deaths are difficult to predict without a highly complex hybrid model," Shi said. "This latest [model](#) could be the best tool available for predicting and treating sepsis and preventing fatalities."

Shi said that as more human data on sepsis becomes available, this type of work may be further developed into an easy-to-use visualization tool that can predict sepsis progression, test proposed treatments prior to preclinical experiments and eventually help in clinical decision-making.

**More information:** Zhenzhen Shi et al. An Agent-Based Model of a Hepatic Inflammatory Response to Salmonella: A Computational Study under a Large Set of Experimental Data, *PLOS ONE*

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Provided by Kansas State University

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