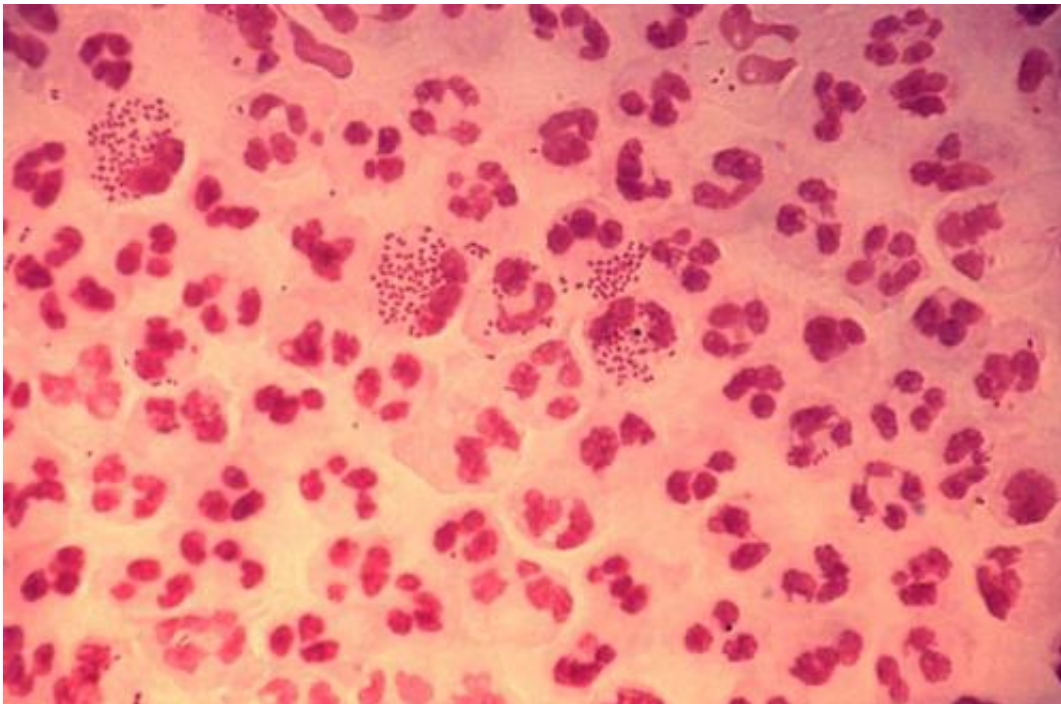


Mouse models may not accurately mimic severity of gonorrhea infection

September 4 2018



Credit: CDC

There is an urgent need to develop a vaccine to prevent gonorrhea infection due to rapidly increasing incidence and growing antibiotic resistance. BUSM researchers (in collaboration with University of Toronto researchers) have been investigating the use of animal models of gonorrhea, to study how the infection evolves and for potential use to determine the efficacy of next generation vaccines. They found that the

mouse model may not fully reflect the severity of the infection and the types of immune responses seen in humans.

Gonorrhea is a rapidly worsening [public health threat](#). In 2017 more than 550,000 new cases of [gonorrhea](#) were reported to the Centers for Disease Control and Prevention (a 67 percent increase from 2013), while the World Health Organization places global yearly incidence at 106.1 million cases. Researchers believe these figures may underestimate the actual disease burden by up to two-thirds. In addition, there is significant evidence that gonorrhea is becoming increasingly drug-resistant. According to most experts in the field, these factors make it even more essential that we develop effective gonorrhea vaccines and have adequate animal models in which to test their efficacy.

""The use of models in infectious diseases to examine pathogenesis and potential vaccine development is fraught with difficulties as many of these human specific pathogens have evolved mechanisms of infection and immune evasion specific for humans. It is essential that when models are used, the details of their infections are fully examined to ensure they at least somewhat mimic what occurs in humans," said Lee M. Wetzler, MD, Professor of Medicine and Microbiology.

More information: Ian P. Francis et al, Murine host response to *Neisseria gonorrhoeae* upper genital tract infection reveals a common transcriptional signature, plus distinct inflammatory responses that vary between reproductive cycle phases, *BMC Genomics* (2018). [DOI: 10.1186/s12864-018-5000-7](https://doi.org/10.1186/s12864-018-5000-7)

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