

# New clues behind the resilience of a leading sexually transmitted pathogen, Chlamydia

October 14 2014

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In the advanced online edition of *Molecular Biology and Evolution*, authors Domman, et al. have explored factors behind the resilience of the most common sexually transmitted disease in the U.S., chlamydia, with an estimated 1 million infected.

The research team sequenced 4 new strains of close genetic cousins of chlamydial pathogens, and examined these with existing DNA data. They found an extensive and robust shuffling of the genomic deck between chlamydia families has played a major role in the evolution of the pathogen, often serving to outwit and exploit its hosts. They also identified genomic hotspots that seem to play a key role in adaptation and survival, with many having an unknown function. Of note, these [gene families](#) were most commonly found to have specific protein features gained from their eukaryotic hosts. By combining their molecular analysis with cell-based assays, the authors demonstrated that these are thought to be secreted proteins that interfere with their hosts' defenses.

The authors argue that the evolutionary forces at work behind the diversity of chlamydiae are the result of a unique confluence of birth and death gene evolutionary cycles. In this cycle, new gene copies often arise by gene duplication, with the copies persisting or adapting into new roles within the genome for varying lengths of time, or dying off and being lost randomly. "One of the most surprising findings is that a similar mode of evolution has so far only been observed in fungi, plants, and animals." says Matthias Horn who led the research team. Such factors

can provide the research community with new clues into how [chlamydia](#) has emerged as a human scourge, as well as novel targets for next-generation therapeutics.

"Our study highlights the importance of taking advantage of the tremendous diversity of environmental microbes to improve our knowledge about the evolution of microbial pathogens," said author Domman.

Provided by Oxford University Press

Citation: New clues behind the resilience of a leading sexually transmitted pathogen, Chlamydia (2014, October 14) retrieved 21 March 2023 from <https://phys.org/news/2014-10-clues-resilience-sexually-transmitted-pathogen.html>

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