

Newly identified strains of Chlamydia trachomatis could produce new diseases

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A new study led by a scientist at Children's Hospital Oakland Research Institute (CHORI) is the first to conclude that Chlamydia trachomatis is evolving at a rate faster than scientists first thought or imagined.

Chlamydia trachomatis is a bacterium that is the leading cause of sexually transmitted diseases and the second leading cause of blindness worldwide. Scientists believe the bacterium is evolving through a process called recombination where genes from one or more strains combine to create new strains and – theoretically – new diseases.

The study is featured in the November issue of *Genome Research* and was led by Dr. Deborah Dean MD, MPH, senior scientist at Children's Hospital Oakland Research Institute (CHORI). Her research suggests that since Chlamydia trachomatis evolves through recombination where one or more strains combine, the traditional method of studying a single gene to track the transmission of the bacterium is wrong. "What we found is an organism that not only evolves rapidly, but in ways that we thought were rare. We also discovered that this organism can customize its attack," said Dr. Dean. "Consequently, the constant flux of the bacterium could serve as a gateway for new emerging diseases, but more research needs to be conducted to understand if and how this is happening."

600 million people are infected across the globe with Chlamydia trachomatis and 8 million are already blind or severely visually impaired. In some parts of third-world countries, more than 90% of the population



is infected. Chlamydia trachomatis has a variety of strains; different strains are responsible for different diseases. Some strains cause sexually transmitted diseases while others cause eye infections. Blinding trachoma is caused by repeated eye infections that cause scarring, which result in the eyelashes turning in-wards. Bacterial infection develops as the eyelashes scratch the surface of the eye, which eventually heals by scarring, resulting in blindness.

Previously, the organism was identified using a single gene, ompA, and the protein encoded by that gene, MOMP. In this study, the clinical strains, which are samples of Chlamydia trachomatis currently responsible for human disease today, were compared to standard reference strains that have been laboratory adapted over the last few decades. By studying multiple strains, the researchers discovered that the strains that were identified as the same strain were actually different.

The next step will be to study clinical strains in comparison with laboratory reference strains to decipher exactly how different strains cause disease and whether new diseases are emerging as a result of the emergence of new strains. "Large-scale comparative genomics will be necessary to understand the precise mechanisms underlying Chlamydia trachomatis recombination and how other species of chamydiae may evolve and transfer from animals to humans."

Source: Children's Hospital & Research Center at Oakland

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