

## **Chlamydiae - how to trace who has been with whom. An unsexy task about sexual infections**

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Background: Chlamydia trachomatis is the bacterial species causing most sexually transmitted infections. It is of high importance for the public health since it causes reproductive tract diseases as salpingitis (äggledarinflammation), ectopic pregnancy (utomkvedshavandeskap) and infertility. Chlamydia infections are often asymptomatic and therefore there are two important ways to detect infected persons: 1./ generous examination among persons in sexually active age groups and 2./ contact tracing of partners to known persons with chlamydia infection.

We have recently performed a major study where DNA sequencing of the ompA gene in C. trachomatis was used to improve the contact tracing work and the epidemiological understanding of sexual networks (Lysén et al, J Clin Microbiol 2004, 42:1641-7). Although 29 different genotypes of C. trachomatis were identified ompA sequencing does not provide enough variation for strain separation. In order to increase the resolution of molecular epidemiology new methods are needed.

Task: First, to develop a sequence based multi locus target system for identification of C. trachomatis strains.

The work consists of PCR and DNA sequencing technology, where candidate loci for sequencing will be tested.

Bioinformatics is used for identification of the optimal sequence targets and to achieve the highest resolution of the genotyping system.

Second, if there is time, the system will be evaluated on a clinical contact tracing material.

If expected results are achieved you will be coauthor of a publication.

Expected time length: Preferably 20 weeks, but 10 weeks is possible