

Chlamydiae - how to trace the spread of chlamydial infections: An unsexy task about sexually transmitted bacteria

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Background: Chlamydia trachomatis is the bacterial species causing most sexually transmitted infections which may end up in ectopic pregnancy (utomkvedshavandeskap) and infertility. It is in some regions also causing eye infections (trachoma) leading to blindness. Thus it is of high importance for the public health world wide.

We are doing studies of sexual networks by sequencing C. trachomatis genes and link such data to contact tracing patterns of infected persons (Lysén et al, J Clin Microbiol 2004, 42:1641-7, Klint et al, J Clin Microbiol 2006, 44: 4066-4071).

To achieve a high resolution we have developed a multi locus sequence typing system (MLST) that improves the possibility to perform molecular epidemiology (Klint et al, J Clin Microbiol 2007, 45:1410-4).

Tasks:

1. Optimization of our MLST system to simplify the performance.
- 2a. To apply our MLST system on a field study of trachoma infections in Gambia. Molecular epidemiology will here increase the knowledge of how the disease is spread in the population.
- 2b. To investigate if our MLST system can be useful for characterization of sexually transmitted chlamydia strains from populations in different countries. We have preliminary data that indicates that some sexual networks are highly internationalized.

The work consists of PCR and DNA sequencing technology on clinical samples. Bioinformatics is used for identification of the optimal sequence targets in the genotyping system.

Projektet kan även göras som konventionellt examensarbete.