Projektarbete finnes 2008

Chlamydia - how to trace a mutant escaping detection systems and contact tracing

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. In 2006 a new variant of *C. trachomatis* (nvCT) was discovered and it escapes commonly used detection systems. In some Swedish counties it constitutes over 30% of all chlamydia cases, but its spread is still poorly understood.
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).

Task: To improve our MLST system by optimizing target regions.
To apply MLST on chlamydia cases and study the clonality and spread of the new variant in different parts of Sweden as well as analyzing international contact patterns of *C. trachomatis*.
There is also an option to further characterize one MLST target gene in several chlamydia species and study recombination events and phylogenetics.

The work consists of PCR and DNA sequencing technology on clinical samples and contact tracing materials. Bioinformatics is used for identification of the optimal sequence targets in the genotyping system and to analyze recombination events in Chlamydiae.

Projektet kan göras som konventionellt 10 eller 20 p projekt.

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