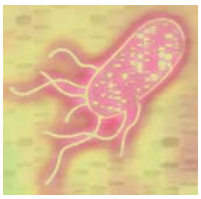

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ECIBUG: Tackling malicious *Chlamydia* infections using genomic analysis

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Project Description

Chlamydia is a devious bacterial genus, which only can reproduce from within host cells, and causes chronic infections that are extremely difficult or impossible to treat. Once in the human body, the bacteria creep into a variety of different cells before tapping their energy reserves and reprogramming the cell's own signalling system in such a way that the cell is not killed off by the intruder. At the same time, the host cell is immediately ordered to produce new *Chlamydia* bacteria, unaware that it has been taken hostage by a parasite. About 70 per cent of all people are infected with *Chlamydia*, but the majority of these will not suffer from any symptoms. Ultimately, the development of the disease depends on the respective conditions in the host cell as well as on the specific species of *Chlamydia* involved. Today, *Chlamydia trachomatis* and *Chlamydia pneumoniae* are the most dangerous of the known variants. *Chlamydia trachomatis* can cause blindness, uteral infections or infertility, whereas *Chlamydia pneumoniae* affects cells in the lungs, causing serious lung disease.

Moreover, *Chlamydia* has been found in patients with vascular diseases such as arteriosclerosis, but in such cases it is not yet known what exact role the bacteria plays. The researcher consortium ECIBUG, which brings together nine academic groups from four different countries under the roof of the *ERA-NET Pathogenomics*, will be exploring the pathogenic *Chlamydia* species on a molecular level. Based on genomewide analysis techniques, the scientists are able to silence targeted cell signals on the host side with the aim of filtering out the most important proteins and signalling pathways that ensure the bacteria's prosperity within the cells. As a result of this analysis, the researchers hope to find a means of tackling the therapeutic resistance that makes chlamydial infections so deadly. Alongside, another group of scientists will be following up previously completed research and investigating new treatment possibilities with the goal of identifying the most promising targets in bacteria-host interactions. Following this, new therapeutic molecules will be designed and tested for their relevance with high throughput screening procedures. Other researchers in the ECIBUG network will be using animal models to conduct a detailed analysis of the still unclear role that *Chlamydia* plays in vascular diseases.