



Genome-wide analysis of the key mechanisms of *Enterococcus faecalis* infections

Project Coordinator



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Project Description

Bacteria of the *Enterococcus* genus make up part of the normal gut flora in humans and animals. However, specific variants are also dangerous disease-provoking agents, putting hospital patients with a weak immune system at particular risk from serious urinary infections or sepsis. One of the most frequent troublemakers is *Enterococcus faecalis*, the treatment of which is becoming difficult, as the bacteria are displaying increasing resistance to common antibiotics. In recent years, there have been a number of extensive studies about *Enterococcus faecalis*, identifying a wide range of disease-relevant factors on the genetic level. However, little is known about the larger molecular health risk pattern of *Enterococcus* infections.

In order to change this situation, five researcher groups from four different countries have come together under the roof of the *ERA-NET Pathogenomics*. Using a systematic screening approach, the goal of this consortia is to unravel potential key mechanisms in the development of *Enterococcus* infections and to answer the following questions: Which surface proteins enable the bacteria to colonize the gut and to expand into deeper tissue layers? How does the bacteria interact with the human immune system? What are the differences between harmless and dangerous variants and which characteristics play a role in antibiotic resistance? Based on the previously decoded genome sequence of a clinically important strain of *Enterococcus faecalis*, the scientists will establish a library of genetically engineered strains, with which they hope to identify important factors involved in the emergence of diseases, before analysing them in large-scale screening systems. The researchers aim is to shed light on approximately 230 genes, whose role will be explored and analysed in detail. In such a way, it is hoped to provide more information on a molecular level about the development of diseases caused by *Enterococcus faecalis*. Based on these results, the key disease-relevant mechanisms of infection processes will be studied in an animal model, with the aim of identifying new means of therapeutic treatment.

