



## Focusing on *Escherichia coli*: What causes a useful intestinal bacterium to become a health risk?

### Project Coordinators



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### Project Description

The human intestines are colonised by hundreds of different bacteria species, and *Escherichia coli* is one of the most common and well known. Like all the other bacteria of the intestinal flora, *E. coli* is essential for the proper functioning of the body: the rod-shaped bacteria produce substances that humans are not able to make themselves, or only in insufficient quantities – vitamin K for example, needed for blood clotting. However, there are *E. coli* variants that are far from harmless: Some relatives of the more useful bacteria are capable of causing diarrhoea or, outside the intestines, urinary infections, which can lead to death for elderly individuals or those with a weak immune system. Treating these extraintestinal *E. coli* species, which are known as ExPEC, is becoming more of a challenge, as they have developed a strong resistance to the most common antibiotics. Moreover, ExPEC variants are also responsible for infections in poultry, which carries the risk of transmission to humans.

Now, 14 researcher groups from seven different countries have come together under the roof of the *ERA-NET Pathogenomics* to focus on these ExPEC strains. They will be shedding light in particular on the factors by which normally harmless and useful *E. coli* species develop into disease-causing agents. Based on these results, the scientists hope to develop new diagnostic, therapeutic and preventive approaches in the fight against diseases caused by ExPEC strains. In previous studies, the researchers have discovered that the dangers posed by these strains are closely related to specific factors that have increased their endurance, as well as their potential to cause diseases. Moreover, *E. coli* species are known for their ability to receive the genetic information of these factors from other closely related organisms. It is now assumed that ExPEC strains accumulate and emphasise these harmful characteristics - the significant difference from the more useful *E. coli* variants. Using functional genomics tools, the researchers in the ERA-NET consortia will analyse these abilities, as well as the interactions between the bacteria and the host cells. Furthermore, they will compare non-pathogenic with pathogenic strains in order to identify more characteristics on a genetic level that play a role in the emergence of disease. Based on these results, the researchers also hope to uncover the mechanisms that are responsible for the widespread resistance to antibiotics displayed by many *E. coli* strains.

