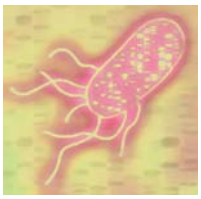

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1st Round of Funding 2007

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HELDIVNET: Analysing the genetic variability of the *Helicobacter pylori* bacterium

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Project Description

Helicobacter pylori is a tightly spiralled bacterium, which at any one time is responsible for infections in half of the world's population and in recent years has been pinpointed as causing gastric ulcers, gastric cancer and gastric mucosal inflammation. To survive in the acidic surroundings, the bacterium produces, among others, the urease enzyme, which forms a protective ammoniac layer. This in turn provokes the stomach to produce more gastric acid. How and why this process gets out of control and causes ulcers, inflammations or cancer is yet not understood in detail. Especially mysterious is the fact that bacterial colonisation alone is apparently not responsible for the symptoms of disease. Scientists believe that one reason for this lies in the enormous genetic diversity and variability of *H. pylori* strains. During infection, an *H. pylori* genome is able to alter rapidly via the exchange of genetic material with other non-related *H. pylori* strains. This genetic aspect is also a focus of the HELDIVNET consortia. Seven researcher teams from four different countries have come together under the umbrella of the *ERA-NET Pathogenomics* to broaden the understanding of *Helicobacter* infections and their genetic originations, using a wide range of approaches and post-genomic methods of analysis.

In one project, the scientists will be applying themselves to the evolutionary genetic development of the many different strains of *H. pylori*. According to recent studies, published at the beginning of 2007, the bacterium has accompanied human life for at least 60,000 years and has its origins in Africa, as is also assumed of human beings. Based on previously accomplished genetic analyses, the scientists are now focusing on the historical development of all populations of *H. pylori* – with the aim of drawing a global map of the genetic diversity of the bacterium. At the same time, the researchers want to look at the consequences of genetic multiplicity on the ability of the bacterium to act as infection agent. Using genetic comparisons with other non-pathogenic but related strains, the scientists will be decoding the most disease-relevant factors. Furthermore, the researchers in the consortia are focusing on the genetic activity of chronic disease processes to determine the possible adaptive strategies of the bacterium in relation to the respective host environment. One project will be using a specific animal model, the Mongolian Gerbil, with which the researchers hope to reveal the most relevant cancer-causing factors.