

Chasing EHEC Via Computer: Scientists in Germany Provide Free Access to Enteric Pathogen's Genetic Regulation Data

ScienceDaily (June 10, 2011) — Just a few genes make enterohaemorrhagic *E. coli* (EHEC) extremely dangerous to humans. If it were not for these genes, EHEC would hardly differ from harmless enteric bacteria. Bioinformatics scientists from the Saarbrücken Cluster of Excellence want to exploit this similarity to find starting points for effective drugs against the EHEC pathogen. In a very short time, the scientists have constructed EhecRegNet, a database and analysis platform that incorporates all known interactions between enteric *E. coli* genes. Using integrated simulations, genetic switches for the dangerous EHEC genes can be identified much faster and used medically. The virtual laboratory will thus help biomedical scientists and pharmacists all over the world to develop new drugs.

All human beings carry roughly one to two kg of bacteria in their bodies. The most common enteric bacterium is *Escherichia coli*, which is also the best-studied microorganism on earth. "Its genetic composition has been documented in detail and we know of around 3,500 gene interactions, i.e., ca. 40% of the regulatory processes that go on in the bacterium," says Jan Baumbach, who heads a research group at the Cluster of Excellence for computer science at Saarland University. Together with his team at the Max Planck Institute for Informatics in Saarbrücken, he quickly realised that the current rampant EHEC pathogen is closely related to normal intestinal bacteria. "We assume that no more than ten genes make the EHEC pathogen life-threatening. Some genes emerged a long time ago, over the course of evolution, but others were modified through an inter-bacterial exchange of plasmids. It is a kind of primitive sex that the bacteria use to transmit genetic information. This often leads to resistance to antibiotics," the bioinformatics scientist explains.

His research team has registered all the information concerning the harmless enteric bacteria's genome and interactions in a database, which also lists the genetic data of the dangerous EHEC pathogen. On the computer, the EhecRegNet system compares the genetic data of the EHEC bacteria with the data from harmless bacteria to track down genetic switches in EHEC. The goal is to use these switches to disable the genes which cause severe renal failure in some patients. "Genes can be switched on and off, much like a light bulb. But first you have to find the right switch. At the moment, you could say that we are throwing stones at the light bulb to put out the light. We still do not know where the switches are for EHEC, but we do know where they are located in evolutionarily related harmless bacteria. That is our starting point," says Baumbach. The computer simulations will allow scientists to locate the switches for dangerous genes much faster than with expensive testing in biomedical laboratories.



Just a few genetic mutations is all it takes to turn the common enteric bacterium, Escherichia coli, into the dangerous enterohemorrhagic E. coli (EHEC) strain. (Credit: MPI for Developmental Biology: Juergen Berger)