Danish researchers have sequenced and analyzed the genome of a bacterium that can feed off coal tar. It lives in symbiosis with another bacterium that can recycle its partner’s waste. Researchers hope that this sustainable bacterial duo can transform toxic substances into useful materials.
Nevertheless, mapping the genome also led to an unpleasant surprise.

Danish researchers have a new bacterium in their spotlight. Called *Acinetobacter johnsonii C6*, it was discovered in 1994 on the site of a gas works in Fredensborg, north of Copenhagen. It seemed to thrive in the toxic wood preservative creosote – a dark viscous fluid made from coal tar. Now researchers from the Technical University of Denmark have mapped the bacterium’s genome because they hope to use its special properties in other settings.

“This bacterium is not just fascinating biologically. We hope that we can use its unique abilities to break down materials such as aromatic hydrocarbons that are present in coal and oil as well as plastics and pesticides. The genomic data show that it contains the enzymes we hoped to find and additional ones we did not expect, so we hope we can use this bacterium to dispose of substances that are otherwise difficult to break down,” explains co-author Søren Molin from the Novo Nordisk Foundation Center for Biosustainability at the Technical University of Denmark.

**Can thrive on almost anything**

Nevertheless, this bacterium is especially interesting for a completely different reason. *Acinetobacter johnsonii C6* can live in symbiosis with another bacterium, *Pseudomonas putida*, which is already being used to purify contaminated soil because it can convert styrene into biodegradable polyhydroxyalkanoates. This has enabled materials such as polystyrene foam to be recycled despite otherwise being
categorized as not biodegradable.

“These two bacteria can coexist symbiotically – a metabolic dependence in which each one needs the other. We hope to use this dependence to establish a stable consortium of *Acinetobacter johnsonii* C6 to break down unusable or harmful substances and *Pseudomonas putida* to use its waste products further as the basis for producing new usable materials.”

The best way these two bacteria can coexist is in a biofilm – thin films of bacteria stuck together by a type of chemical glue. Biofilms are already known from deposits in nature such as on stones in a riverbed and in sewage treatment plants where they break down contaminants.

“The unique collaboration between these two bacteria integrated into a biofilm makes this very interesting and industrially relevant in addition to the individual biotechnological bacteria used today. These bacteria can thrive on almost anything. In contrast, *Escherichia coli* bacteria, for example, are much less robust and flexible because they cannot tolerate or use many chemicals,” explains one of the driving forces behind the project, Sünje Johanna Pamp from the National Food Institute of the Technical University of Denmark.

**A multidrug-resistant surprise**

Nevertheless, mapping the genome of *Acinetobacter johnsonii* C6 provided an unpleasant surprise. The researchers discovered several antibiotic resistance genes in this bacterium that enables it to survive several antibiotics such as chloramphenicol, trimethoprim and cefoxitin. This is especially important
because bacteria often transfer antibiotic resistance genes between each other.

“We definitely do not want to create a new problem while solving another one. If we had started to use these bacteria to break down toxic substances on a large scale, we might have disseminated their antibiotic resistance genes. It is therefore fantastic that we can investigate the bacteria genonomically so we can remove such problematic genes before working with them further,” explain Sünje Johanna Pamp and Søren Molin.

The spread of bacteria that resist most of the available antibiotics is a growing problem. Some Acinetobacter species are among the most resistant; this is why they are difficult to contain in hospitals and therefore can cause a broad spectrum of infections such as pneumonia and meningitis. The new knowledge may therefore also prove to be useful in this respect.

“These results illustrate well how the current boundaries between infectious diseases, cleaning up contaminated sites, biotechnology, and food production are extremely fluid. Similar microorganisms and mechanisms can be relevant in many situations. The new genome-based techniques enable research to be carried out in major interdisciplinary collaborations instead of previously, when scientific disciplines were completely separate.”

Researchers from the National Food Institute and the Novo Nordisk Foundation Center for Biosustainability of the Technical University of Denmark have published “Draft genome sequence of Acinetobacter johnsonii C6, an environmental isolate engaging in interspecific metabolic
interactions” in Genome Announcements.

Søren Molin  
Professor

The major research interest of the past 10 years has been microbial biofilms in relation to cell–cell interactions and developmental processes. The knowledge obtained in the course of this work is now being further developed in connection with detailed studies of microbial adaptation and evolution in cases of chronic infection. These current research activities are based on the assumption that fundamental studies of bacteria physiology and ecology are essential to understand and eventually interfere with such microbial infections. The investigations employ several methods providing global information about the cells’ genomes and functional genomics. In particular, specific clones of bacteria infecting the airways of people with cystic fibrosis are being studied. In connection with these studies, the evolution of antibiotic resistance is an important topic, and the current focus point is the resistance mechanisms involved in tolerance to antimicrobial peptides. The development of various types of laboratory model systems for simulating human infections in vitro has been added to the research programme.

Sünje Johanna Pamp  
Associate Professor

Humans are host to a remarkable diversity of microbes that are key to our health and well-being, but the microbiome of humans and animals can also be the source of infectious diseases and contribute to a variety of complex diseases. My research aims at unravelling the mechanisms by which microorganisms adapt, evolve and interact in space and time – from the perspective of single cells to complex host-associated microbial communities. We integrate approaches from genomics, microbial ecology, evolution, classical and molecular microbiology and clinical and veterinary medicine to provide insight into: • the biogeography of pathogens; • microbe–microbe interactions; • microbe–host immune system interactions; • antimicrobial resistance and tolerance; • beneficial functions of the microbiota structure; and • the function of microbial communities (biofilms). Through interdisciplinary approaches, our research has already revealed the identity and predicted function of important uncultivated members of human and animal microbiomes (such as segmented filamentous bacteria) and their impact on host immune system maturation, provided initial insight into the microbial interactions of opportunistic pathogens (such as Staphylococcus aureus and Pseudomonas...
aeruginosa) and led to a strategy for specifically targeting physiologically distinct microbial subpopulations, resulting in a successful combined antimicrobial treatment strategy. The ultimate goal is to provide better strategies for preventing and controlling microbial infections and complex microbial diseases to benefit society.
Molecular cause of type 2 diabetes can also cause Parkinson’

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