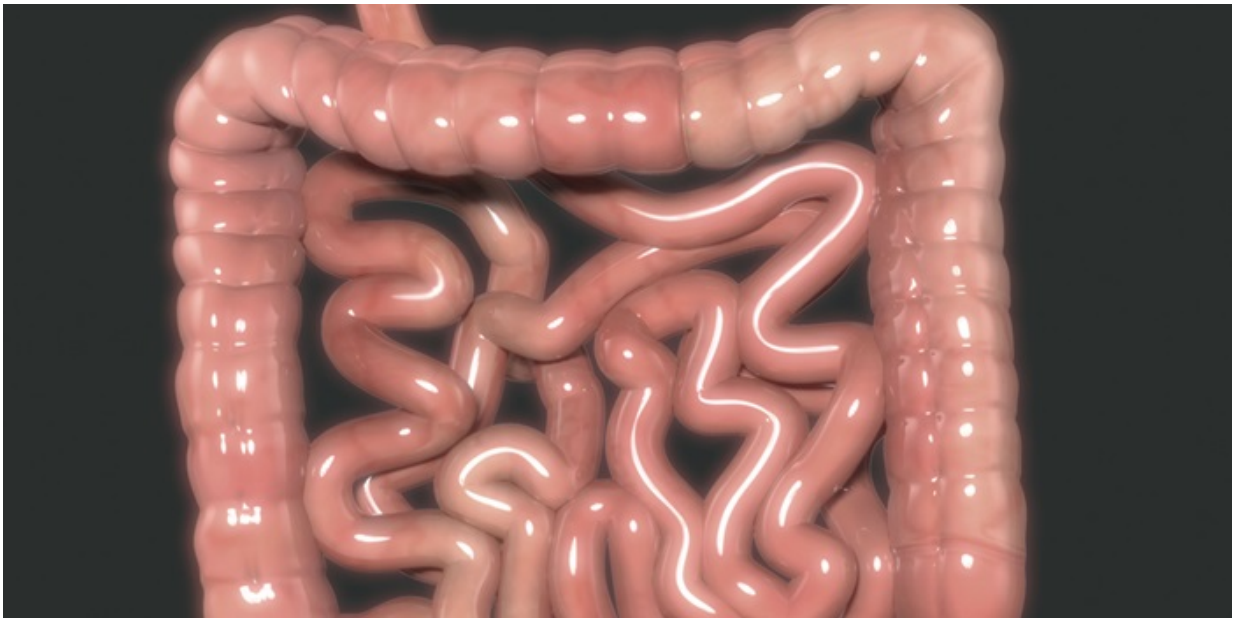


# One step closer to personalized antibiotic treatment

February 10 2017

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Credit: Technical University of Denmark

Microbes in the gut can "disarm" antibiotics, leading to antibiotic resistance and incurable infections. A new method makes it possible to quickly detect resistance genes and, hence, choose the most efficient type of antibiotic treatment.

Taking antibiotics to fight an infection won't necessarily solve your problems. Often, natural occurring bacteria in the gut harbor several

resistance genes. This means that the gut bacteria may exchange genes with the infectious bacteria, resulting in [antibiotic resistance](#). Therefore, knowing the resistome—i.e. the pool of resistance genes present in the gut microbiota—can improve treatment immensely.

Now researchers from The Novo Nordisk Foundation Center for Biosustainability—DTU Biosustain—at Technical University of Denmark have developed a super-fast cheap method called poreFUME that can shed light on the pool of resistance genes in the gut.

"With this method, you will get an overview of the resistome in 1-2 days, and, hence, be able to start the treatment of the infection sooner and with better results than before," says Eric van der Helm, Postdoc at The Novo Nordisk Foundation Center for Biosustainability—DTU Biosustain—at Technical University of Denmark.

The research has recently been published in the journal *Nucleic Acid Research*.

## **Antibiotics resistance is causing 700,000 annual deaths**

The poreFUME method using nanopore sequencing is very rapid compared to current methods, because it doesn't require growth of the faecal bacteria, which takes time and can be difficult. Also, the data from the device is streamed in real time, so the user doesn't need to wait until the end of a 'run' to access information about the experiment.

Today, getting resistome-data from a patient takes weeks. In the meantime, the resistome profile might change dramatically, and the patient will suffer from failing health.

Every year 700,000 people die of resistant infections, in particular hospitalized patients; and the problem seems to be growing. For many patients, a quick assessment of their personal pool of [resistance genes](#) in their feces can be lifesaving.

"Our research shows, that this method provides a promising alternative to other sequencing methods and that it can be used to rapidly profile the resistome of microbial communities in for instance the gut. We are quite convinced, that rapid resistome profiling could lead to personalized [antibiotic treatment](#) in high risk patients," says Professor and co-author Morten Sommer from DTU Biosustain.

## **Cheap runs make the difference**

The study was carried out as a collaboration between DTU and co-author Dr. Willem van Schaik from the University Medical Center Utrecht, who provided access to an [intensive care unit](#) patient (ICU).

In this study, five feces samples from the ICU patient were assessed. After lung transplantation surgery, due to Chronic obstructive pulmonary disease (COPD), the patient was treated with four different kinds of antibiotics to prevent and fight infections. Samples were collected both upon admission to intensive care unit, during stay and several months after hospitalisation.

The results showed that the poreFUME method was 97% accurate, when compared to standardized resistome profiling methods. This percentage is sufficient when measuring the resistome.

Furthermore, the poreFUME method is much cheaper than current methods, primarily due to the low cost of the so-called MinION; a small handheld DNA-sequencing device, which scientists can start to use for 1,000 Dollars. In comparison, conventional so-called next generation

sequencing devices are priced at between 50,000 Dollars and 10 million Dollars.

"If hospitals can purchase equipment for resistome profiling cheaper than today, it opens up for better profiling of more patients and hopefully fewer cases of bacterial resistance," says co-author and Researcher Lejla Imamovic from DTU Biosustain.

**More information:** Eric van der Helm et al, Rapid resistome mapping using nanopore sequencing, *Nucleic Acids Research* (2017). [DOI: 10.1093/nar/gkw1328](https://doi.org/10.1093/nar/gkw1328)

Provided by Technical University of Denmark

Citation: One step closer to personalized antibiotic treatment (2017, February 10) retrieved 11 July 2024 from <https://medicalxpress.com/news/2017-02-closer-personalized-antibiotic-treatment.html>

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