Metagenomic analysis software reveals new causes of superbug emergence

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Researchers from ITMO University and Center of Physical and Chemical Medicine have developed an algorithm capable of tracking the spread of antibiotic resistance genes in gut microbiota DNA and revealed additional evidence of resistance gene transfer between bacterial species. The method can not only contribute to the development of effective therapy schemes, but also curb the spread of superbugs. The results of the research were published in *Bioinformatics*.

In recent years, the spread of antibiotic resistance has become a global health care problem. As a consequence of excessive antibiotics use in medicine and agriculture, gut microbiota accumulate antibiotic resistance genes in their DNA or metagenomes. On the one hand, these genes help the normal flora to survive. However, recent studies show that gut microbiota are capable of sharing resistance genes with pathogens, thus making them resistant to available therapies. In this light, studying the spread of resistance genes is especially important.

Programmers from ITMO University with colleagues from the Research Center of Physical and Chemical Medicine developed an algorithm called MetaCherchant that makes it possible to explore the drug resistance gene environment and see how it changes depending on bacteria species. "We created a tool that enables scientists to have a closer look at the difference between gene surroundings in two or more samples of microbiota. We can analyze microbiota samples collected from different people or from the same person at different times, for example, before and after antibiotic treatment," says Vladimir

Ulyantsev, associate professor of the Computer Technologies Department at the ITMO University. "Based on the obtained data, we can suggest how a particular resistance gene could spread from one microbial species to another."

Studies of the antibiotic resistance gene environment are primarily important for designing effective antimicrobial treatment schemes. "Using MetaCherchant, we can analyze how microbiota contributes to the spread of resistance to a particular antibiotic class. Looking forward, it is possible to predict the antibiotics to which pathogens are most likely to spread resistance. On the other hand, we can also find drugs with low resistance risk. This, in turn, will help us adjust and tune specific therapies. This is the question of the next couple of years," says Evgenii Olekhnovich, lead author and researcher at the Center of Physical and Chemical Medicine.

Potential applications of the algorithm are not limited to gut microbiota genes analysis, since the program can be also used to study genome samples from soil, water or sewage. "We can evaluate the spread of resistance within a single bacterial community, such as gut microbiota, as well as between different communities. This allows us, for example, to identify global pathways of antibiotic resistance spread through the environment," says Evgenii Olekhnovich. "The problem of resistance is complex and requires a complex approach, where our tool can be really useful."

Provided by ITMO University

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