

Patients who have been diagnosed with severe bacterial infections such as sepsis, pneumonia and even skin and soft tissue infections require hospitalization, often in intensive care settings. Regardless of the type of infection or hospital ward, an antibiotic is needed to treat bacterial infections. Antibiotics are drugs that are included in the most important elements of modern medicine and are widely used both in outpatient care and in hospitals.

In Poland, *Acinetobacter* spp. strains are one of the more frequently isolated bacteria in intensive care units. The most popular species is *Acinetobacter baumannii*, but others such as *A. lwoffii* or *A. ursingii* are also increasingly marking their presence. It happens that they are not properly identified. Another problem faced by doctors is the increasing resistance of *Acinetobacter* to antibiotics used in therapy. It often turns out that these bacteria are only sensitive to one of the available drugs, and it is not suitable for every patient.

The project will enable detailed characterization of bacterial strains of the genus *Acinetobacter* that cause infections in humans, including the accurate identification of less common species. Their drug resistance and virulence will be determined in detail. The latest research methods will be used, including sequencing of the whole microbial genome. This is the method that currently allows the most accurate characterization of bacterial strains. Understanding the epidemiology of infections with *Acinetobacter* spp. strains using modern sequencing methods will make it possible to understand the transmission pathways of microorganisms and/or resistance genes and the level of their horizontal transfer between the inanimate hospital environment and infected patients. The study will also test methods that could be used in the future in the event of an epidemic in the hospital ward.

In addition, the research project will contribute to improving the daily practice of microbiological diagnostics, which will allow to obtain better results necessary for targeted microbial therapy and will contribute to reducing the risk of emergence of drug-resistant strains and outbreaks.