

The aim of this project is evaluation on the relationship between MDR efflux systems activity and antimicrobial susceptibility profile of clinical *Stenotrophomonas maltophilia* strains. The second objective is investigation of new efflux systems in *S. maltophilia* genome.

Nowadays, the main pathogenicity researches on Gram-negative rods concern *Enterobacteriaceae* family. However, the increasing role of other bacteria species is being observed. *S. maltophilia* it is one of the most frequently isolated non-fermentative Gram-negative rods responsible for nosocomial infections. It is an opportunistic pathogen, especially dangerous for patients with immunodeficiencies, extensive burns, prolonged hospitalization, cystic fibrosis. It can cause many severe infections, including pneumonia, meningitis, bacteremia, which achieve, in case of bacteremia, even 69% mortality rate.

*S. maltophilia* infections are difficult in therapy, because clinical strains are often highly resistant to many groups of antimicrobial agents. The activity of MDR (multi-drug resistance) efflux systems is one of the most important resistance mechanisms of *S. maltophilia*. The MDR pumps are able to remove different classes of antibiotics and chemioterapeutics, as well as disinfectants, from bacterial cells. The preliminary research demonstrated prevalence of efflux systems from ABC family and several pumps from RND family in *S. maltophilia* isolates. Taking into consideration great number of MDR efflux systems in closely related *Pseudomonas aeruginosa* species, it is necessary to explore new efflux systems also in *S. maltophilia* genome.

The investigations will include a group of over 100 clinical *S. maltophilia* strains isolated from patients hospitalized in Warsaw. The first step of research will be detection of MDR efflux systems from RND family. Then, the contribution of selected efflux systems to antimicrobial resistance will be estimated using antimicrobial susceptibility tests and real-time RT-qPCR method. Genome sequencing of few selected strains with unusual resistance phenotype will enable to detect new efflux systems in *S. maltophilia* genome.

Every year the increasing number of *S. maltophilia* resistant strains and patients with immunodeficiencies is being observed. Therefore, it is very significant to enlarge the knowledge about opportunistic pathogens, resistance genes and resistance mechanisms. No investigation regarding MDR efflux systems among clinical *S. maltophilia* strains isolated in Poland has been conducted, the global researches are fragmentary. The presented project will be the first analysis performed on such a large-scale (all efflux pumps from RND and ABC families will be sought) among the large group of clinical isolates. The proposed analysis would enable an in-depth characteristics of strains and would provide the knowledge about current epidemiological situation and strain resistance in Poland. They would also give the possibility of comparing of the Polish strains with those isolated in different parts of the world. Genome sequencing of selected strains will enable to detect new efflux systems in *S. maltophilia* genome and it will enlarge the global knowledge concerning resistance mechanisms in *S. maltophilia* isolates. Moreover, obtained data will bring useful knowledge of the resistance mechanisms and the treatment of *S. maltophilia* infections, not only in Poland, it will be helpful in assessing the percentage probability of contribution of the efflux systems overexpression in *S. maltophilia* resistance.