

This proposal refers to epidemiology of antimicrobial resistance (AMR) in pathogenic bacteria that is a key issue in infectious diseases and public health today. Specifically, the project concerns *Pseudomonas aeruginosa*, a Gram-negative common nosocomial pathogen in which virulence and AMR largely contribute to high infection morbidity and mortality. It will be focused on strains producing metallo- β -lactamases (MBLs) which are the most potent enzymes hydrolyzing carbapenems, the last resort antibiotics in the infection treatment. MBLs are the major acquired AMR mechanism in *P. aeruginosa*, observed globally. Recent studies have revealed that most of AMR, including MBLs, accumulates in a few pandemic *P. aeruginosa* clones, such as ST235 or ST111. MBL-producing *P. aeruginosa* (MPPA) in Poland has been observed since 1998, and early studies demonstrated its strictly regional epidemiology in five geographic areas in 1998-2004, comprising clonal spread of several genotypes or horizontal transmission of plasmids with MBL genes. From the mid-2000s the National Reference Centre for Susceptibility Testing (NRCST) in Warsaw has been observing dynamic increase in MPPA cases and their spread all over the country. From 2005 to 2015 1314 cases were confirmed in 258 hospitals and 37 outpatient clinics in all of the 16 administrative regions of Poland.

The general objective of the project is to elucidate the mechanism(s) of the MPPA growth in 2005-2015 in Poland, by providing a comprehensive and updated view of its molecular epidemiology, compare it with the early situation in 1998-2004, and with other countries. The broad and proportional representation of ~500 isolates from each year, region and most of the clinical sites would address both the temporal and geographic aspects of the MPPA spread. The study would explain the nature of the dissemination, considering clonal spread, horizontal transfer of MBL genetic determinants, and the *de novo* selection or importation. Interregional and international comparisons would allow identifying and characterizing *P. aeruginosa* pandemic clones, subclones, individual genotypes and/or MBL genetic determinants playing prominent roles in the MPPA increase over the decade. The results will be of basic relevance for AMR epidemiology and infection control in Poland, and will contribute to the international knowledge on MPPA and *P. aeruginosa* in general. Specific genotypes and mobile elements with MBL genes will be excellent candidates for further studies, using genomics and active experiments.