In contrast to other fields of medicine, infectiology is currently in crisis, creating a huge global problem for public health. It has been largely due to antimicrobial resistance (AMR) in pathogenic bacteria, which owing to multiple and complex factors rapidly grows all over the world, resulting in more and more untreatable infections. The AMR-associated danger has been publicly equalled to global warming and international terrorism, and become a concern of not only public health authorities, but also various political bodies. In 2016 a UK Government's report estimated that by 2050 AMR may be causing yearly ~10 000 000 deaths in the world (https://amr-review.org/). Among the microorganisms that are responsible for the situation, the major position is occupied by carbapenemase-producing *Enterobacterales* (CPE) that by definition are resistant to the largest and most important class of antibiotics, β-lactams, including carbapenems, the last-resort drugs in the treatment of severe hospital infections. CPE are notoriously co-resistant to multiple other antimicrobial classes, eliminating most or all convenient and evidence-based therapeutic options.

One of the indispensable activities in combating AMR is epidemiological research, aimed at understanding the basis (origins, ways and mechanisms) of the emergence and spread of AMR pathogens. In the 1990s epidemiology of bacterial infections was revolutionized by the implementation of molecular biology techniques to studies on pathogenic strains, allowing for a large progress in addressing the role of its two major components. The first is clonal dissemination of the pathogens, and it has been now well-evidenced that bacterial species segregate clones with enhanced epidemicity, *i.e.* spreading more readily than others. The second aspect is the horizontal transmission of AMR genetic determinants in bacterial populations. These two phenomena are largely contributing to the AMR global crisis. Nowadays we are experiencing the next technological revolution, being application of whole-genome sequencing (WGS). WGS is superior to traditional molecular approaches by the amount of data provided and the highest possible discriminatory power, resulting in the unprecedented, finest characterization of the most dangerous infective microorganisms.

This project refers to one of the four main groups of CPE, namely organisms producing the so-called VIM/IMP-type carbapenemases. These are the oldest type of carbapenemases, in Europe represented mostly by VIMs. The first VIM CPE in Poland emerged in 2006, and since then the National Reference Centre for Susceptibility Testing (NRCST) in Warsaw has been observing their stepwise increase and territorial spread. Our previous study on ~120 Polish VIM/IMP CPE isolates from 2006-12, using classical molecular approaches, revealed striking specificity of these organisms when compared to other countries, and a number of their very interesting characteristics. The new application proposes a WGS analysis of all ~1000 isolates recovered in ~180 hospitals all over the country from the first case in 2006 to the end of 2019. This will be the first genomic epidemiology study on Gram-negative pathogens in Poland, and one of the largest performed so far on VIM/IMP CPE on the international scale. It would contribute to the current knowledge on evolution, routes and mechanisms of spreading of the dangerous organisms, especially with respect to newly identified and other potential high-risk AMR clones. It may also deliver important data for surveillance performed at the national and European levels.