Sequence-based typing methods have revolutionized population, epidemiological and evolutionary studies of many bacterial species over the last 15 years, including numerous human pathogens. This refers mostly to the multi-locus sequence typing (MLST) approach, relying on the comparative sequence analysis of 7 house-keeping genes. Among others, it has allowed identifying and characterizing strains, clones or lineages with increased epidemic potential, including the pandemic or "high-risk" clones. These organisms are often responsible for the majority of infections caused by a species, moreover, these usually acquire and accumulate most of antimicrobial resistance (AMR) observed in a species. MLST and other sequence-based, fully standardized typing approaches are essential in the era of the severe crisis in infectiology, in large part associated with the AMR dissemination in populations of pathogenic bacteria. Therefore, as many as ~100 MLST schemes have been developed so far.

This project proposes setting-up of an MLST scheme and database for *Pseudomonas putida*, which would be the 3rd scheme for the genus *Pseudomonas*. Similar to many other members of this genus, *P. putida* basically is an environmental species, but from the 1990s it has been increasingly recovered from hospital infections and identified as a cause of outbreaks in high-risk wards (*e. g.* neonatal, oncological, intensive care). Moreover, *P. putida* has been more and more often observed as an organism readily acquiring and accumulating AMR mechanisms, including metallo-β-lactamases (MBLs). MBLs are specialized in the hydrolysis of carbapenems, the last-resort antibiotics in the treatment of severe nosocomial infections, caused by multi-drug-resistant Gram-negative bacteria, and so these are recognized as one of the most relevant AMR mechanisms today. Therefore, the MLST scheme for *P. putida* should meet live interest among researchers in epidemiology of infections and AMR. In its 2nd part, the project assumes performing a comprehensive molecular epidemiology analysis of MBL-producing *P. putida* (MPPP) isolates, collected over ~14 years in hospitals all over Poland. These were identified as agents of serious infections. Because of its quantitative, geographic and temporal scale, the analysis would be one of the largest epidemiological studies on *P. putida* carried out so far. It should allow verifying the hypothesis that similar to many other species, *P. putida* segregates specific genotypes which may adopt better to the nosocomial environment, and spread and persist in there, causing a risk for predisposed patients.