Intensive and uncontrolled use and misuse of antibiotics, not only in medicine, but also in animal breeding and agriculture, have provoked the worldwide spread of highly resistant bacteria. At the beginning, bacterial resistance was noted in hospital setting, but now antibiotic-resistant strains are isolated from the environment. Antibiotic resistance genes are regarded as biotic pollutants and threat for human health. Mobile genetic elements (plasmids and transposons) are responsible for the dynamic spread of resistance genes among cells of the same or even different bacterial species through horizontal gene transfer.

The aim of this project is to characterize the resistome of urban air. The resistome is the collection of all the antibiotic resistance genes in both pathogenic and commensal bacteria. To achieve this goal, we will qualitatively and quantitively characterize the resistome of the air in Poznań, Łodź and Rybnik (one of the most polluted cities in Poland), and, as a reference air little affected by anthropogenic activity, in Wielkopolski National Park. Because >99% of microorganisms cannot be cultured in laboratory conditions, only analyses of metagenome (the pool of all genes present in a given habitat) can provide comprehensive information on the resistome of a given environment. Therefore, both cultivable and metagenomic approaches, with the use of quantitative PCR methods (real-time PCR and ddPCR) will be applied. Analysis of meteorological data, air quality index (AQI) and the concentration of PM2.5 and PM10 will allow determining if the air resistome is associated with air pollution. Moreover, analysis of microbial population composition will allow establishing its association with the presence and abundance of antibiotic resistance genes.

The results of this project will provide data on urban air as a conduit for antibiotic-resistant bacteria, including those resistant to the last-resort antibiotics, like carbapenems, colistin or vancomycin. Bioinformatic analyses would determine correlation between taxonomic composition of bacterial population and antibiotic resistance genes. Clonal analysis of isolates with alert resistance mechanisms will answer the questions whether the same clones are prevalent in different sites. Results of the project will enable comprehensive characteristics of environmental resistomes and will contribute to global strategy for controlling and preventing the spread of antimicrobial resistance.