

An epidemic is the occurrence of a greater than expected number of cases at a given time and place. Epidemics have accompanied humanity since the dawn of time and have very serious consequences. It is estimated that one of the most serious historical epidemics in human history, the Black Death caused by the bacterium *Yersinia pestis*, caused the deaths of around 60% of Europe's population. There are many factors that contribute to the development of an epidemic of an infectious disease. These factors are, amongst others, congregating people in a small area, lack of proper hygiene or ventilation of the rooms. For the development of the disease, the patient's immune status is important - children, the elderly or chronically ill are usually more susceptible to infection. Importantly, the factors that determine more frequent disease transmission may be within the pathogen itself. Identification of such factors enables rapid intervention of medical services in the case of diagnosing infection with a particularly dangerous pathogen variant. Identification of factors affecting pathogen transmission is therefore important to successfully stop the spread of an epidemic, preferably at an early stage.

One of the most serious bacterial diseases of the modern world is tuberculosis, caused by *Mycobacterium tuberculosis*. *M. tuberculosis* are bacteria in which no horizontal gene transfer has been found. Thus, all genetic and phenotypic variability of these bacteria is determined by duplications, deletions, and above all, by single nucleotide polymorphisms. Bacterial variation is therefore conditioned by relatively subtle changes in their genomes, and not, as is the case with other bacterial species, by acquiring new genes for virulence. It is therefore not clear whether there are *M. tuberculosis* factors that affect the transmission of the disease, or whether the transmission of this disease is related only to the condition of the host and environmental conditions.

Our research hypothesis assumes that there are factors that increase the frequency of tuberculosis transmission that are inside the tuberculosis bacilli. In our research, we will use a collection of *M. tuberculosis* strains collected at the Institute of Tuberculosis and Lung Diseases. Our Institute is a reference laboratory for tuberculosis in Poland. We will select strains from the collection, which will be assigned to the "high transmission" or "low transmission" group, 250 strains per each group. We want to investigate whether there are features that differ in both groups. These studies will be conducted at the level of the occurrence of the characteristic phenotypic features of the mycobacteria, the characteristic host response to the mycobacteria, and the level of variability in the DNA of the mycobacteria. The obtained results will be verified in experimental conditions, using genetically modified *M. tuberculosis*. The research will be conducted in cooperation with the Institute of Medical Biology of the Polish Academy of Sciences and the Biobank Laboratory of the University of Lodz. These facilities have a large experience in mutagenesis of *M. tuberculosis* and whole genome DNA sequencing, respectively. We expect that the results of our research will identify new factors favoring transmission of tuberculosis and thus allow for more effective control of this dangerous disease in the world.