In 1896 Sir William Osler, one of the most prominent infectious diseases specialist, stated: „Humanity has but three great enemies: fever (a synonym of infectious disease), famine and war; of these by far the greatest, by far the most terrible, is fever". Unfortunately, in spite of an enormous advance in medicine this sentence has not lost its importance, because infectious diseases are the second, after heart diseases, leading cause of death worldwide. We continuously have problems not only with "old" pathogens, but more and more often with new, so called emerging pathogens. An emergence phenomenon of new pathogens is usually associated with changes in our environment, frequently caused by ourselves. Processes associated with agriculture, deregulation of water ecosystems, globalization, may contribute to removing natural barriers protecting us from potentially dangerous microbes. It should be emphasized that microbes are great opportunists, which thanks to their natural predisposition to adaptation e.g., via interspecies gene transfer, rapidly evolve and acquire new features that facilitate them colonization of new hosts. *Escherichia albertii* is a good example of such emerging pathogen, recognized as a cause of intestinal infections in human and birds. *E. albertii* at some degree shows similarity to enteropathogenic (EPEC), enterohemorrhagic (EHEC) and avian-pathogenic (APEC) strains of *Escherichia coli*, a bacterium well known for a long time. However, due to a recent recognition of *E. albertii* (2003 year) and lack of its standard identification methods, our knowledge about its biology, ways of transmission and pathogenic potential is very scant. Thus, the aim of our project is to solve these issues, based on epidemiological and virulence studies, supported by the newest molecular biology techniques. The project was intended to include a complexity of the emergence process of pathogens, where not only understanding of interaction between hosts and microbes is important, but also ecological interactions among microbes e.g,, a process of genes exchange, and transfer of microbes between various hosts e.g., animals and humans. Therefore, the project will elucidate also such issues as a coexistence of E. albertii with aforementioned pathogenic *E. coli* strains (known as pathotypes), and a potential influence of *E. albertii* on their evolution as gene's donor.

The project includes *in vitro* basic researches that will be accomplished to determine phenotypic e.g., biochemical and antigenic features, and genetic characteristics e.g., relatedness, virulence genes patterns and their expression in *E. albertii* strains from various sources (environment, animals, food, humans). The results will be supported by assessment of *E. albertii* virulence level based on *in vitro* assays of adhesion properties (a major virulence mechanism of this bacterium) to human cell cultures. Thanks to these studies reservoirs and ways of transmission of *E. albertii* will be recognized, and they will allow to answer the question about existence of specific pathotypes and/or commensal strains of *E. albertii*, like in the case of sisterly species *E. coli*. A key part of the project are basic researches in the field of bacterial genomics, intended to recognition of genetic variability of *E. albertii* as a species, based on estimation of a sum of all its genes, i.e. pangenome and its similarity with pangenome of *E. coli* using *in vitro* and *in silico* assays. To that end, next-generation sequencing (NGS) of whole *E. albertii* genomes will be performed with subsequent bioinformatic analysis of the data and their further comparison with data deposited in public databases e.g., GenBank. It is worth to emphasize, that NGS of microbial genomes is an invaluable tool in understanding bacterial evolution on a scale unattainable a few years ago, and thanks to public databases various comparative analyses can be done for pathogens from around the world, thus facilitating tracing of outbreaks and ways of transmission or gene exchange events.

Pioneering character of the project results not only from the fact of choosing of poorly known bacterial species, that is *E. albertii*, as the target of study, but also its close relatedness with *E. coli*, one of the most important bacterium in medicine. *E. coli* is enormously variable and adaptable bacterium, remaining with us in permanent an arm race, being a very tricky enemy with access to huge arsenal of weapons, such as various virulence factors (toxins, capsules, adhesins) produced by more than dozen of pathotypes causing infections either in animals and humans. This issue can be well illustrated by the recent emergence of *E. coli* O104:H4, i.e. a hybrid strain combining adhesion ability with production of Shiga toxin, which was responsible for outbreak of diarrhea in Germany in 2011. Thus, potential threats associated with *E. albertii* may not only be limited to its direct ability to cause infections, but also its role as an ally of pathogenic *E. coli* strains. To summarize, it should be emphasized that our team has experience with work with this bacterium, and the isolation of *E. albertii* from a child with acute diarrhea (2010 year) in our Department was the first such report from Poland, and the genome sequence of this isolate was the first complete sequence of this species deposited in public database GenBank.