One of the main challenges we shall face in the 21th century is providing sufficient amount of nutritious, high quality food for the whole human population. Experts estimate that the number of people on Earth will reach 9.2 billion in 2050. Potato is already called the crop of the future due to its incorporation in international food safety and hunger limitation programmes (International Potato Center, Research for Development). Nowadays, potato is one of the main components of the human diet and its total yield is lower only than that of corn, rice and wheat (FAO, 2012). Aside from the fact that Poland is 7th top producer of potato worldwide (FAO, 2012), our country holds the highest *per capita* consumption of fresh potatoes in Europe (USDA Foreign Agricultural Service, 2015). The changes in dietary habits and lifestyle within the Polish society did not influence this parameter so far.

Many diseases affect potatoes in the field or in storage. Among the most destructive are soft rot and blackleg caused by bacteria from the genera *Dickeya* and *Pectobacterium*, including *Dickeya solani*. It is worth to underline that *D. solani* as a new species was established just 2 years ago and the emergence of bacteria belonging to this species was correlated with elevated loss in the European potato production sector. Total economic losses resulting from soft rot and blackleg on potato are estimated to reach 20% of the total yield, for example in the Netherlands it is around 30 mln € every year. Currently available control procedures are based only on prevention methods, namely: using certified pathogen-free seed potatoes, limiting the number of generations in the field or avoiding contamination by harvesting under optimal weather conditions with clean agricultural machines.

D. solani are Gram-negative rods with flagella. Because this species was established quite recently, not much is known about the molecular mechanisms of its pathogenicity. So far, it was reported that *D. solani* strains are more virulent than the strains of *D. dianthicola*, that were thought to dominate on potato fields. The former pathogens are also better competitors against saprophytic potato microflora. Long-term monitoring studies of pectinolytic bacteria in Poland showed that *D. solani* was isolated from potato plants, but not from the waterways. Moreover, certain *D. solani* strains vary significantly when it comes to the abilities to macerate potato tissue, or in the activities of plant cell wall-degrading enzymes functionally linked with pathogenicity i.e. pectinases, cellulases, proteases. Besides, differences in the efficacy of iron acquisition and motility were demonstrated. Taking into account that *D. solani* strains exhibit high level of genomic homogeneity, phenotypic diversity between distinct isolates is a curious issue.

The aim of the proposed project is to broaden fundamental knowledge about the mechanism of infection development caused by the unsatisfactorily characterised phytopathogenic bacterium - *D. solani*. We will evaluate the sequential turning on of the virulence genes expression during ongoing infection in potato tissue caused by *D. solani*. Moreover, we will examine the expression dynamics of the virulence genes and compare obtained virulence genes expression profiles between three distinct *D. solani* strains. Strains included in the gene expression analysis will be the ones most varying in the phenotypic traits functionally linked with the virulence of pectinolytic bacteria. We also want to define the pathogenicity factors that are the key contributors to certain stages of progressing infection.

In the frames of the proposed project we shall investigate 20 *D. solani* strains, originating from different European countries (including Poland) that are deposited in the IFB UG & MUG collection of phytopathogenic bacteria (comprising about 400 *Dickeya* sp. strains), for the differences in phenotypic traits that are important for virulence i.e. ability to macerate potato tissue, proteases, pectinases, cellulases and siderophores production and motility. Three *D. solani* strains most divergent in the above mentioned features shall be used for the pathogenicity assays on potato tubers. Macerated potato tissue will be harvested every 8 h post-inoculation until 72 h and frozen immediately in the liquid nitrogen. Then total mRNA will be isolated from the rotten tissue and cDNA shall be synthesized. Implementing comparative genomic approach will lead to the selection of *D. solani* genes coding for virulence factors for qPCR-based gene expression analysis.

Basic research hypothesis is that the gene expression of certain *D. solani* virulence factors is turned on at different stages of the infection process. **In the terms of the second research hypothesis,** we postulate that diverse isolates of *D. solani* vary in their main virulence factors gene expression profiles regardless high level of genetic homogeneity. **Third research hypothesis** states that it is possible to reveal the most important virulence determinants of *D. solani* for certain stages of the ongoing plant infection process.

Summarizing, unveiling the molecular basis of pathogenicity in this recently established species of high economic impact is innovative and fits to the domain of basic research. Results collected thanks to this founding shall contribute to the development of molecular phytopathology.