Helicobacter pylori is a common gastric colonizing bacterium, identified in 50-60% of the human population. In most cases, its presence does not cause any negative consequences, but some infected people develop gastric and duodenal ulcers, as well as gastric cancer. herefore, it is important to understand the mechanisms that allow this bacterium to survive in the stomach and infect the host. In the future, this knowledge could facilitate design of modern drugs and development of effective treatments.

To successfully infect the human body the *H. pylori* bacteria must produce specific virulence factors which are (1) essential for the survival of the bacteria under harsh conditions in the stomach (e.g. the enzyme urease neutralizing acidic pH) and during the first stages of infection; (e.g. adhesins that allow bacteria to stably adhere to epithelial cells), (2) enable maintenance of a long-term and successful infection (e.g. VacA toxin and extracellular proteases that damage the host cell structure). In this process, the adaptations of bacterial cells that enable the efficient uptake of nutritional substances and metal ions, and the removal of harmful compounds are also important.

The cellular envelope of Gram-negative bacteria is composed of two membranes, the inner /cytoplasmic membrane and the outer membrane, between which there is a periplasmic space with a peptidoglycan layer. The periplasm is a cellular compartment which is responsible for many key processes, including the transport of nutrients, metal ions, and virulence factors. Cellular envelope is also a first line of defense against unfavorable external factors. For these reasons, the proper functioning of the cell envelope is essential for the maintenance of homeostasis of the whole bacterial cell and is crucial in the process of host infection.

One of the methods of controlling basic life processes is proteolysis. This process allows for the removal of non-functional proteins, the accumulation of which may be toxic to the cell, as well as for the modification of protein activity (activation or inactivation). Until now, studies on the function of periplasmic proteases of Gram-negative bacteria have been conducted mainly on the model bacterium *Escherichia coli*, while the knowledge of *H. pylori* proteases is limited. The aim of this project is to understand a functioning mechanism of the extracytoplasmic proteases in the *H. pylori* cell: identify their protein substrates, discover cellular processes whose proper functioning is disturbed by the lack of proteases, and study the role of these proteases during the growth of bacteria under physiological and stressful conditions. The successful implementation of the planned research tasks should expand our knowledge of the *H. pylori* cell physiology which is also related to *H. pylori's* ability to cause infection.