Ribosomes are large structures built of proteins and ribonucleic acid and are present in every living cell. The ribosome's task is to synthesise all the proteins needed by the cell, i.e. the process of translating messenger RNA (mRNA) into protein. It is known that ribosomal ribonucleic acid (rRNA), which is the most important building block of the ribosome is 'decorated' with chemical modifications that are present on individual nucleotides. In bacterial ribosomes, the most common modification is nucleotide methylation. According to many scientific reports, most modifications are accumulated in the functional regions of ribosomes, where they have a function in stabilizing the ribosome structure, providing 'checkpoints' for the correctness of the ribosome structure prior to the start of the translational activity, and a few of them provide resistance to antibiotics that could cause damage to the ribosome and thus inhibit protein biosynthesis. However, none of these modifications are essential for the survival of the bacteria in the environment. Current reports indicate that ribosomes within a single cell may be 'decorated' differently in response to different environmental signals, which may influence the type of cellular response to these signals.

Campylobacter jejuni, which is our model organism, is currently one of the leading causes of bacterial gastroenteritis in humans worldwide. The main source of this bacterium is raw or undercooked meat from various poultry species. In some patients, as a consequence of experiencing such an infection, peripheral nervous system symptoms in the form of numbness and loss of sensation in the limbs (Guillain-Barre syndrome) may occur. Therefore, we believe that understanding the mechanisms of pathogenesis and virulence as precisely as possible is extremely important in the context of public health and food safety. Our previous studies and literature data indicate that methylation of the cytidine nucleotide at position 1402 (C1402), located in the decoding centre of the ribosome, the region where protein biosynthesis begins, is implicated in the virulence of various pathogens. In the case of *C. jejuni*, the loss of one or both methylations at this site resulted in a reduction in the motility, biofilm formation, and invasion of intestinal epithelial cells, which are the most important virulence factors for this bacterium. Our research project proposal aims to verify this relationship and elucidate its mechanisms. We want to find out how C1402 methylation regulates the translation process of specific genetic information. The experiments we have designed will allow us to determine how environmental conditions affect this process and, consequently, how the external environment can affect the cell's response to signals from it at the level of regulation of the translation process. Changes in C1402 rRNA methylation will be linked to changes in the virulence of these bacteria in a series of experiments comparing motility, biofilm formation, invasion of the host’s intestinal cells, and survival in the immune system cells. These relationships will also be reflected in the gene expression changes (determination of the type and amount of specific mRNA molecules) and proteome (determination of all proteins and their amounts) of the pathogen, which will be determined using Real-Time quantitative PCR and mass spectrometry, respectively.

The results of our study will provide a wealth of new information on the regulation of transcription and translation mediated by variation of cytidine 1402 methylation in the decoding centre of the *Campylobacter jejuni* ribosome, in the context of the different environmental conditions that this pathogen has to face both in the production environment and the host. This will allow a more complete understanding of the pathogenesis process and is likely to bring the scientific community closer to developing new strategies to control the spread of this pathogen and its pathogenicity, based on a thorough knowledge of the processes taking place inside the cell of this bacterium.