APRESENTAÇÃO DE PÔSTER - MICROBIOLOGIA

UNDERSTANDING HU AND YBAB NUCLEOID-ASSOCIATED PROTEINS IN HELICOBACTER PYLORI AND CAMPYLOBACTER JEJUNI

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Helicobacter pylori is a flagellated Gram-negative bacterium that survives in the presence of low oxygen, known as microaerophilia, and has the ability to change shape, usually spirally, to a coccoid shape, a mechanism to survive in the host gastrointestinal tract. The transmission of H. pylori is not yet well known, although the fecal-oral seems to be the major infection route. The infection by this bacterium commonly occurs during childhood, but symptoms manifest in adulthood. Infection with this bacterium causes gastritis and duodenal ulcers and is a risk factor for gastric cancer. Campylobacter jejuni is also a microaerophile and Gram-negative bacterium, that only has a spiral shape, and is closely related to H. pylori, but a distinct mucosal pathogen that infects different niches in the mucus layer of the human gastrointestinal tract. Furthermore, this bacterium colonizes chickens with no symptoms, while in humans is the leading bacterial cause of food-borne gastroenteritis in developed countries. In some cases, C. jejuni infection leads to a post-infection complication known as Guillain-Barré syndrome, which is a form of neuromuscular paralysis. Infections caused by both bacteria can be treated with antibiotics; however, the decreasing effectiveness of antibiotics is currently one of the greatest health threats. The World Health Organization (WHO) has

published a list of bacteria for which new drugs are urgently needed, including H. pylori and C. jejuni. Recent studies aimed to identify novel compounds that inhibit the biological activity of pathogenic bacteria have proposed Nucleoid-Associated Proteins (NAPs) as promising targets. NAPs are a group of global regulators that control genome compaction, transcription, replication, and recombination, and are important in metabolic pathways, virulence, and interaction with host cells. HU is one of the most studied proteins of this group and has an important influence on metabolic cycles, even on virulence gene expression, and it is a potential target for the development of therapies against tuberculosis. YbaB is another NAP protein that acts as an anti-repressor of virulence genes in Borrelia burgdorferi, but its roles in other bacteria are yet scarce. In this study, we aimed to clarify the role of HU and YbaB in the bacterial fitness of H. pylori and C. jejuni. The aim is to dissect YbaB and HU regulatory functions in H. pylori and C. jejuni. We will generate ybab and hu mutants strains and make their phenotypic characterization. In addition, transcriptome and ChIP-sequencing analysis will be performed. Finally, moreover, we will screen libraries of molecules to identify compounds that can inhibit the function(s) of these proteins, identifying new classes of compounds that can influence bacterial growth by inhibiting important metabolic pathways.