### scovery of genes required for glycolipids biosynthesis in the gastric pathogen Helicobacter pylori Student Researcher Adedunmola Praise Adewale

## Advisor Danielle Dube <u>Bowdoin College</u> Department of Chemistr and Biochemistr Abstract

Helicobacter pylori (H. pylori) is a Gram negative disease causing bacteria that causes sores in the lining of the stomach called ulcers and gastric cancer H. pylori infects about of the human population and has increasing resistance to antibiotic treatment like triple therap making it a high priorit pathogen b W O for which new antibiotics are needed ipopol saccharide PS is a molecule found in the outer membrane of Gram negative bacteria that pla s an important role in H. pylori s abilit to colonize and infect the human bod owever the genes responsible for the bios nthesis pathwa of PS in H. pylori remain unknown Based on previous e periments the Dube lab created mutant H. pylori strains b doing an insertional inactivation in genes encoding for putative gl cos Itransferases Comparison of PSbios nthesis in wild t pe H. pylori strains versus mutant H. pylori strains revealed genes that are potentiall involved in PSbios nthesis in H. pylori.

#### Project Objective

PSis a molecule that is found in the outer leaflet of the outer membrane of Gram negative bacteria PSis a ke factor in colonization and resistance of *H. pylori* because it is responsible for the outer membrane permeabilit barrier *H. pylori*'s resistance to immune cells mediates interactions between the bacterium and its environment and is a ke factor in infectivit PSis composed of three main domains lipid A a h drophobic domain embedded in the membrane O antigens responsible for host mimicr that facilitates immune escape and contributes to infectivit and core oligosaccharide a chain of sugar residues that controls the permeation properties of the outer membrane PS bios nthesis is well characterized in other bacteria but remains uncharacterized in *H. pylori* The genes required for PSbios nthesis in *H. pylori* remain largel unknown Due to the importance of PSin *H. pylori* sinfectivit m goal is to shed light on how PSstructures are made b identif ing ke s genes involved in their bios nthesis If we can have information on how structures work we can begin to think about creating small molecules antibiotics that inhibit those ke genes from functioning b preventing the proper sugar coating from being made

#### ethodolog sed

To find out which genes are required in PSbios nthesis I sought to compare the PSprofile in wildt pe *H. pylori* versus mutant *H* 

Proteinase Khelps degrade contaminating proteins Samples were then visualized for their PSprofile b running an electrophoresis gel and staining PS Electrophoresis gel separates samples b molecular weight smaller molecules down the gel and bigger molecules up the gel I stained the PS samples and visualized under a transilluminator

### Result Obtained

Based on PS stain it appears that wildt pe p lori s nthesize full elaborated PS Several of the mutants including and also appeared to s nthesize full elaborated PS B contrast mutant and mutant did not s nthesize full elaborated PS These results indicate that mutant and mutant appears to be involved in PS bios nthesis in *H. Pylori*.

## Sgnificance and Interpretation

utant and mutant did not have full elaborated PSlike wildt pe WT *H. pylori* which tells me that both mutants might be involved in PSbios nthesis pathwa This information is important because we can use it to figure out the order in which PSgl cos lation genes function and ultimatel create small molecule inhibitors that target ke genes from functioning b preventing the proper sugar coating from being made

Figures and charts

PSbios nthesis pathwa

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