A genetic screen to identify novel *Helicobacter pylori* virulence factors using *Saccharomyces cerevisiae* as a model eukaryotic cell.

A Thesis

Presented To

Eastern Washington University

Cheney, Washington

In Partial Fullfilment of the Requirements

for the Degree

Master of Science

By

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Fall 2013

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ABSTRACT

Helicobacter pylori is a spiral, gram-negative bacterium that colonizes the stomachs of approximately 50% of the World's population overall and is a major etiological agent of human gastric adenocarcinoma. Of infected individuals, only 10-15% develop severe gastric disease due to environmental factors, host genetic factors, and more significantly, genetic differences in the infecting *H. pylori* strains. Type I strains of *H. pylori* contain a 40-kb cytotoxin-associated pathogenicity island (*cag* PAI) that encodes and secretes the CagA protein into host epithelial cells via a type IV secretion system. To date, CagA is the only identified effector protein of the *cag* PAI. The goal of this study was to identify novel *H. pylori* virulence factors, to further elucidate their role in *H. pylori* virulence and their potential as novel effectors of the *cag* PAI. In the work presented here, we generated an *H. pylori* genomic plasmid library and screened this library in *Saccharomyces cerevisiae* for toxic effects. We initially identified 2 candidate *H. pylori* virulence factors, however, after further analysis these candidates were not toxic to *S. cerevisiae* and are no longer genes of interest. To identify novel *H. pylori* virulence factors, others in the lab are addressing pitfalls found in this study to conduct a better-structured screen that we believe will be successful in identifying *H. pylori* genes of interest.

ACKNOWLEDGMENTS

I thank Dr. Andrea Castillo for her guidance and support. Christopher Hansen and Nathan Phillips for their technical assistance. We thank John Geiser of Western Michigan University for the pJG482 plasmid and Sue Biggins for the *S. cerevisiae* W303 strain.

This work was supported by a mini-grant from the Eastern Washington University Biology Department.

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