

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

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By

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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.

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## TABLE OF CONTENTS

<u>ABSTRACT</u>	<u>iv</u>
<u>ACKNOWLEDGEMENTS</u>	<u>v</u>
<u>LIST OF FIGURES AND TABLES</u>	<u>viii</u>
<u>INTRODUCTION</u>	<u>1-22</u>
1.1 <i>H. pylori</i> infection of humans, good or bad	1-2
1.2 <i>H. pylori</i> prevalence and transmission	2-4
1.3 <i>H. pylori</i> infection, diverse disease outcomes	4-5
1.4 Diversity of the <i>H. pylori</i> genome	5-6
1.5 One clinically important variation among <i>H. pylori</i> strains is the presence or absence of type IV secretion systems (T4SS's)	6-8
1.6 The translocation of CagA into host epithelial cells	8-9
1.7 CagA affects on host cells	9-10
1.8 Additional <i>H. pylori</i> virulence factors	10-11
1.9 Host immune response to <i>H. pylori</i>	11=16
1.10 <i>H. pylori</i> diagnosis and treatment	16-18
2.1 Identification and function prediction of bacterial effector proteins	18-19
2.2 Using <i>Saccharomyces cerevisiae</i> as a model to identify and examine novel bacterial virulence proteins	19-21
2.3 Successful use of <i>S. cerevisiae</i> to identify novel virulence factors	21-22
<u>MATERIALS AND METHODS</u>	<u>23-28</u>
Bacteria strains, growth conditions, media and antibiotics	23-24
The pJG482 plasmid	24
<i>H. pylori</i> pJG482-m library construction	25
pJG482-m <i>H. pylori</i> library analysis	25-26
Screening the pJG482-m <i>H. pylori</i> library for toxicity in <i>S. cerevisiae</i>	26
Identification of candidate pJG482-m <i>H. pylori</i> library clones	26-27
Identification of <i>H. pylori</i> genes that inhibited <i>S. cerevisiae</i> growth	27
Analysis of candidate <i>H. pylori</i> virulence factors	27-28

<u>RESULTS</u>	<u>28-39</u>
pJG482-m <i>H. pylori</i> genomic library	28-32
Screening the pJG482-m <i>H. pylori</i> library for toxicity in <i>S. cerevisiae</i>	33-36
Identity of toxic <i>H. pylori</i> genes	37-38
Library vector, pJG482-m without insert conferred growth defects in <i>S. cerevisiae</i>	38-39
<u>DISCUSSION</u>	<u>40-49</u>
<i>S. cerevisiae</i> potential to identify novel <i>H. pylori</i> virulence factors	40-41
<i>S. cerevisiae</i> model system identified virulence proteins in many bacterial species	41
Incomplete screen of the <i>H. pylori</i> genome	42-43
Small TYCs	43-44
<i>S. cerevisiae</i> growth defects independent of <i>H. pylori</i> DNA insert expression	44-45
pJG482-m alone isolated in <i>S. cerevisiae</i> toxicity screen	45-46
pJG482-m recombination with <i>S. cerevisiae</i>	46-47
Future direction	47-49
Conclusions	49
<u>SUPPLEMENTARY INFORMATION</u>	<u>50-53</u>
<u>LITERATURE CITED</u>	<u>54-62</u>
<u>VITA</u>	<u>63</u>

## LIST OF FIGURES AND TABLES

### FIGURES

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1. Stomach gastritis introduced by <i>H. pylori</i> infection	13
2. pJG482-m construction	29
3. Isolation of <i>H. pylori</i> genomic DNA fragments	30
4. Construction of the pJG482-m <i>H. pylori</i> genomic library in <i>E. coli</i>	31
5. <i>H. pylori</i> pJG482-m genomic library analysis	32
6a. Mechanism for <i>H. pylori</i> DNA fragment expression	33-34
6b. Replica plate technique used to assay <i>H. pylori</i> pJG482-m clones expressed in <i>S. cerevisiae</i>	34
7. Analysis of TYCs in <i>S. cerevisiae</i>	35
8. Final analysis of TYCs toxicity in <i>S. cerevisiae</i>	36
9. PCR of toxic yeast candidates (TYCs)	37
10. Re-analysis of candidate <i>H. pylori</i> virulence factors	39

### TABLES

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1. Identification of <i>H. pylori</i> genes	38
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