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

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

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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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