

Probing *H. pylori* cancer protein

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Infection with the stomach-dwelling bacterium *Helicobacter pylori*—particularly strains producing the oncoprotein CagA—is a strong risk factor for gastric cancer.

Previous studies found that a region called the +59 motif in the transcript for CagA (the RNA "copy" of the gene that includes the template for [protein production](#)) is associated with high levels of CagA protein and premalignant disease.

Now, Timothy Cover, MD, John Loh, Ph.D., and colleagues have explored how the +59 motif and a nearby stem-loop structure affect CagA gene expression. They found that mutations that disrupt the stem-loop structure reduced levels of the transcript and protein by decreasing the stability of the mRNA. Mutations that altered the +59 motif also reduced transcript and protein levels, but did not impact mRNA stability.

The [results](#), reported in the February issue of *Infection and Immunity*, point to determinants of CagA gene expression and improve understanding of a factor that influences the risk of premalignant and malignant changes in the stomach.

More information: John T. Loh et al. Role of a Stem-Loop Structure in *Helicobacter pylori* cagA Transcript Stability, *Infection and Immunity* (2018). [DOI: 10.1128/IAI.00692-18](https://doi.org/10.1128/IAI.00692-18)

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