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Trial of systematic identification of long non-coding RNAs critically involved in chronic inflammation by *H. pylori* infection

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Abstract

There is growing evidence that long non-coding RNAs (lncRNAs) play important roles in a wide-repertoire of biological processes. A number of recent studies show lncRNAs have distinct molecular functions (such as molecular scaffolds, guidance or molecular decoys) and appear to be involved in all aspects of gene regulation. It is very likely that lncRNAs also play critical roles in chronic inflammation and related carcinogenesis, however there are very few reports on lncRNAs involved in chronic inflammation.

The goal of this study is to comprehensively identify novel long non-coding RNAs that are critically involved in chronic inflammation and related carcinogenesis. To achieve this goal, we decided to analyze *Helicobacter pylori*-associated gastritis and gastric cancer as a model to study the chronic inflammation.

To identify candidate lncRNAs, we have applied the ChIP-Seq (chromatin immunoprecipitation followed by high-throughput sequencing) technology to clinical endoscopic biopsy specimens. We first optimized ChIP-Seq procedures to enable the global analysis of small numbers (<100,000) of cells extracted from gastrointestinal endoscopic biopsy specimens. We applied crypt isolation technique to get epithelial cell fraction from the biopsy specimen. Utilizing the optimized small-scale protocol, we characterized global histone modification patterns in normal stomach tissues, *Helicobacter pylori* associated gastritis and gastric cancers. We developed an original lncRNA database based on several public databases. We then examined histone methylation status around putative lncRNAs and generated a list of candidate lncRNAs that may be important for chronic inflammation and carcinogenesis. In order to narrow the list down, we also utilized publicly available multi-omics data (such as ENCODE data), and performed integrated analysis using bioinformatics.

Here we would like to show the background and concept of this study, and we will also report the progress on this project.