

Protein interaction network can respond *Helicobacter pylori* infection?

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Helicobacter pylori (*H pylori*) is a gram negative bacterium which infects about 50% of the world population. *H pylori* colonization causes a strong systemic immune response. Various tools have been employed to identify the relationship between *H pylori* and gastric cancer, including c-DNA microarrays. However, most of these methods did not consider the systematic interaction of biological components.

A research team from South Korea studied the complex reaction of gastric inflammation induced by [Helicobacter pylori](#) (*H pylori*) in a systematic manner using a protein interaction network. Their study will be published on September 28, 2009 in the *World Journal of Gastroenterology*.

The results showed that the scale-free network showing the relationship between inflammation and carcinogenesis was constructed. Mathematical analysis showed hub and bottleneck proteins, and these proteins were mostly related to [immune response](#). The network contained pathways and proteins related to *H pylori* infection, such as the JAK-STAT pathway triggered by interleukins. Activation of nuclear factor (NF)-kB, TLR4, and other proteins known to function as core proteins of immune response were also found. These immune-related proteins interacted on the network with pathways and proteins related to the cell cycle, cell maintenance and proliferation, and transcription regulators such as BRCA1, FOS, REL, and [zinc finger](#) proteins. The extension of nodes showed interactions of the immune proteins with cancer-related proteins. One extended network, the core network, a

summarized form of the extended network, and cell pathway model were constructed.

The researchers drew a conclusion that immune-related proteins activated by *H pylori* infection interact with proto-oncogene proteins. The hub and bottleneck proteins are potential drug targets for gastric inflammation and cancer.

Their study showed how a systematic approach such as the network construction produces meaningful information. It also offered a relatively easy and simple framework to understand the complexity of cellular interactions having functional importance. Therefore, the application of this tool may be an alternative to find important genes and drug targets in other diseases and in complex biological systems.

More information: Kim KK, Kim HB. Protein interaction network related to Helicobacter pylori infection response. World J Gastroenterol 2009; 15(36): 4518-4528, www.wjgnet.com/1007-9327/15/4518.asp

Source: World Journal of Gastroenterology ([news](#) : [web](#))

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