

# Researchers identify four distinct mechanisms that contribute to gastric cancers

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Scientists at A\*STAR's Genome Institute of Singapore (GIS) headed a study that discovered four processes by which gastric cancer is formed. This is extremely important since gastric cancer is the second most common cause of cancer deaths worldwide, claiming almost 750,000 lives annually, 60% of which are Asians.

Using what is known as next-generation sequencing technologies, GIS scientists were able to provide a comprehensive view of the gastric cancer [genome](#), characterizing micro- and macro-scale mutations. This led to the identification of four distinct processes that cause mutations in gastric cancer. One of these was found to have a targeted impact on genes and is potentially triggered by [bacterial infection](#). The other processes were found to have impact throughout the genome, and included oxidative damage processes and the failure of DNA proof-reading mechanisms.

The discovery of the mutative actions of these processes provides essential clues to the formation of gastric cancers, paving the way for diagnostics and targeted therapy.

The findings were published online in the December 2012 issue of *Genome Biology*.

First author and GIS Principal Investigator Dr Niranjan Nagarajan said,

"Cancers are constantly evolving, and therefore understanding how they do so is important for finding new treatments. Mutational processes in cancer had not previously been shown to have a targeted impact on the genome and on genes. With this study, we show evidence of this for the very first time. This is truly exciting since it moves us a critical step towards understanding and finding a cure for gastric cancer."

Co-author and GIS Principal Investigator Dr Patrick Tan said, "This is the first time gastric cancers have been analyzed at the whole genome level. This work further showcases the reputation of Singapore as a world-leader in [gastric cancer](#) research."

"Our study demonstrates that sequencing gastric tumours not only allows the identification of mutations in the [human genome](#) but also reveals micro-organisms and their pathogenic gene content," added Dr Axel Hillmer, GIS Principal Investigator.

GIS Executive Director, Prof Ng Huck Hui said, "This is a very exciting study that probed into the genomic signature of gastric cancers. Through the analysis of somatic mutations occurring in gastric cancers, this team has identified several interesting genes which have profound implications in cancers."

**More information:** Nagarajan, N. et al., Whole-genome reconstruction and mutational signatures in gastric cancer. *Genome Biology*. December 2012.

Provided by Agency for Science, Technology and Research (A\*STAR), Singapore

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