

MEDIA RELEASE FOR IMMEDIATE RELEASE

19 APRIL 2018

ARTIFICIAL INTELLIGENCE HELPS TO PINPOINT ROOTS OF GASTRIC CANCER

Singapore – In a pioneering study, scientists at A*STAR’s Genome Institute of Singapore (GIS) have developed new machine learning computer models¹, a type of artificial intelligence (AI), to accurately pinpoint cancer mutations². They have also discovered new mutations in non-coding DNA (specifically, DNA that does not encode for proteins) which may cause gastric cancer. Furthermore, the innovative methods and technology developed through this study will aid researchers in understanding the impact of mutations in non-coding DNA in other cancer types.

Cancer is one of the leading causes of death worldwide and gastric cancer (also known as stomach cancer) is the fourth most lethal cancer³ in the world. It arises from mutations in the DNA that lead to abnormal cell growth. Much has been learnt about cancer through the study of two percent of DNA that comprise our genes. However, the other 98%, termed non-coding DNA, is still mostly uncharted territory. Non-coding DNA regulates activity of the genes and there is increasing evidence that mutations in these regions can also contribute to cancer.

In this project, two new AI methods were created to scan the entire genomes of 212 gastric cancer tumours in a few months. The analysis would have otherwise taken 30 years to complete on a standard modern computer. Using computer clusters at GIS and the National Supercomputing Centre (NSCC) Singapore, the analysis uncovered several new cancer-associated mutation hotspots located throughout the genome. It also provided new evidence that mutations in the non-coding DNA may cause cancer by altering the 3-dimensional (3D) genome structure.

Dr Anders Skanderup, Principal Investigator at GIS and lead scientist of the study, said, “We focus on computational and data-driven approaches to study the root of cancer so as to develop better strategies to combat it. Our findings suggest that mutations at 11 non-coding sites regulating the 3D genome structure are staggeringly frequent. Approximately one in every four gastric cancer patients have mutations at these specific sites.”

He continues, “These non-coding mutations are also frequent in other types of gastrointestinal cancers such as colorectal, pancreatic and liver cancer. Therefore, they can be used as biomarkers to detect and monitor the progression of gastrointestinal cancers too.”

¹ SMuRF: Portable and Accurate Ensemble-based Somatic Variant Calling; W. Huang, Y. Guo, K. Muthukumar, P. Baruah, M. Chang, A. Skanderup.

² Mutation hotspots at CTCF binding sites coupled to chromosomal instability in gastrointestinal cancers; Y. Guo, M. Chang, W. Huang, W. Ooi, M. Xing, P. Tan, Nature Communications, 2018.

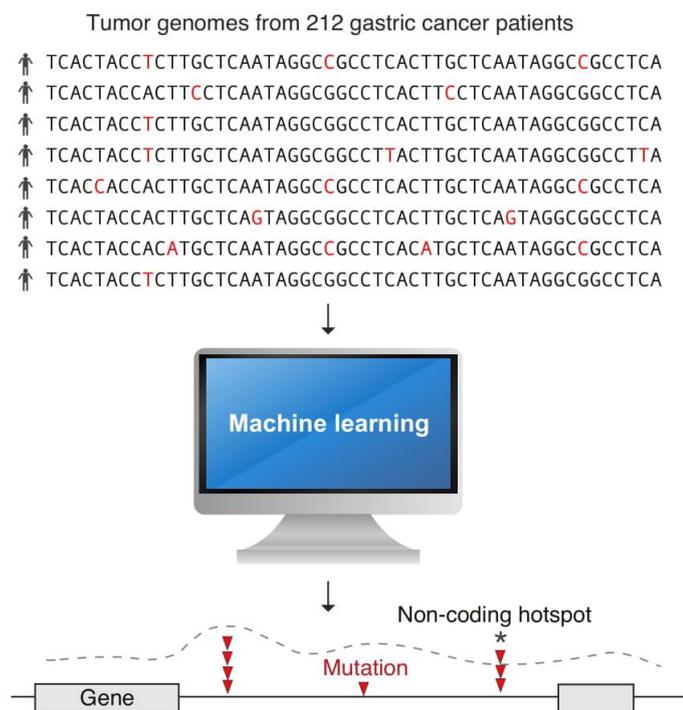
³ World Health Organization - <http://www.who.int/mediacentre/factsheets/fs297/en/>

Professor Patrick Tan, Director of Singhealth Duke-NUS Institute of Precision Medicine (PRISM), Deputy Executive Director of A*STAR's Biomedical Research Council, and co-lead scientist said, "Sophisticated machine learning techniques such as the one developed in this study are absolutely essential towards decoding the information encoded in our genomes. If experimentally validated, these findings point towards a mechanism of cancer development missed by previous studies." Professor Tan is also a professor at the Cancer & Stem Cell Biology Programme in Duke-NUS Medical School.

Professor Ng Huck Hui, Executive Director of GIS, said, "Previous studies focus solely on profiling mutations in the protein coding regions of our DNA, which makes up a mere two percent of our DNA. So, it has been an open question for ages whether we are missing vital information by overlooking the other vast 98%. This is the first study investigating the impact of non-coding DNA mutations in gastric cancer and we anticipate that it will inspire new research to further uncover the mechanisms and impact of these specific mutations."

These results were published in [Nature Communications](#) on 18 April 2018.

IMAGES



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Novel AI methods used to scan the whole genomes of 212 gastric cancer tumours, which identified new cancer-associated mutation hotspots in the non-coding regions.

Notes to Editor:

The research findings described in this media release can be found in the scientific journal Nature Communications, under the title, “Mutation hotspots at CTCF binding sites coupled to chromosomal instability in gastrointestinal cancers” by Yu Amanda Guo¹, Mei Mei Chang¹, Weitai Huang^{1,2}, Wen Fong Ooi³, Manjie Xing^{3,4}, Patrick Tan^{4,5} and Anders Jacobsen Skanderup¹.

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About A*STAR’s Genome Institute of Singapore (GIS)

The Genome Institute of Singapore (GIS) is an institute of the Agency for Science, Technology and Research (A*STAR). It has a global vision that seeks to use genomic sciences to achieve extraordinary improvements in human health and public prosperity. Established in 2000 as a centre for genomic discovery, the GIS will pursue the integration of technology, genetics and biology towards academic, economic and societal impact.

The key research areas at the GIS include Human Genetics, Infectious Diseases, Cancer Therapeutics and Stratified Oncology, Stem Cell and Regenerative Biology, Cancer Stem Cell Biology, Computational and Systems Biology, and Translational Research.

The genomics infrastructure at the GIS is utilised to train new scientific talent, to function as a bridge for academic and industrial research, and to explore scientific questions of high impact.

For more information about GIS, please visit www.gis.a-star.edu.sg.

About the Agency for Science, Technology and Research (A*STAR)

The Agency for Science, Technology and Research (A*STAR) is Singapore's lead public sector agency that spearheads economic oriented research to advance scientific discovery and develop innovative technology. Through open innovation, we collaborate with our partners in both the public and private sectors to benefit society.

As a Science and Technology Organisation, A*STAR bridges the gap between academia and industry. Our research creates economic growth and jobs for Singapore, and enhances lives by contributing to societal benefits such as improving outcomes in healthcare, urban living, and sustainability.

We play a key role in nurturing and developing a diversity of talent and leaders in our Agency and Research Institutes, the wider research community and industry. A*STAR oversees 18 biomedical sciences and physical sciences and engineering research entities primarily located in Biopolis and Fusionopolis.

For more information on A*STAR, please visit www.a-star.edu.sg.

About Duke-NUS Medical School Singapore

The Duke-NUS Medical School (Duke-NUS) was established in 2005 as a strategic collaboration between the Duke University School of Medicine, North Carolina, USA, and the National University of Singapore (NUS). Duke-NUS offers a graduate-entry, four-year MD (Doctor of Medicine) training programme, anchored on an innovative model of self-directed learning. The School also offers MD/PhD and PhD programmes.

Duke-NUS has five Signature Research Programmes: Cancer and Stem Cell Biology, Neuroscience and Behavioural Disorders, Emerging Infectious Diseases, Cardiovascular and Metabolic Disorders, and Health Services and Systems Research.

The collaboration between Duke-NUS and Singapore Health Services (SingHealth) has established an Academic Medical Centre to advance our joint pursuits in clinical care, research and education to transform medicine and improve lives.

For more information, please visit www.duke-nus.edu.sg.