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SINGAPORE SCIENTISTS DISCOVER NEW VIRUSES THAT IDENTIFIES HIGH-RISK INDIVIDUALS OF CANTONESE CANCER

Singapore – Scientists from the Agency for Science, Technology and Research's (A*STAR) Genome Institute of Singapore (GIS) have identified two new Epstein-Barr Virus (EBV) viral variants associated with cancers, including nasopharyngeal carcinoma (NPC) (the most common head and neck cancer in Singapore[1]), gastric cancer, and several kinds of lymphomas[2].

The discovery of these EBV viral variants paves the way for the implementation of effective intervention programmes that may reduce the disease's incidences in Asia. The study was published in _Nature Genetics_ on 17 June 2019.

EBV infected individuals from the Cantonese dialect group are known to have a 20-time higher risk (20 to 40 cases per 100,000 individuals per year) of developing NPC than people from other regions or populations. Hence, NPC is also known as the Cantonese Cancer.

The Epstein-Barr virus (EBV) was discovered in 1964[3] and is the first human virus to be associated with cancers.

In the current study, scientists from the GIS, Sun Yat-sen University Cancer Center, Institute of Zoology of Chinese Academy of Sciences, as well as several other collaborating research institutes, sequenced a large batch of viral genomes from NPC patients and healthy controls (individuals with EBV infection but did not contract NPC) from both NPC-endemic and non-endemic regions. They discovered a unique EBV strain that is associated with increased risk of developing NPC.

Individuals infected by this unique EBV strain have 11 times higher risk for developing NPC than the non-carriers. Currently, over 40% of individuals in southern China are infected by this high-risk EBV strain and about 80% of the NPC cases in the Cantonese dialect group are driven by this high-risk EBV strain. This unique strain seems to have originated in Asia, followed by expansion in NPC-endemic regions.

Dr Liu Jian Jun, Deputy Executive Director at GIS and lead author of the study, said, "The importance of the EBV viral variants in the development of NPC and its striking epidemic among Cantonese dialect group have been poorly explored in the past. This study provided novel insights into the NPC endemic, and potentially provides the basis for implementing effective intervention programmes to reduce its incidences."

Professor Ng Huck Hui, Executive Director at GIS, said, "The discovery of these high-risk EBV viral variants has important implications for public health efforts to reduce the burden of NPC, particularly among Cantonese speakers. Testing for these variants enables the identification of high-risk individuals for routine clinical monitoring to detect

[1] https://www.singhealth.com.sg/news/medical-news/head-and-neck-cancer-and-multidisciplinary-care

[2] Kieff, E.R., A.B. Epstein-Barr Virus and Its Replication. in Field's Virology 2603-2654 (Lippincott Williams & Wilkins, Philadelphia, 2007).

[3] Epstein, M.A., Achong, B.G. & Barr, Y.M. Virus Particles in Cultured Lymphoblasts from Burkitt's Lymphoma. Lancet 1, 702-3 (1964).

NPC early. Primary prevention through the development of vaccines against high-NPC-risk EBV strains is expected to greatly reduce the incidence rate of Cantonese Cancer."

IMAGES

Cantonese infected with high-risk Epstein-Barr virus (EBV) strains are susceptible to nasopharyngeal carcinoma (NPC)

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Notes to Editor:

The research findings described in this media release can be found in the scientific journal *Nature Genetics*, under the title, "Genome sequencing analysis identifies high-risk Epstein-Barr virus subtypes for nasopharyngeal carcinoma" by Miao Xu[1,2,12], Youyuan Yao[1,11,12], Hui Chen[3,12], Shanshan Zhang[1,12], Su-Mei Cao[1], Zhe Zhang[4], Bing Luo[5], Zhiwei Liu[6], Zilin Li[2], Tong Xiang[1], Guiping He[1], Qi-Sheng Feng[1], Li-Zhen Chen[1], Xiang Guo[1], Weihua Jia[1], Ming-Yuan Chen[1], Xiao Zhang[1], Shang-Hang Xie[1], Roujun Peng[1], Ellen T. Chang[7], Vincent Pedergnana[3], Lin Feng[1], Jin-Xin Bei[1], Ruihua Xu[1], Mu-Sheng Zeng[1], Weimin Ye[6], Hans-Olov Adami[6,8], Xihong Lin[2], Weiwei Zhai[3,9,10], Yi-Xin Zeng[1], Jianjun Liu[3].

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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.a-star.edu.sg/gis.

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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.

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