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中文

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NYCU Study Reveals Hidden Liver Cancer Risk in Non-Hepatitis Patients



Edited by Chance Lai

Many people in Taiwan are aware that hepatitis B and C viruses are major risk factors for liver cancer. However, new research

One of Asia's largest studies on non-viral liver cancer

The study is among the

shows that even individuals without these infections may still face a significantly increased risk—driven by genetic variation.

A research team led by Professor Mei-Hsuan Lee at the Institute of Clinical Medicine, College of Medicine, National Yang Ming Chiao Tung University (NYCU), has uncovered critical genetic factors linked to liver cancer risk in non-viral populations. By integrating data from the **Taiwan Precision Medicine Initiative (TPMI)**, **Taiwan Biobank**, and the **Taiwan Liver Cancer Network (TLCN)**, the team analyzed genomic, clinical, and longitudinal health data from more than 70,000 Taiwanese adults. The study was published in the international journal *JHEP Reports*.

Genetic variants linked to up to a threefold increase in risk

few globally—and one of the largest in Asia—to specifically examine liver cancer risk in individuals without hepatitis B or C infection. By excluding viral cases and focusing on so-called “non-viral liver cancer,” the researchers were able to establish a clearer understanding of genetic susceptibility.

With nearly a decade of follow-up data, the study provides robust longitudinal evidence with both clinical and public health relevance, laying the groundwork for more precise risk prediction models.

Cross-institutional collaboration showcases Taiwan’s precision medicine strength

The research was led by NYCU’s Institute of Clinical Medicine, in collaboration with Academia Sinica, the Taiwan Precision Medicine Initiative, the Taiwan Biobank, the Taiwan Liver

The study identified variants in the PNPLA3 and SAMM50 genes as significant contributors to liver cancer susceptibility. Individuals carrying multiple risk variants were found to have a 2.6 to 3.4 times higher likelihood of developing liver cancer over time.

Importantly, the findings challenge long-standing assumptions about liver cancer risk. Even in the absence of fatty liver disease—a condition often associated with metabolic dysfunction—these genetic variants independently elevated cancer risk.

“Liver cancer is no longer just a viral disease,” said Prof. Lee. “Our findings highlight that genetic and metabolic pathways play equally critical roles. In the future, genetic risk profiling could be incorporated into public health strategies for early

Cancer Network, and multiple medical centers.

The study highlights Taiwan’s global competitiveness in integrating large-scale biobank resources, data science, and precision medicine.

identification and
prevention."

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Contact Us



Yangming Campus

Address :

No. 155, Sec. 2, Linong St. Beitou Dist., Taipei City 112304, Taiwan

Phone : +886-2-2826-7000

Chiaotung Campus

Address :

No. 1001, Daxue Rd. East Dist., Hsinchu City 300093, Taiwan

Phone : +886-3-5712121

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