

# New evidence for genetic bases of liver cancer reported

July 1 2013

---

The Asian Cancer Research Group (ACRG), an independent, not-for-profit company in collaboration with BGI, the world's largest genomics organization, and The University of Hong Kong (HKU), jointly announced the publication of findings from a study of recurrent mutations in hepatocellular carcinoma (HCC), one of the most deadly cancers worldwide, in the international journal *Genome Research*. The study provides new insights into potential therapeutic intervention strategies for this common form of liver cancer.

HCC is a primary malignancy of the [hepatocytes](#), generally leading to death within 6-20 months after diagnosis. This type of cancer is more common in parts of Africa and Asia, where the patients with hepatitis B or C are at risk for [liver cancer](#), even if they have not developed cirrhosis. HCC has limited treatment options such as surgical resection of the tumor at its early stage, and the molecular basis of its occurrence and development remains poorly understood.

In this study, researchers used whole genome sequencing (WGS) to survey a cohort of 88 matched HCC tumor and normal samples from Hong Kong for investigating alerted genes and the pathways implicated in HBV-associated HCC. They found that TP53 was the most commonly mutated [tumor suppressor gene](#), accounting for 35.2% in the HCC cohort. Generally, the patients with tumors containing TP53 mutations exhibited poor survival.

The Wnt/?-Catenin signaling pathway is central for liver functions and is

frequently abnormal activated in the carcinogenesis of HCC. Researchers in this study found  $\beta$ -catenin maybe the most frequently mutated oncogene. In addition to  $\beta$ -catenin, they found relative high [mutation rates](#) in genes in the JAK/STAT pathway, which may act as a major oncogenic driver in HCC [tumor progression](#).

Hancheng Zheng, group leader of this project at BGI, said, "Liver cancer is intractable to nearly all currently available anti-cancer targeted therapies. Our findings in this study provide a better understanding of molecular basis of hepatocarcinogenesis and provide new clues to improving the diagnosis and treatment of liver cancer in the future."

"We detected a series of genes and pathways implicated in HBV-associated HCC using whole genome sequencing, which contribute to a better understanding of the tumor biology and targeted drug screening," said Dr. James Hardwick, Vice President of ACRG, and Director of Informatics & Analysis at Merck, "The ACRG was established to fuel research directed towards improving our understanding of cancers affecting Asian populations. By working together, we are able to generate important breakthroughs that can be transformed to better fight against liver cancer in the future."

"As clinicians, we are very excited about the several prevalent and actionable mutations identified from the study, including activating mutations of JAK1, which warrant testing several existing inhibitors for the treatment of the disease preclinically and clinically," said Dr. Ronnie Poon, Chair Professor and Chief, Division of Hepatobiliary and Pancreatic Surgery, The University of Hong Kong.

Provided by BGI Shenzhen

Citation: New evidence for genetic bases of liver cancer reported (2013, July 1) retrieved 16

April 2024 from

<https://medicalxpress.com/news/2013-07-evidence-genetic-bases-liver-cancer.html>

This document is subject to copyright. Apart from any fair dealing for the purpose of private study or research, no part may be reproduced without the written permission. The content is provided for information purposes only.