

Researchers identify new gene involved in the development of liver cancer

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Virginia Commonwealth University researchers have identified a new tumor-promoting gene that may play a key role in the development of liver cancer. Levels of the gene's expression are significantly higher in more than 90 percent of patients with the disease compared to their healthy counterparts.

Researchers at the Virginia Commonwealth University Massey Cancer Center and the VCU Institute of Molecular Medicine hope the findings could lead to an effective therapy to target and inhibit the expression of this gene and result in inhibition of cancer growth.

Hepatocellular carcinoma, HCC, or [liver cancer](#), is the fifth most common cancer and the third leading cause of cancer deaths in the world. Treatment options for HCC include chemotherapy, chemoembolization, ablation and proton-beam therapy. [Liver transplantation](#) offers the best chance for a cure in patients with small tumors and significant associated [liver disease](#).

In the study published online the week of April 19 in the Early Edition of the journal [Proceedings of the National Academy of Sciences](#), researchers employing a series of molecular studies identified the new oncogene called LSF, and observed that LSF levels are significantly higher in HCC patients compared to healthy individuals.

Further, the team found that LSF plays an important role in the development and progression of HCC, and that inhibiting LSF can reverse the aggressive properties of human liver [cancer cells](#). They have also identified the molecular mechanism by which LSF promotes the growth of tumors.

"Researchers have been studying the role of LSF for more than 25 years in fields outside of cancer, but our work is the first demonstration that LSF plays an important role in HCC," said principal

investigator Devanand Sarkar, Ph.D., MBBS, assistant professor in the Department of Human and [Molecular Genetics](#) in the VCU School of Medicine, and Harrison Endowed Scholar in Cancer Research at the VCU Massey Cancer Center and a member of the VCU Institute of Molecular Medicine.

"We show a novel mechanism of HCC development by LSF that provides us with fresh insight into the complex etiology and mechanism of carcinogenesis process. Because LSF is increased in such a high percentage of patients, it could be a potential target for therapeutic intervention," he said.

According to Sarkar, LSF is a transcription factor, which means it can directly regulate the expression of genes. The team has identified specific genes, such as osteopontin, that are directly induced by LSF.

"Osteopontin is a key player in regulating tumor development and progression and the identification of a master regulator of osteopontin, such as LSF, is a very important discovery," said Sarkar.

The team is currently testing small molecule inhibitors of LSF as a possible therapy for HCC in animal models.

"Analysis of LSF level in biopsy material may one day be used as a prognostic marker for HCC. Clinicians may be able to design treatment strategies based on the LSF level of a patient. For example, a patient with higher LSF level will respond more to LSF inhibitors. Newer combinatorial strategies can be developed incorporating LSF inhibition in one arm," he said.

Provided by Virginia Commonwealth University

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