c-Met may be a biomarker for metastatic hepatocellular carcinoma

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Targeting c-Met may be a promising personalized treatment method for approximately 45 percent of patients with hepatocellular carcinoma (HCC) who have c-Met-positive tumors, according to study results presented at the Fourth AACR International Conference on Molecular Diagnostics in Cancer Therapeutic Development.

HCC is the most common primary malignant tumor of the liver; c-Met is a receptor for hepatocyte growth factor that appears to drive liver cancer growth, invasion and metastasis.

"Current therapies for HCC patients are 'one size fits all.' We propose that molecular profiling will enable better therapy for HCC patients with a c-Met positive tumor," said Hanning You, M.D., Ph.D., postdoctoral fellow working in the laboratory of C. Bart Rountree, M.D., in the departments of pediatrics and pharmacology, at the Pennsylvania State University College of Medicine, Hershey, Pa.

Using a preclinical translational study to validate c-Met as a target for HCC, You and colleagues found c-Met was highly overexpressed in metastatic liver cancer cells.

"By targeting c-Met we were able to suppress tumor growth in vivo and kill these metastatic liver cancer cells," said You.

Since c-Met inhibitor stopped proliferation and tumor growth of metastatic HCC cells, the researchers concluded that c-Met might be a potential personalized target of metastatic HCC. In addition, they found that results of a separate meta-analysis of six studies and 1,051 patients showed that c-Met activation is associated with poor prognosis in HCC.

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