Novel Biomarker to Predict Response to CDK9 Inhibitors

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Technology description

Summary of Invention

Hepatocellular carcinoma (HCC) is the most common type of liver cancer and the third-leading cause of cancer-related mortality worldwide. The MYC oncoprotein, amplified in ~33% of hepatocellular carcinomas, is a well-validated but currently undruggable driver of HCC. Overexpression of MYC causes uncontrolled cell proliferation by affecting multiple cellular processes including gene transcription, DNA replication, and protein translation.
Through an RNAi screen, MSK investigators identified CDK9 (cyclin-dependent kinase 9) as required for proliferation of MYC-overexpressing liver tumors. Furthermore, MSK investigators found that liver tumors which overexpress MYC are sensitive to CDK9 inhibitor treatment, while liver tumors with normal MYC expression levels are less sensitive to CDK9 inhibitor treatment. Therefore, CDK9 inhibitors could be used to treat liver cancers, and potentially other tumor types, which have elevated levels of MYC.

Key Publications

Huang C-H. et al., CDK9-mediated transcription elongation is required for MYC addiction in hepatocellular carcinoma.Genes and Development, 28(16), 2015 (PubMed ID: 25128497)

Market Need

Hepatocellular carcinoma is the most common type of primary liver cancer, and its incidence rate continues to increase. In 2016, there will be an estimated ~35K new cases of HCC in the U.S., and there are over ~55K patients currently living with liver cancer in the U.S.

Application area

Initial application of hepatocellular carcinoma (HCC), with potential expansion to include other tumor types with elevated levels of MYC

Institution

Memorial Sloan-Kettering Cancer Center

Inventors

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