

5th International Conference on

Cancer Genomics

August 08-09, 2016 Las Vegas, USA

Global analysis of DNA methylation in hepatocellular carcinoma by a liquid hybridization capture-based bisulfite sequencing approach

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Epigenetic alterations such as aberrant DNA methylation of promoter and enhancer regions, which lead to atypical gene expression has been associated with carcinogenesis. In hepatocellular carcinoma (HCC), genome-wide analysis of methylation has only recently been used. For a better understanding of hepatocarcinogenesis, we applied an even higher resolution of the promoter methylome analysis to identify previously unknown regions and genes differentially methylated in HCC. Optimized liquid hybridization capture-based bisulfite sequencing (LHC-BS) was developed to quantitatively analyze 1.86 million CpG sites of individual sample from 8 pairs of HCC and adjacent tissues. By linking the differentially methylated regions (DMRs) in promoters to the differentially expressed genes (DEGs), we identified 12 DMR associated genes. We further utilized Illumina MiSeq combining bisulfite sequencing PCR approach to validate the 12 candidate genes. Seven genes, including SMAD6, IFITM1, LRRC4, CHST4 and TBX15 with promoter hyper-methylation and CCL20 and NQO1 with promoter hypo-methylation in HCC were confirmed in additional 78 HCC pairs by Illumina MiSeq platform. These data highlight the novel methylome profiling provides a cost-efficient approach to determine candidate genes in human HCC that may contribute to hepatocarcinogenesis. Our work provides further information critical for understanding the epigenetic processes underlying tumorigenesis and prognosis of HCC.

Biography

Qian Chen has completed her PhD from Queen's University of Belfast, Northern Ireland and Postdoctoral studies from National Institute of Health, USA. She serves as a Physician & Clinical Assistant Professor of Medicine, Gastrointestinal Department and Endoscopy Unit at Affiliated Tongji Hospital of Huazhong University of Science and Technology (HUST), China. She has published more than 11 papers in reputed journals and has been serving as an editorial board member of reputed.

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