DNA methylation of tumor suppressor genes in hepatocellular carcinoma

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Abstract

The basic unit of chromatin is a nucleosome included an octamer of the four core histones and 147 base pairs of DNA. Posttranslational histones modifications affect chromatin structure resulting in gene expression changes. CpG islands hypermethylation within the gene promoter regions and the deacetylation of histone proteins are the most common epigenetic modifications. The aberrant patterns of methylation localized in normally unmethylated CPG islands mediate chromatin compaction resulting in gene silencing and cancer induction. The current review article aimed to assess and analyze the available literature on the tumor suppressor genes (TSGs) hypermethylation in hepatocellular carcinoma (HCC). For this review article, the suitable studies were obtained by searching PubMed, SCOPUS, NCBI, and Ovid database from 1995 up to September 2018 with the MeSH terms combined with free terms. A total 1483 Items were identified in SCOPUS (n = 459), PubMed (n = 832), Ovid (n = 118), and other reference sources (n = 74). After the assessment, 73 manuscripts were included in the current study. In total, 13 genes were found to have the most effect on HCC. Therefore, we selected them to evaluate as candidate genes in this cancer. TSGs can affect cell cycle during various stages of the cycle an at the cell cycle checkpoints. The hypermethylation of these genes results in chromatin compaction and TSGs silencing which induces HCC.

Keywords: Carcinoma, Genes, Methylation, Tumor Suppressor