

Recent Advance of Histone Modification in Gastric Cancer : A Review

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Abstract: Epigenetics play important roles during development progress of tumor. The histone modifications are the most important constituted field. Recently, accumulating research focused on exploring the roles of those modifications in regulating tumorigenesis. Moreover, the dysregulation of histone modifications is supposed to have vital clinical significance. Numerous histone modifications have the potential to be prognostic biomarkers, monitoring response of therapy, early diagnostic markers. Herein, we review the recent advances of histone modifications involving development of gastric cancer. Gastric cancer (GC) is one of the most frequent tumors in the world. Stomach adenocarcinoma is a heterogeneous tumor, turning the prognosis prediction and patients' clinical management difficult. Some diagnosis tests for GC are been development using knowledge based in polymorphisms, somatic copy number alteration (SCNA) and aberrant histone methylation. This last event, a posttranslational modification that occurs at the chromatin level, is an important epigenetic alteration seen in several tumors including stomach adenocarcinoma. Histone methyltransferases (HMT) are the proteins responsible for the methylation in specific amino acids residues of histones tails. Here, were presented several HMTs that could be relating to GC process.

Keywords: Acetylation, gastric cancer, histone modification, methylation, phosphorylation.

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