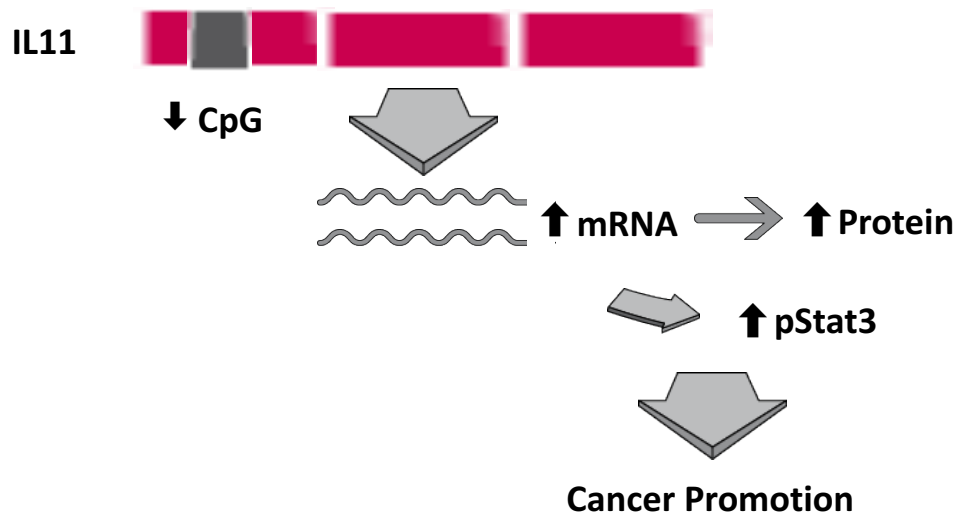


Epigenetic Modifications of IL11 Gene in Human Colon Cancer Cells

Calantha Yan, Hong Wang, Chung S. Yang
Rutgers, The State University of New Jersey

IL11 was found to be upregulated in digestive tract cancers in The Cancer Genome Atlas Database. In our colon carcinogenesis mouse model, we performed genome wide gene expression and DNA methylation analyses and our data suggested that IL11 upregulation in mouse colon tumors is associated with its DNA demethylation. To establish the role of epigenetic regulation in IL11 expression in human cancer, we studied the DNA methylation of IL11 in 10 commonly used colon cancer cell lines. According to the University of California Santa Cruz's genomic database there are 3 methylated CpG clusters in human IL11 gene in colon cancer Caco-2 cells. We designed PCR primers to amplify these 3 clusters for bisulfite converted DNA for sequencing. DNA was extracted from the cell lines and we are working on the PCR optimization. If we could successfully identify the DNA methylation site in cell lines, we will further characterize IL11 methylation in human colon cancer samples.



When the CpG island is demethylated the IL11 gene is expressed. mRNA levels rise which result in an increased amount of protein. The occurrence of phosphorylation of STAT3, the key downstream signaling event of IL11, goes on to promote colon tumor cell growth and tumorigenesis.