Methylation of miRNAs in UC colitis

Summary

Colorectal cancer (CRC) is a feared complication of chronic ulcerative colitis (UC) and the mortality of patients diagnosed with CRC in the setting of UC is higher than for sporadic CRC. Thus, a reliable screening assay that can identify UC patients at risk for the development of CRC is needed. Researchers at the Baylor Center for Gastrointestinal Cancer Research have discovered a unique panel of methylated miroRNA (miRNA) signatures that can be utilized to enhance surveillance and diagnosis UC-associated neoplasia.

Key Investigator
Ajay Goel, PhD

Field
Colorectal Cancer

Technology
miRNA biomarkers

Key Features
Cancer screening
Development of biomarkers

Stage of Development
Preclinical proof of concept

Status
Available for licensing
Available for research collaboration

Patent Status
Patents pending
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Market

UC is a chronic disease that effects the innermost lining of the large intestine. Carcinogenesis UC occurs in a histologically stepwise manner involving accumulation of genetic and epigenetic alterations that can occur in both non-neoplastic and neoplastic epithelium of patients with UC -associated neoplasia. Patients with UC are at increased risk for developing CRC, and the cumulative risk of developing UC-associated CRC increases with the duration and extent of the disease. To improve surveillance efficacy, more effective markers for identifying patients at high risk for UC-associated CRC are needed.

Technology

miRNAs are non-coding RNA molecules of approximately 21-23 nucleotides in length that regulate target gene expression by interfering with their transcription or by inhibiting translation. In several types of neoplasia, aberrant methylation of promoter-region CpG islands, as an epigenetic DNA modification, is associated with transcriptional inactivation of tumor suppressor genes; and can result in tumorigenesis. In colon tissues, CpG islands methylated in cancer have been divided into two groups: those that display cancer-restricted methylation (type C), and those that are methylated in (initially) normally aging epithelial cells (type A).

This technology demonstrated for the first time that methylation of a combination miRNA-1 ,miRNA-9, miRNA-124, miRNA-137 and miRNA-34b/c in rectal tissues are robust biomarkers for early detection of UC-associated cancer. Thus, methylation of these 5 miRNAs collectively suggest that this sequence of events occurs early in dysplasia-carcinoma sequence and could be used as a basis for a diagnostic method for UC associated neoplasia.

For more information about the Baylor Center for GI Cancer Research see:
http://www.baylorhealth.edu/GiResearch