# Methylation of miRNAs in UC colitis

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## Technology description

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. 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.┬áPatients 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.

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