Molecular Targets in Early Detection and Differentiation of Inflammatory Bowel Disease Associated Colon-Rectal-Anal Cancer Disparities


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To identify proteins and genes of interest and confirm their presence in colonic layers of IBD-associated colorectal cancer (CRC) specimens.

METHODS

To detect changes for UC, we compared UC to CC and UC to NL; and for CC, we compared CC to UC and CC to NL.

Statistical analyses, Leave-One-Out Cross-Validation (LOOCV) and Weighted-Leave-One-Out-Cross-Validation (WLOOCV) were performed on each cross-validation test. The results of the leave-one-out cross-validation tests (p values) are listed in Table 1.

The significances of these genes to CRC initiation has not been elucidated.

RESULTS

Table 1:

1A 12 μm tissue section is placed on a gold-coated MALDI target.

2A histology-directed approach was used to robotically deposit matrix in areas of interest (mucosa, submucosa, inflamed, uninflamed) on the tissue sections.

Flexible Compounds (WFCPC) were used to determine significant features.

Laser Capture Microdissection (LCM) of colonic submucosa from UC, CC, and NL (cc), and normal (NL) vials was performed.

The submucosal mRNA was extracted using the PicoPure ™ RNA Isolation kit.

Comprehensive gene expression analysis of the pooled mRNA from each group was then performed using the Affymetrix GeneChip® Gene 1.0 ST Array System.

Eleven features were found with the smallest p-values with an overall accuracy = 82% (p<0.0001), Table 2.

Table 2:


FIG1: PROTEOMIC BIOMARKER PIPELINE

FIG2: WORKFLOW FOR HISTOLOGY-DIRECTED PROFILING (MALDI MS)

FIG3: HIGH THROUGHPUT ANTIBODY PRODUCTION OF NOVEL GENE/PROTEIN IN THE EVENT ANTIBODIES NOT AVAILABLE COMMERCIALY

FIG4: VALIDATION TECHNOLOGY OF GENE BY QUANTITATIVE RT-PCR

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