

SNPs in the cachexia pathway predict outcomes in colon cancer

USC Case # 2016-116

Market Opportunity:

Colorectal cancers (CRC) are the third leading cause of cancer-related deaths in the United States and account for an \$8 billion market. Cancer cachexia is a significant cause of morbidity and mortality and affects the majority of patients with advanced cancer. It commonly affects late-stage CRC patients, leading to substantial and progressive functional impairment. Cachexia itself might be a direct result of malignancy as well as some of the chemotherapeutics used to treat it such as bevacizumab. It is known that genes involved in the cachexia pathway play a critical role in the development and progression of CRC. However, we still have a poor understanding of whether polymorphisms in these genes can predict clinical outcomes in patients treated with bevacizumab.

USC Solution:

USC researchers have identified novel, small nucleotide polymorphisms (SNPs) in the cachexia pathway that affect treatment outcomes in colorectal cancer patients. Patient tissue samples screened for certain SNPs had a high correlation with prolonged survival with Irinotecan and Bevacizumab treatment. Detection of these novel biomarkers can be easily achievable via PCR-based assays.

Value Proposition

- Novel biomarkers for predicting efficacy of existing cancer treatments
- Opportunity to improve progression free survival in colorectal cancer
- High correlation of SNP genotype with improved patient outcomes

Keywords:

Colorectal cancer, pharmacodiagnosics, diagnostics, biomarkers, oncology, cachexia, SNPs, precision medicine, personalized medicine



Applications

- Diagnostic tool for predicting treatment outcomes in colorectal cancers

Stage of Development

- Validated in samples from two distinct clinical cohort studies
- Available for exclusive and non-exclusive license

Intellectual Property

Status:

Provisional Patent Filed

Key Publication:

[“Molecular Pathways: Cachexia Signaling—A Targeted Approach to Cancer Treatment.” Clin Cancer Res. 2016; 22\(16\):3999-4004.](#)

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