miRNAs for Prognosis and Prediction of Metastases

Summary

During colorectal cancer (CRC) development, neoplastic cells may acquire the ability to invade or spread to distant organs through complex processes including directional activation of proteolytic enzymes, epithelial-to-mesenchymal transition (EMT) and translocation of cancer cells. The ability to predict those patients in which the cancer could metastasize will alter treatment paradigms. Researchers at the Baylor Center for Gastrointestinal Cancer Research have discovered unique metastasis-specific microRNA (miRNA) signatures that could predict prognosis and distant metastasis in CRC.

Key Investigator
Ajay Goel, PhD

Field
Colorectal Cancer

Technology
miRNA biomarkers

Key Features
- Cancer screening
- Development of blood -based assays

Stage of Development
Preclinical proof of concept

Status
Available for licensing
Available for research collaboration

Patent Status
Patents pending
WO2013096888
WO2014145612

Contact

Melissa Acosta, PhD
(214) 820-7528
Melissa.acosta@BSWHealth.org

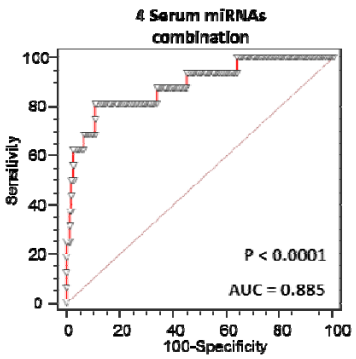
Market

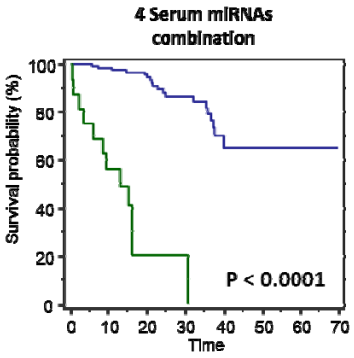
CRC is the most prevalent of GI cancers, causing 600,000 deaths worldwide each year, and is the second biggest cause of cancer death in the US. Colorectal cancer is also a significant contributor to US health care costs, with over $12 billion spent on treatment each year. Management of CRC is dependent on clinic-pathologic features. Metastasis formation is the major cause of death in patients with colorectal cancer, and depending on tumor stage, liver metastases occur in 20% to 70% of patients, and lung metastases in 10% to 20% of cases. However, all current staging systems have their shortcomings and limitations. To date, it is not possible to prospectively identify the patients that will suffer from metastases related to CRC. Thus, there is a dire need to identify highly robust biomarkers that can clinically determine cancer prognosis and predict patient outcome.

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. Tumor-derived miRNAs are present within the circulation in stable forms that are protected from endogenous ribonuclease activity resulting in the possible prognostic utility of these serum-based miRNAs.

A combination analysis of serum miRNAs revealed that miR-21, miR-885-5p, miR-200c and miR-203 predicted liver metastasis with a high sensitivity and specificity. Receiver operating characteristic (ROC) analysis revealed that a change in expression of all 4 miRNAs could discriminate between patients with metastasis and patients without. Thus, the panel of 4 serum-based miRNAs is a prognostic panel of tumor recurrence and predictive panel of CRC metastasis as well as poor prognosis.





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