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The role of microbiome perturbations in colorectal cancer: Diagnostic, therapeutic or both?

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There is encouraging evidence for using a stool-based composite microbial non-invasive diagnostic for colorectal cancer. Through our meta-analysis, we analyzed eight global cohorts, re-analyzing the raw 16S rRNA gene sequencing data to find consistent biomarkers such as *Parvimonas micra, Fusobacterium* sp. and *Streptococcus anginosus* robust to demographic and technical heterogeneity across the studies. We further evaluated which microbial markers in colorectal cancer tissue biopsy, directly at the disease interface were consistently elevated across cohorts, the extent to which they were detectable in fecal samples from the same colorectal cancer case and the pathways through which they might operate. We noticed OTUs elongated to genus *Parvimonas, Fusobacterium* and *Streptococcus* elevated in biopsies as well. Inferred functional analysis identified differences in amino acid and lipid metabolism, likely driven by the altered abundances of *Fusobacterium, Leptotrichia, Enterobacteriaceae, Comamonadaceae and Ruminococcaceae*. While promising, to be truly generalizable for the public, a microbial diagnostic for colorectal cancer must overcome challenges in terms of confounding the microbial signal by other co-existing morbidities such obesity, type-2 diabetes, and IBD or the intake of over-the-counter or prescribed medications which is known to influence the gut microbial content. Along with diagnostic avenues, *in vivo* studies have characterized Wnt-β-catenin signaling cross-talks with microbial communities and host immune system and can be causal in inflammation-driven colorectal cancer. Recent studies have demonstrated that the immune-modulator effectiveness of CTLA-4 and PD-PDL1 based therapy is microbiota dependent and lays ground to prove the utility of microbiome modulated immunotherapy for all cancers.

Biography

Manasi S Shah has completed her PhD from the University of Texas School of Public Health. She then worked briefly with Second Genome Inc., as a consultant and is a current postdoctoral study from Stanford University School of Medicine. Currently working as a Staff Bioinformatics Scientist at Thermo Fisher Scientific, Manasi has authored a couple of microbiomes focused papers and is currently working on a grant award she received to improve the Axiom microbiome array capabilities.

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