Microbial dysbiosis in colorectal cancer and its persistence after curative surgery
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Introduction

Increasing evidence points towards gut microbiota influence on CRC. Globally, CRC is the second most common cancer, and the fourth leading cause of cancer-related deaths. CRC is a global disease with developing and developed countries equally affected.

WHAT IS THE HUMAN MICROBIOME?

The human microbiome is the second genome of the human body where microorganisms establish a symbiotic relationship with its host in complementing metabolic deficits, protection from invading pathogens and maintaining immune homeostasis.

WHAT IS THE RELATIONSHIP?

Increasing evidence points towards gut microbiota influence on CRC development through virulence factors from pathogenic bacteria, suggesting a close correlation between certain bacteria and CRC.

OUR PURPOSE

In this study, we seek to examine alterations in co-abundant bacterial strains in CRC patients before and after surgery and compare them to healthy individuals.

Methods

1. DNA extraction
2. 16S sequencing
3. Sequencing reads

Results

- Figure 1: Fecal bacterial compositions are different between Healthy and CRC patients. (A) Top bacterial phyla present in all samples. (B) Comparisons of bacterial alpha diversity in CRC to Healthy control group.

- Figure 2: Log fold change in abundance of bacterial ASVs that are significantly different in CRC post-op compared to pre-op (alpha ≤ 0.0001, * denotes Benjamini-Hochberg adj < 0.0001).

- Figure 3: Log fold change in abundance of bacterial ASVs that are significantly different in CRC post-op compared to pre-op (alpha ≤ 0.0001, * denotes Benjamini-Hochberg adj < 0.0001).

- Figure 4: KEGG gene enrichment analysis heatmap showing KOs that contributed to the enriched pathways associated with different comparisons.

Conclusion

1. High diversity is associated with health and temporal stability, while a relative lack of diversity is often observed in the microbiota of CRC patients.
2. Curative surgery resulted in the reversion of some bacterial strains (i.e., Bacteroidetes spp.) to a "healthy" level but not others (i.e., Eubacterium coprostansgenogroup).
3. Certain bacterial groups which were found in equal abundance in "healthy" patients were increased after surgery (i.e., A. muciniphila) suggesting a complex dynamics of bacteriome field-change associated with the presence of CRC.