The human microbiome and colorectal cancer

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Outline

- Introduction to the human microbiome
- Technologies to assess the microbiome
- Human microbiome and colorectal cancer
- Future directions
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Microbiota and the tree of life

- Microbes
- Bacteria
- Archaea
- Fungi
- Protists
- Viruses
- Microbiome: collection of microbial genes

Alpha and beta diversity

**Alpha diversity**
- Counts (Taxonomy/OTUs)
- Shannon index
- Simpson index
- Chao1
- PD tree

**Beta diversity**
- Bray-Curtis
- UniFrac

**Forest 1**
Alpha diversity = 3

**Forest 2**
Alpha diversity = 6

Beta diversity
- 2 shared
- 5 different
PCoA plot: Clustering by body site

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History of microbial research

Image: http://learn.genetics.utah.edu/content/microbiome/study/
Present day study

Fecal collection methods

- No Solution
- RNAlater
- 95% Ethanol
Stability

Accuracy

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Colorectal cancer worldwide

Source: GLOBOCAN 2012 (IARC)
Meat and colorectal cancer

MEAT AND CANCER HOW STRONG IS THE EVIDENCE?

IARC CARCINOGENIC CLASSIFICATION GROUPS

Processed meats have been given Group 1 classification

- Salami
- Sausages and hot dogs

Includes

Bacon

Causes cancer

Probably causes cancer

GROUP 1

GROUP 2A

GROUP 2B

GROUP 3

GROUP 4

These categories represent how likely something is to cause cancer in humans, not how many cancers it causes

Red meats have been given Group 2A classification

- Pork
- Beef
- Lamb

(Does not include chicken or fish)

WE WILL BEAT CANCER SOONER

cruk.org

Cancer Research UK (http://gloriousnutrition.co.uk/processed-meat-popularity-decreasing-due-to-cancer-link/)
Meat and the gut microbiome

Microbiome and colorectal cancer (U.S.)

Ahn et al (2013) *JNCI*
Microbiome and colorectal cancer (U.S.)

Case enrichment
- *Fusobacterium*
- *Veillonellaceae*
- *Anaerovorax*
- *Porphyromonas*
- *Atopobium*

Control enrichment
- Firmicutes overall
- Lachnospiraceae

Ahn et al (2013) *JNCI*
Meta-analysis of 16S rRNA gene studies

Meta-analysis of 16S rRNA gene studies

Potential mechanisms

Drewes et al (2016) *BJC*
Conclusions

- There is promise for fecal microbial markers to enhance FOBT or FIT tests for colorectal cancer screening.

- All previous studies have been cross-sectional.

- Prospective studies (and studies with multiple serial samples) are needed to understand microbial associations with colorectal cancer etiology.
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Future directions

- Optimization of collection method for multiple technologies
- Collect fecal samples in prospective cohort studies
- Quality control standards to evaluate reproducibility
- Standardization of methods for extraction, sequencing, and bioinformatics for data pooling and meta-analyses
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