

The Gut Virome: A Neglected Factor in Colorectal Cancer

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Outline

A) Brief on human virome and cancer risk factors

- Human Virome
- Virome-related diseases
- Cancer risk factors
- Mechanism of virome carcinogenesis
- B) Gut virome and colorectal cancer (CRC)
- Microbiota in CRC
- Gut virome composition
- Gut virome in CRC





Brief on human virome and cancer

Gut virome and colorectal cancer (CRC)





What is human virome?

- the repertoire of all viruses on the surface and inside our body
- Infect both human cells and microbes
- Some can cause disease, while others are asymptomatic
- Different composition due to anatomical sites

Human virome-related diseases



Cancer risk factors

Mechanism of viral carcinogenesis

- Cell proliferation
- Apoptosis
- Cell cycle
- DNA damage

Brief on human virome and cancer

Gut virome and colorectal cancer (CRC)

• The abundance of microbes in CRC tissue is different from normal tissue.

Microbiota in CRC

- Compared to health tissue, *Fusobacterium* is more abundant while *Bacteroides* is less abundant in CRC tissue.
- *Fusobacterium* is the key phylotype that contribute to the dysbiosis in CRC patients.

Microbiota-related mechanisms in CRC carcinogenesis

- By metabolites or genotoxins
- Procarcinogenic bacteria and opportunistic bacteria
- Activate carcinogenic signaling pathways
- Molecular changes lead to CRC progression

Known bacteria in CRC

Unknown bacteria and virus in CRC

Gut Virome composition

- Gut virome contains 13204 viral populations, including prokaryotic viruses and eukaryotic viruses.
- 96.1% of gut viral populations are bacteriophages, 3.8% are eukaryotic viruses.

Viruses in CRC

- Several eukaryotic viruses can be detected in CRC samples
- Negative association with these viruses

ia ID C	Fusobacterium (OTU 4)- Bacteroides (OTU 68)- Porphyromonas (OTU 146)- Blautia (OTU 25)- Akkemansia (OTU 87)-
H Bacter	Clostridium_XVIII (OTU 220) Blautia (OTU 32) Ruminococcaceae (OTU 222) Phascolarctobacterium (OTU 24) Bacteroides (OTU 42)
	2 4 6 Mean Accuracy Decrease
D	Siphoviridae (Cluster 115)
Virus ID	Siphoviridae (Cluster 315)
	0.5 1.0 1.5 2.0 Mean Accuracy Decrease
Е	Siphoviridae (Cluster 115)
be ID	Bacteroides (OTU 68) - Fusobacterium (OTU 4) - Myoviridae (Cluster 109) - Myoviridae (Cluster 95) -
Micro	Siphoviridae (Cluster 315) - Unclassified (Cluster 162) - Clostridium_XIVa (OTU 191) - Siphoviridae (Cluster 18) - Porphyromona dace ae (OTU 46) -
	0.5 1.0 1.5 2.0 Mean Accuracy Decrease

Bacteriophage in CRC

- *Fusobacterium* was the primary driver of the bacterial association with colorectal cancer
- Bacteriophages(belong to Siphoviridae and Myoviridae) play a role in tumorigenesis
- Both bacterial and viral microbes were found to drive the community association with cancer

Bacterial OTUs

Bacteriophages and bacteria in CRC

 low correlation between bacterial and viral relative abundances

How bacteriophage promotes CRC

- Phages alter bacterial community
- Space for opportunistic bacteria
- Adhere, colonize and may establish biofilm
- Oncogenic bacteria transforms epithelial cells and disrupt tight junctions.

Other conceptual models

Kill the winner

Phages act as predators of overgrowed

bacteria

Biological weapon

Phages are used by commensal bacteria to kill bacterial competitor

Community shuffling

A host reaction induced phages to act

negatively on their host

Emergence of new bacterial strains

Phages operate as reservoirs of genetic

diversity, without killing bacteria

Summary

- Human virome has been associated with diverse cancers and diseases.
- Bacteriophages can alter gut bacterial community thereby promoting CRC progression indirectly.
- More researches need to be done to elucidate how phages influence CRC.

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Thanks for listening!

