Microbiome and GI Cancers

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- Consulting Immuron, Niche, ProbioTech, Seres, Takeda
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Outline



- Introduction to the microbiome
- Microbial alterations in GI malignancies
- Clinical implications

What's This Microbiome That Everyone's Talking About?

- >10x microbial cells (~100 trillion) than human
- Microbes: 1 3% of body's mass
 - 99% of all bacteria are commensal
- Humans possess 23,000 genes
 - Microbes contribute ~3,300,000 genes
- Phyla present
 - Firmicutes and Bacteroidetes: >90%
- Functions such as colonization resistance
- Alterations associated with disease states

Gilbert et al. Nature Medicine. 24, 392-400; Scott et al. Gut. 68(9): 1624-32.



Let's Get the Terminology in Order



Microbiota: The microorganisms that live in an established environment



Microbiome: The combined genetic material of the microorganisms in a particular niche



Metabolome: Functional properties of the gut microbiota



Dysbiosis: A derangement in the microbiota

Proportion of Cancers Attributable to Infections



Other infections Hui

Human herpes virus-8 Epstein-Barr virus Human papillomavirus Hepatitis C virus

Hepatitis B virus

Most Common Infection-Attributable Cancers



canceratlas.cancer.org

Is it just single organisms that are associated?

Microbes and GI Cancers: An Age-Old Tale



Pop et al. *Pharmaceutics*. 2022, 14(7), 1463, https://patient.gastro.org/tag/h-pylori/.



Is *H pylori* a Single Organism Pathogenesis?



Wroblewski et al. Clin Microbiol Rev. 2010 Oct;23(4):713-39. Abreu et al. Gastroenterology. 2014;146:1534–1546.

Microbiome and CRC in 1969...

Bacteria and the aetiology of cancer of the large bowel

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in geographical distribution (Doll, 1967; Doll, Payne, and Waterhouse, 1966; Davis, Knowelden, and Wilson, 1965) and, with the exception of Japan, the disease is more prevalent in developed than in underdeveloped countries. The reason for this variation is not known but epidemiological evidence suggests that environmental factors may be involved. It is claimed that immigrants from areas with a low incidence of cancer of the large bowel tend to show the same high incidence of this cancer as the local population (Haenszel and Dawson, 1965; Buell and Dunn, 1965). Changes in dietary habit may be especially important (Wynder and Shigematsu, 1967; Buell and Dunn, 1965) and diet is known to affect the nature and distribution of bacteria in the faeces (Hoffmann, 1964; Dubos, 1965).

Among the important metabolic activities of intestinal bacteria is the degradation of bile salts (Hill and Drasar, 1968). It seems possible that some of the bacteria in the bowel could convert bile salts, or steroids in the diet, into carcinogens; Haddow (1958) has reviewed the ways in which it is possible, in the laboratory, to convert deoxycholate into 20-methylcholanthrene, a potent carcinogen.

We have, therefore, compared the bacterial flora of the faeces from people in England, an area with a high incidence of cancer of the large bowel, with that from people in Uganda, where the incidence is low. We have also compared the abilities of English and Ugandan strains of faecal bacteria to degrade bile salts and have examined the products of bile degradation in English and Ugandan faeces.

MATERIALS AND METHODS

Samples of freshly voided faeces from 48 healthy Ugandan adults living in and around Kampala and from 40 healthy English adults living in London were examined, Specimens were preserved for transport and storage as a 10% suspension in meat infusion broth containing 10% 334

Cancer of the large bowel shows marked variations and McLeod, 1969); the bacteria have been found to survive well under these conditions. Specimens were cultivated by the methods described previously (Drasar, 1967) with minor modifications. Approximately equal numbers of English and Ugandan specimens were examined on each day of testing in order to compensate for minor fluctuations in culture media, incubation temperatures, and operational techniques.

Methods for investigating the degradation of bile salts are described elsewhere (Hill and Drasar, 1968; Aries, Crowther, Drasar, and Hill, 1969).

RESULTS AND DISCUSSION

Our findings are summarized in the Table. The same

TABLE

BACTERIAL COUNTS OF FAECES FROM 40 ENGLISH AND 48 DGANDAN ADDIT TS1

Organism	English	Ugandan	P ²
Bacteroides	97+06	8-2 + 1-1	<0.001
Bifidobacteria	9.9 ± 0.3	9.3 ± 0.6	<0.001
Aerobic streptococci	7.0 ± 0.8	7.8 ± 0.9	0-01
Enterococci	5.7 ± 1.3	7.0 ± 1.2	0.01
Lactobacilli ·	60 ± 16	7.2 ± 1.1	0-01
Yessta	1.3 ± 1.8	3.1 ± 2.0	0-01
Enterobacteria	7.5 ± 1.2	80 + 08	>0.05
Clostridia	44 ± 18	40 ± 19	>0.05
Veillonellae	44 ± 21	$5-3 \pm 1-4$	>0.05
Filamentous fungi	1.4 ± 1.2	2.2 ± 1.2	>0.05

Arithmetic mean of log₁₀ organisms per g wet weight ± standard

"Agreed values obtained from both the student / test and the x" test. *Agreed value obtained from both a rank test and the x* test.

groups of bacteria occurred in both populations but there were significant quantitative differences. Although the dominant bacteria in both populations were non-sporing anaerobes (bacteroides and bifidobacteria), the English specimens contained 30 times more bacteroides than did the Ugandan. Streptococci, enterococci, lactobacilli, and yeasts occurred in significantly greater numbers in the glycerol frozen on solid carbon dioxide (Drasar, Shiner, Ugandan specimens, No significant differences were

BACTERIAL COUNTS OF FAECES FROM 40 ENGLISH AND 48 UGANDAN ADULTS¹

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Bifidobacteria	9.9 ± 0.3	9.3 ± 0.6	<0.001
Aerobic streptococci	7.0 ± 0.8	7.8 ± 0.9	0.01
Enterococci	5.7 ± 1.3	7.0 ± 1.2	0.01
Lactobacilli	6.0 ± 1.6	7.2 ± 1.1	0.01
Yeasts	1.3 ± 1.8	3.1 ± 2.0	0.01
Enterobacteria	7.5 ± 1.2	8.0 ± 0.8	>0.02
Clostridia	4.4 ± 1.8	4.0 ± 1.9	>0.02
Veillonellae	$4 \cdot 4 \pm 2 \cdot 1$	5.3 ± 1.4	>0.02
Filamentous fungi	1.4 ± 1.2	$2 \cdot 2 + 1 \cdot 2$	>0.023

¹Arithmetic mean of \log_{10} organisms per g wet weight \pm standard error.

²Agreed values obtained from both the student t test and the χ^2 test. ³Agreed value obtained from both a rank test and the χ^2 test.

Microbial Alterations in Colo-Rectal Cancer



Current Opinion in Physiology

Sayed et al. Curr Opin Physiol. 2021, 22:100451.

Fusobacterium Nucleatum and CRC





Microbial sequences

(101,000 reads; median per sample)





PathSeg analysis

Is *F* nucleatum a Single **Organism Pathogenesis?**



Xu et al. Front Microbiol. 2023 Mar 21;14:1100873.

Is F nucleatum Ready for Practice?

Metronidazole improved survival in mice with CRC with *F nucleatum*

? Targeted antibiotics

? Targeted microbiome therapeutics

Diets that may promote intestinal inflammation, based on EDIP score

Higher risk of *F nucleatum* – positive CRC but not CRC that do not contain these bacteria

Bullman S et al. Science. 358(6369): 1443–1448; Liu et al. Clin Gastroenterol Hepatol. 2018 Oct;16(10):1622-1631.e3.

How Does Dysbiosis Relate to Carcinogenesis?

- No accepted quantitative definition of a 'normal' microbiome
- Persistent departure from a homeostatic state, towards a cancer promoting and/or sustaining phenotype



Dysbiosis is specific to an individual, the disease and the ecological niche

Gilbert et al. Nature Medicine. 24, 392–400; Scott et al. Gut. 68(9): 1624–32.

Microbiome Interactions with Carcinogenesis



Rahman et al. Biomed & Pharmacother. 149 (2022) 112898.

Microbiome and Cancer Biology



Rahman et al. Biomed & Pharmacother. 149 (2022) 112898.

What's Happening in Therapeutics?



Search conducted on April 10, 2023. Cancer Res. 2019;79(13 Suppl): Abstract nr 2839; VedantaBiosciences.com.

ClinicalTrials.gov

Microbiome therapeutic in metastatic RCC



Dizman et al Nature Medicine 28, pages 704-712 (2022)



Future Directions for Research

Large, international cohort studies

Prospective longitudinal sampling

More focus on interventional, rather than purely observational studies

Integration of microbiome analysis with other oncological research projects

Standardization and transparency in reporting microbiome research

Where Are We at in 2023?

True associations with *H pylori* and viral Hepatitis

Interactome: A tripartite, multi-directional framework of environment, epigenetic/genetics and the microbiome

No direct evidence: commensal microbiome causes cancer

Plausible mechanisms by which the human microbiome may cause cancer

2023: No microbiome therapeutics available for cancers