

Dietary microbial modulation for colorectal cancer prevention in the Hong Kong Chinese population

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Colorectal cancer (CRC) is one of the most common malignancies worldwide.¹ A higher incidence of CRC is observed in more developed regions than under developed regions, and changes in lifestyle and dietary habits are believed to attribute to this increased incidence.¹ In Hong Kong, CRC has been the most common cancer since 2013, with more than 5000 new diagnoses annually.² The dietary habits of people in Hong Kong have changed from the traditional Chinese diet to include more fast food and processed food with less diversity. Although the association between microbiota and the risk of CRC is indistinct, the undoubted fact is that patients with CRC have less diverse microbiota than their healthy counterparts.³ In this commentary, we discuss the potential benefits of resuming a traditional Chinese diet to mitigate microbial risk in CRC in the Hong Kong Chinese population.

Microbial risk in developing colorectal cancer

Most microbial species in the gastrointestinal tract belong to *Firmicutes*, *Bacteroidetes*, *Proteobacteria*, and *Actinobacteria* species. Gut microbiota form a highly complex ecosystem composed of thousands of species and strains which interact with one another, the substrates, and the host. A patient's risk for CRC may be determined through microbial profiling, with recent evidence showing that altered microbiome environment, or dysbiosis, in the gut and pathogenic bacterial colonies overgrowth has implications for cancer development.^{4,5} Some gut microbiomes—known as CRC microbial markers—have been identified as promoting colorectal tumorigenesis.⁵ Certain unfavourable bacteria, including *Fusobacterium nucleatum*, *Escherichia coli*, *Bacteroides fragilis*, *Clostridium hathewayi*, and *Bacteroides clarus* have been identified to be more abundant in patients with CRC,^{6,7} whereas beneficial bacteria are less abundant.⁸ Moreover, dysbiosis is observed in patients with CRC, among a cluster of chronic diseases, such as, inflammatory bowel disease, diabetes mellitus, and obesity.^{9,10} The commonality among these diseases is chronic inflammation, which is an important factor in the

development of CRC. Some microbiomes induce inflammation via lipopolysaccharides, whereas others are correlated with elevated serum C-reactive protein.¹¹ Whatever the cause of the change in microbiota, the abnormality in composition is a potentially important aetiological factor in the initiation and progression of CRC, and diet is undeniably a key player.¹²

Westernisation is a global phenomenon

The American Institute for Cancer Research and the World Cancer Fund¹³ recommend a diet that is high in fibre, rich in whole grains, and has little or no red meat or processed meat to reduce the risk of cancer development. In contrast, contemporary diets in Hong Kong and other developed regions are low in fibre, high in processed foods including food additives, refined sugar, and hydrogenated fats.^{14,15} In a study comparing the cancer risk in rural Africans with that in African Americans, the higher fibre, lower animal fat, and lower protein in the rural African diet were associated with reduced cancer risk.^{16,17} Ou et al¹⁶ also reported that microbial metabolites moderated by dietary intake can influence CRC risk. Nevertheless, different dietary components may have various effects on CRC risk. The current literature on microbial-diet-host interaction is diverse and includes metabolic cross-feeding of microbes, substrate degradation of dietary fibres, and microbiome as moderators of host physiology and behaviour.¹⁸

Traditional Chinese diet

One dietary approach in lowering CRC risk involves restoring beneficial gut microbiota, thus strengthening intestinal barrier against pathogenic bacteria, increasing intestinal motility, and lowering a pro-inflammatory state.^{19,20} This can be achieved by adopting a diversified diet such as the Mediterranean diet, which is high in vegetables and legumes; high in fruits; high in grains; moderate in plant protein rather than animal protein; and moderate in dairy. The traditional Chinese diet shares some of these

characteristics. Woo et al¹⁴ found that the dietary habits of the Chinese population in four major cities, evaluated using the Mediterranean Diet Score, were compatible with, if not closer to adhering to, the Mediterranean diet than those of the Greek population. The authors found that cuisines varied yet remained culturally distinctive, and the only sub-populations in Hong Kong with less adherence to the Mediterranean diet were the younger generation and men, with 50% and 51%, respectively, achieving a high Mediterranean Diet Score.¹⁴ The authors also found that the Mediterranean Diet Score was indicative of the preservation of traditional Chinese dietary habit, with scores of at least 80% from a rural Chinese population.¹⁴

Conclusion

Hippocrates once said, “All disease begins in the gut.” Although not completely true, the trillions of microbes that live on our skin and within our body are crucial to human health. Although there is a lack of definitive causation between microbiota and CRC, the synergetic effect of a diversified diet can improve the overall anti-inflammatory prospects of the host and promote a healthy gut by creating a balanced microbiome. With further mechanistic studies to understand the multi-axial microbial-diet-host interaction, we hope to deduce a microbiota-driven dietary recommendation decision tree to optimise the growth and balance of gut microbiota.

Author contributions

Concept or design: WYY Lin.

Acquisition of data: WYY Lin.

Analysis or interpretation of data: WYY Lin.

Drafting of the manuscript: WYY Lin.

Critical revision of the manuscript for important intellectual content: SC Ng and FKL Chan.

All authors had full access to the data, contributed to the study, approved the final version for publication, and take responsibility for its accuracy and integrity.

Conflicts of interest

All authors have disclosed no conflicts of interest.

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References

- Allemani C, Matsuda T, Di Carlo V, et al. Global surveillance of trends in cancer survival 2000-14 (CONCORD-3): analysis of individual records for 37 513 025 patients diagnosed with one of 18 cancers from 322 population-based registries in 71 countries. *Lancet* 2018;391:1023-75.
- Wong KH. Overview of Hong Kong Cancer Statistics of 2018. Hong Kong Cancer Registry. Available from: <https://www3.ha.org.hk/cancereg/pdf/overview/Overview%20of%20HK%20Cancer%20Stat%202018.pdf>. Accessed 6 Apr 2022.
- Ahn J, Sinha R, Pei Z, et al. Human gut microbiome and risk for colorectal cancer. *J Natl Cancer Inst* 2013;105:1907-11.
- Cozen W, Yu Y, Hwang A, et al. Association between fecal microbiome and colon adenomas and hyperplastic polyps in monozygotic twins. *Twin Res Hum Genet* 2017;20:620.
- Yang Y, Li L, Xu C, et al. Cross-talk between the gut microbiota and monocyte-like macrophages mediates an inflammatory response to promote colitis-associated tumorigenesis. *Gut* 2020;70:1495-506.
- Sears CL, Garrett WS. Microbes, microbiota, and colon cancer. *Cell Host Microbe* 2014;15:317-28.
- Liang Q, Chiu J, Chen Y, et al. Fecal bacteria act as novel biomarkers for noninvasive diagnosis of colorectal cancer. *Clin Cancer Res* 2017;23:2061-70.
- Yu J, Feng Q, Wong SH, et al. Metagenomic analysis of faecal microbiome as a tool towards targeted non-invasive biomarkers for colorectal cancer. *Gut* 2017;66:70-8.
- Ijaz UZ, Quince C, Hanske L, et al. The distinct features of microbial ‘dysbiosis’ of Crohn’s disease do not occur to the same extent in their unaffected, genetically-linked kindred. *PLoS One* 2017;12:e0172605.
- Jurjus A, Eid A, Kattar SA, et al. Inflammatory bowel disease, colorectal cancer and type 2 diabetes mellitus: the links. *BBA Clin* 2016;5:16-24.
- Umoh FI, Kato I, Ren J, et al. Markers of systemic exposures to products of intestinal bacteria in a dietary intervention study. *Eur J Nutr* 2016;55:793-8.
- Irrazábal T, Belcheva A, Girardin SE, Martin A, Philpott DJ. The multifaceted role of the intestinal microbiota in colon cancer. *Mol Cell* 2014;54:309-20.
- Clinton SK, Giovannucci EL, Hursting SD. The World Cancer Research Fund/American Institute for Cancer Research Third Expert Report on diet, nutrition, physical activity, and cancer: impact and future directions. *J Nutr* 2020;150:663-71.
- Woo J, Woo KS, Leung SS, et al. The Mediterranean score of dietary habits in Chinese populations in four different geographical areas. *Eur J Clin Nutr* 2001;55:215-20.
- Jew S, AbuMweis SS, Jones PJ. Evolution of the human diet: linking our ancestral diet to modern functional foods as a means of chronic disease prevention. *J Med Food* 2009;12:925-34.
- Ou J, Carbonero F, Zoetendal EG, et al. Diet, microbiota, and microbial metabolites in colon cancer risk in rural Africans and African Americans. *Am J Clin Nutr* 2013;98:111-20.
- O’Keefe SJ, Li JV, Lahti L, et al. Fat, fibre and cancer risk in African Americans and rural Africans. *Nat Commun* 2015;6:6342.
- Henriques SF, Dhakan DB, Serra L, et al. Metabolic cross-feeding in imbalanced diets allows gut microbes to improve reproduction and alter host behaviour. *Nat Commun* 2020;11:4236.
- Gutiérrez-Díaz I, Fernández-Navarro T, Sánchez B, Margolles A, González S. Mediterranean diet and faecal microbiota: a transversal study. *Food Funct* 2016;7:2347-56.
- De Filippis F, Pellegrini N, Vannini L, et al. High-level adherence to a Mediterranean diet beneficially impacts the gut microbiota and associated metabolome. *Gut* 2016;65:1812-21.