

Original Article

Gut Microbiota Differences Between Colorectal Cancer Patients and Healthy Individuals: Preliminary Findings from Central Taiwan

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Key Words

Colorectal cancer (CRC);

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Purpose. Colorectal cancer ranks third in incidence in Taiwan. Emerging evidence suggests that gut microbiota plays a role in its development. This study aims to investigate the relationship between microorganisms and colorectal cancer in Taiwan and to establish a regional gut microbiome profile.

Materials and Methods. Fecal samples from 133 healthy adults and 131 patients with colorectal cancer were analyzed using 16S rRNA sequencing. Alpha and beta diversity analyses were conducted to assess differences in species, followed by statistical analysis of microbial metabolites.

Results. Healthy individuals showed significantly higher microbial diversity than patients with colorectal cancer. Notably, *Collinsella aerofaciens*, *Eubacterium hallii*, and *Lachnospiraceae* (particularly *Blautia*) were more abundant in the healthy group. *Blautia* may have a protective effect, as suggested by prior literature. Metabolite analysis revealed that healthy subjects favored L-glutamate and L-glutamine biosynthesis, whereas patients with colorectal cancer showed increased pyruvate fermentation to acetone.

Conclusions. This study confirms reduced gut microbiota diversity in patients with colorectal cancer, highlighting a potential link between microbial imbalance and carcinogenesis. These findings provide insights for the development of future cancer prevention strategies. Further studies with larger cohorts and more in-depth metabolite analysis are warranted.

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One of the most common cancers is gastrointestinal cancer, and environmental, genetic, and bacterial factors influence its development. A diverse spectrum of pathogens comprises the gut microbiota, which is crucial for maintaining gut health. Problems in bacterial stability, known as microbiome dysbiosis, have been associated with inflammation and tumor

growth.¹ Key bacterial strains, such as *Fusobacterium nucleatum*, *Bacteroides fragilis*, and *Escherichia coli*, have been suggested by western literature as potential donors to colorectal cancer (CRC).² However, microbiota composition is influenced by local factors, making it necessary to create localized bacterial profiles. In this review, bacterial differences between patients

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with CRC and healthy individuals in Central Taiwan are examined, and changes throughout their tumor microenvironment are discussed.

Materials and Methods

The study aims to compare the gut microbiota of healthy individuals and patients with CRC in Central Taiwan. It also aims to examine differences in their metabolic profiles.

Study design

The study is conducted at China Medical University Hospital since 2023 August to 2024 December. The healthy control samples were obtained from fecal donations voluntarily provided by healthy individuals undergoing routine health checkups at China Medical University Hospital Health Screening Center. The CRC samples were obtained from the bio-film or fecal matter collected from surgical pathology specimens of patients with CRC. Inclusion criteria included clinically diagnosed patients with CRC. Exclusion criteria included: 1. Pathology report not confirming adenocarcinoma. 2. The use of antibiotics within three weeks of sample collection. A total of 131 patients with CRC and 133 healthy controls were included in the research. Two CRC patients were diagnosed with tumors other than adenocarcinoma, and three patients received antibiotics before the sample collection. Therefore, the final samples include 129 healthy individuals and 128 patients with CRC.

Samples analysis

Post-operatively, tumor-associated mucus and intestinal samples were collected. For 16S rRNA sequencing, which targets the V3-V4 and V7-V9 regions, microbial RNA was extracted. Liquid chromatography–mass spectroscopy (LC–MS) was employed to analyze metabolic changes. Statistical analyses were used to assess bacterial variations, including the Mann–Whitney U and Kruskal–Wallis tests.

Results

Characteristics of the patients

Among 128 patients with CRC, 73 were male (57%) and 55 were female (42%), with a median age of 65. The average body mass index (BMI) was 24 (Table 1). The healthy control samples were obtained from fecal donations voluntarily provided by healthy individuals undergoing routine health checkups at China Medical University Hospital Health Screening Center.

Microbiota composition and diversity

The analysis of gut microbiota is divided into four main sections: A. Alpha diversity, B. Beta diversity, C. Microbial variations, D. Functional prediction and metabolic analysis. Each section includes several specific measures described below.

A. Alpha diversity – comparison between groups

A1. Species evenness

This measures how evenly microbial species are distributed within a sample. In our study, the healthy group showed significantly higher species evenness compared to the CRC group. The difference was statistically sig-

Table 1. Characteristics of the patients

Characteristics	Healthy controls N = 129 (50%)	CRC patients N = 128 (50%)
Sex		
Male	62 (48.06%)	73 (57.03%)
Female	67 (51.93%)	55 (42.96%)
Mean age (yrs)	61	65
Mean BMI	24	24
Family history	0 (0%)	10 (7.81%)
Cancer stage		
I		24 (18.75%)
II		40 (31.25%)
III		41 (32.03%)
IV		23 (17.96%)
Location		
Cecum		9 (7.03%)
Ascending		21 (16.40%)
Transverse		15 (11.71%)
Descending		8 (6.25%)
Sigmoid		39 (30.46%)
Rectum		36 (28.12%)

nificant, with a Kruskal–Wallis test p -value of 6.8×10^{-5} ($p < 0.01$). Higher evenness indicates that various bacteria species are present in similar proportion, without one dominating the others. Greater microbial evenness is often linked to a more stable gut environment, whereas lower evenness may suggest microbial imbalance, which is commonly seen in CRC, where certain bacterial may become dominant³ (Fig. 1).

A2. Faith's phylogenetic diversity

This index considers the evolutionary distances among microorganisms in a sample. When the species present are more distantly related, the phylogenetic

diversity is higher. This approach gives a broader picture than just counting species. Higher phylogenetic diversity is usually associated with a more resilient and adaptable microbial community. However, our data reported a p -value of 0.517 ($p > 0.01$) and did not show a significant difference between healthy adults and patients with CRC⁴ (Fig. 2).

A3. Observed species count

This indicates the number of bacterial species detected in a sample. A higher count suggests a more diverse microbial population, often observed in a healthy gut. In contrast, reduced species counts were observed

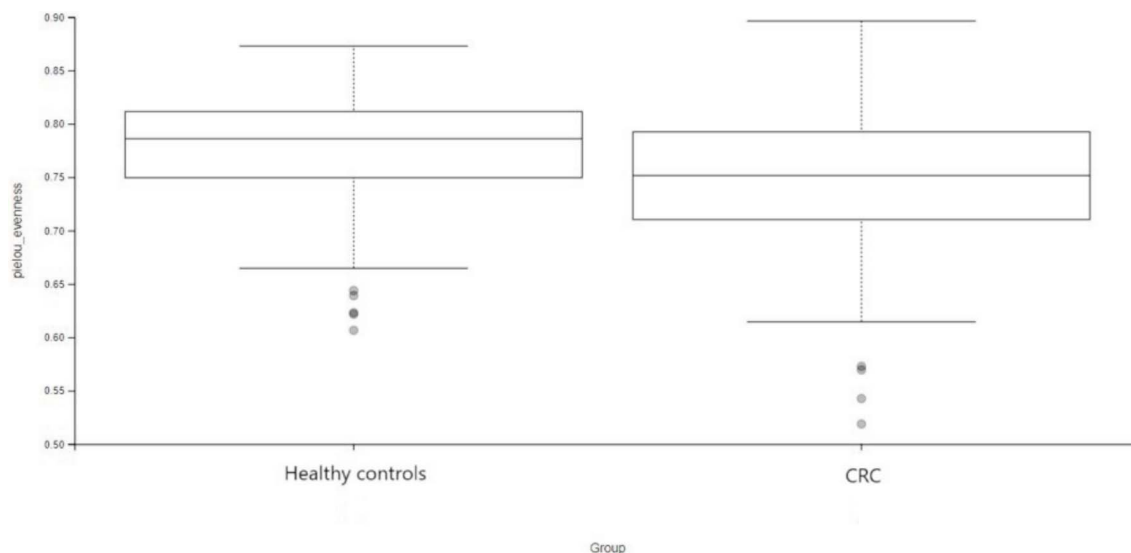


Fig. 1. Evenness: Measures the uniformity of species distribution within a sample.

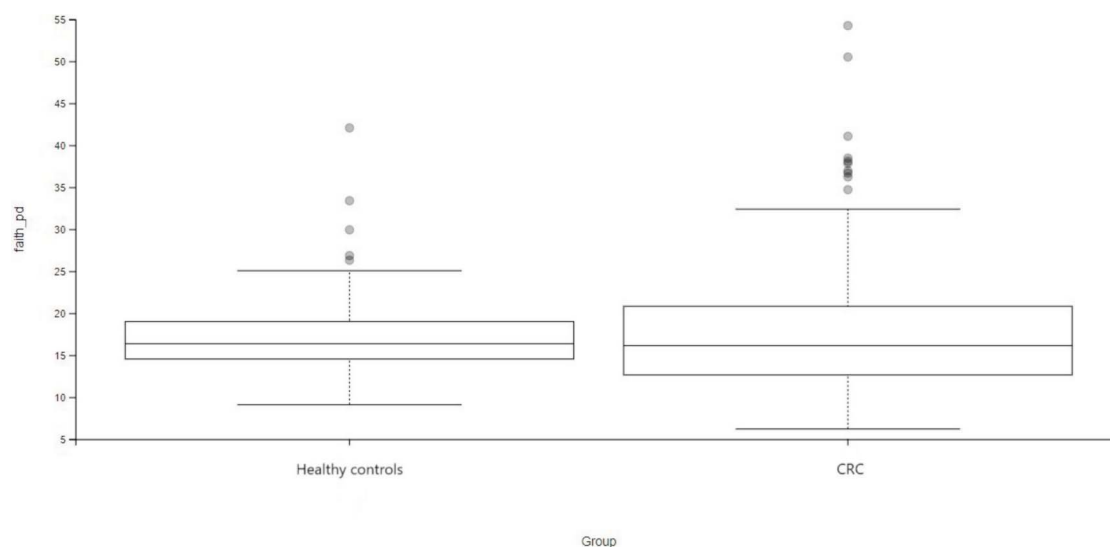


Fig. 2. Faith Phylogenetic Diversity: Considers the phylogenetic distance among microorganisms.

in patients with CRC, which may reflect dysbiosis and disease progression.³ The Kruskal–Wallis pairwise test showed a statistically significant difference between the two groups, with a p -value of 2.35×10^{-12} . This extremely low p -value indicates a highly significant difference in the measured parameter between the healthy group and CRC group, suggesting that the observed variation is unlikely due to chance (Fig. 3).

A4. Shannon index

The Shannon index accounts for both species' richness and evenness. It measures how many different species are present and how evenly they are distributed. A higher Shannon index reflects a well-balanced, diverse microbiome and is often found in healthy individuals. As observed in patients with CRC, lower values may reflect a disrupted microbial community dominated by specific species. The associated p -value was 3.03×10^{-10} in this study, indicating a highly significant difference between the two groups, with a significantly lower Shannon index in the CRC group indicating poor microbiota diversity in patients with CRC (Fig. 4).

B. Beta diversity – comparison between individual samples

B1. Principal coordinate analysis (PCoA)

The principal coordinates analysis (PCoA) illus-

trates the beta diversity of gut microbiota between CRC and healthy people. Similar bacteria melodies can cluster closely together, but samples with different microbial profiles can be found farther off. Blue dots represent CRC individuals, while red dots represent healthy controls. CRC individuals exhibit greater dispersion, which indicates increased inter-individual variation, whereas healthier people cluster more closely, suggesting a more consistent microbial composition.⁵ This difference highlights dysbiosis frequently associated with CRC and reflects specific microbial group structures. Moreover, in CRC studies, microbial profiles in samples from healthy individuals typically cluster more strongly than those from patients with CRC, showing a shift in bacterial compositions during tumor development (Fig. 5).

B2. Differential abundance analysis

This analysis compares the abundance of microbes between individual samples. It is often shown according to the taxonomic hierarchy: Kingdom, Phylum, Class, Order, Family, Genus, Species. This helps identify which bacteria are significantly more or less abundant in patients with CRC than in healthy adults. For example, the proportion of *F. nucleatum* may be significantly higher in samples from the CRC group, whereas members of the *Lachnospiraceae* family may be more common in samples from the healthy individuals (Fig. 6).

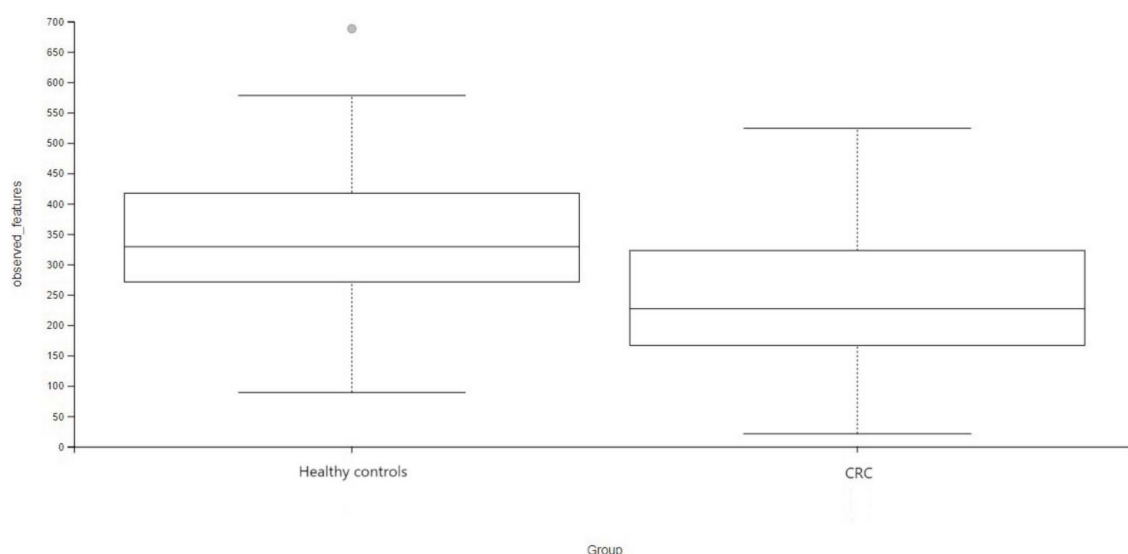


Fig. 3. Observed Species Count: Reflects the actual number of bacterial species detected in the sample.

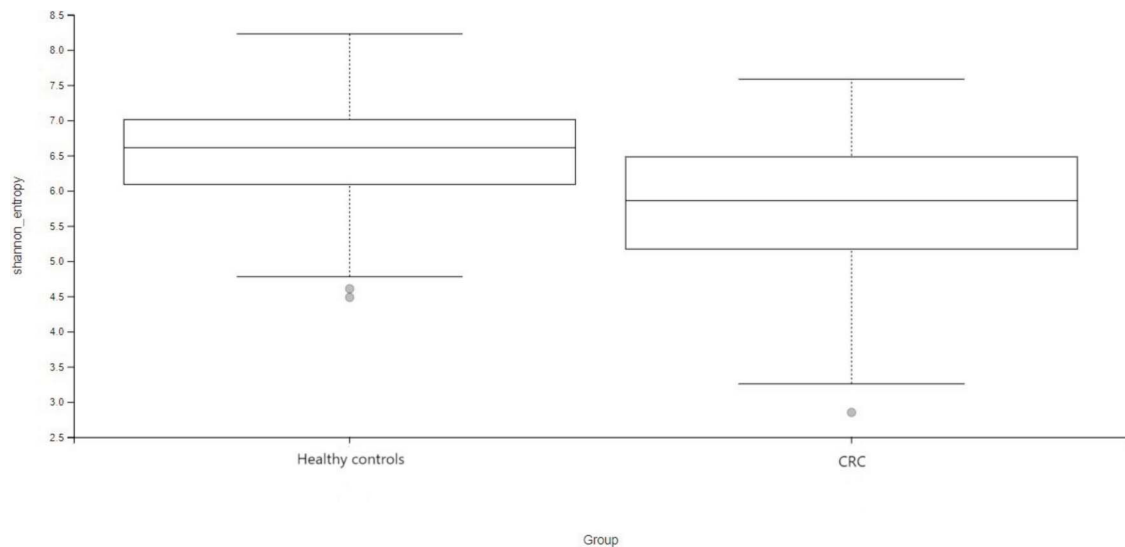


Fig. 4. Shannon Index: Evaluates microbial diversity based on richness and evenness.

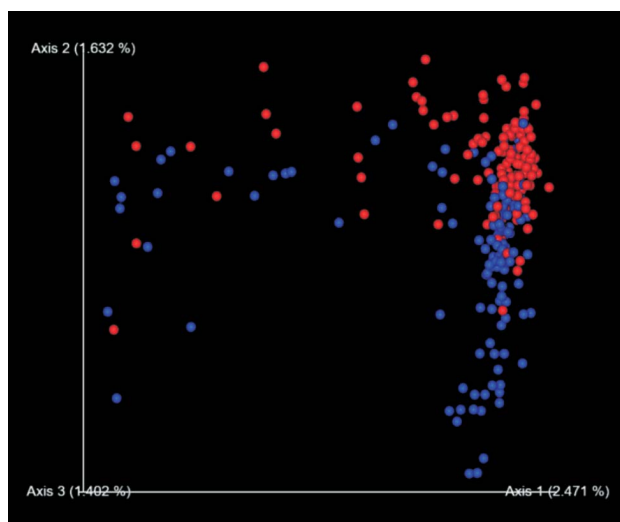


Fig. 5. PCoA visualizes sample similarity, typically displayed in 2D or 3D scatter plots. Closer points indicate more similar microbial compositions. Red bullet: healthy group. Blue bullet: CRC group.

C. Microbial variations

We analyzed the twenty most significantly enriched microbial species in each group using Mann-Whitney U test and Benjamini-Hochberg FDR adjusted p -values (Table 2 and 3). In samples from patients with healthy individuals an increase in cases of *Collinsella aerofaciens*, *Eubacterium hallii*, and *Lachnospiraceae Blautia* (Table 2) were observed, whereas CRC, more cases of *Escherichia-Shigella*, *B. fragilis*,

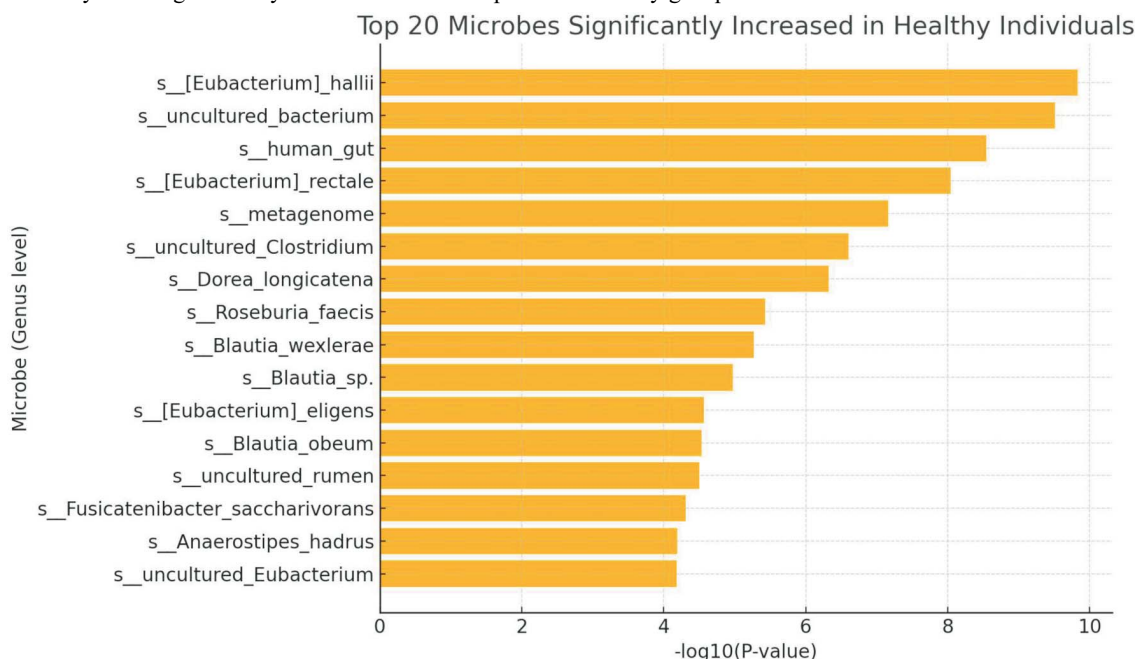
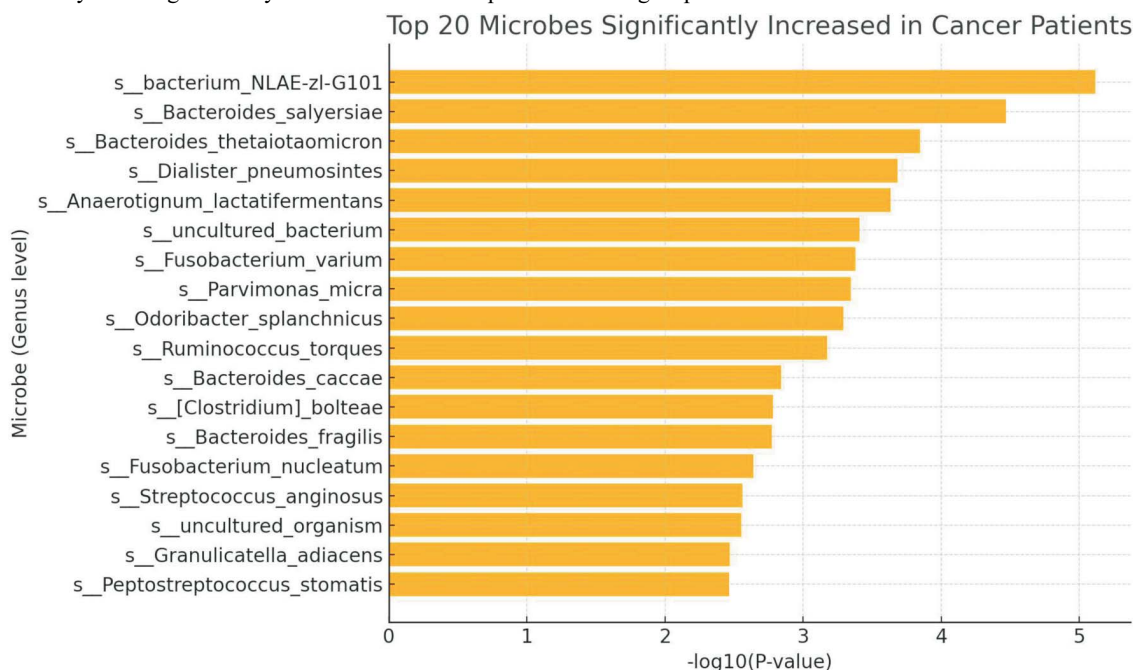


Fig. 6. Differential abundance analysis.

and *F. nucleatum* (Table 4). The findings will be further discussed in the Discussion section.

D. Functional prediction and metabolic analysis

Functional prediction includes two categories: 1. Pathway and 2. Enzyme Commission (EC). In microbiota analysis, these methods are commonly used to infer the metabolic potential of microbial communities based on sequencing data, often derived from 16S rRNA. Pathway prediction provides insights into potential biological processes, whereas EC analysis iden-

Table 2. Twenty most significantly enriched microbial species in healthy group.**Table 3.** Twenty most significantly enriched microbial species in CRC group.

tifies the enzymes that may be responsible for carrying them out. Both are inference-based methods and rely on reference genome databases; therefore, metagenomic or transcriptomic data validation is recommended.⁶ The final goal is to estimate how microbes contribute to host physiology or environmental functions.

Significant differences between the two groups were found in metabolic analysis. The synthesis of L-glutamate and L-glutamine, which are necessary for colon homeostasis, was enhanced in healthy individuals. In comparison, patients with CRC exhibited increased triglyceride fermentation, a metabolic switch

Table 4. Summary of top 5 significantly enriched microbes in healthy and CRC groups

Group	Microbiota name	Taxonomy	<i>p</i> -value (exact <i>p</i> -value)
CRC	Lachnoclostridium (bacterium NLAE-zl-G101)	Lachnospiraceae family, Lachnospirales order	< 0.001 (7.690 ⁻⁶)
	Bacteroides salyersiae	Bacteroidaceae family, Bacteroidales order	< 0.001 (3.410 ⁻⁵)
	Bacteroides thetaiotaomicron	Bacteroidaceae family, Bacteroidales order	< 0.001 (1.420 ⁻⁴)
	Dialister pneumosintes	Veillonellaceae family, Veillonellales-Selenomonadales order	< 0.001 (2.070 ⁻⁴)
	Tyzzzeria (Anaerotignum lactatifermentans)	Lachnospiraceae family, Lachnospirales order	< 0.001 (2.320 ⁻⁴)
Healthy	[Eubacterium] hallii	Lachnospiraceae family, Lachnospirales order	< 0.001 (1.500 ⁻¹⁰)
	Uncultured Blautia bacterium	Blautia genus, Lachnospiraceae family	< 0.001 (3.090 ⁻¹⁰)
	Blautia (human gut)	Blautia genus, Lachnospiraceae family	< 0.001 (2.870 ⁻⁹)
	[Eubacterium] rectale	Agathobacter genus, Lachnospiraceae family	< 0.001 (9.090 ⁻⁹)
	Monoglobus (metagenome)	Monoglobaceae family, Monoglobales order	< 0.001 (6.960 ⁻⁸)

favoring tumor survival (Table 5). EC analysis also revealed significant categorical differences between the two groups; however, no specific biological relevance has been identified in the current literature (Table 6). Further analysis will be discussed in Sections 4.5 and 4.6.

Discussion

CRC is one of the most pervasive malignancies in the world is colorectal cancer (CRC), which has been increasingly linked to gut microbiota dysbiosis. The gut microbiota refers to the complex ecosystem of trillions of microorganisms — including bacteria, viruses, fungi, and archaea — that reside in the human intestine. These microorganisms play a significant role in several physiological processes, including bowel homeostasis, defense immune regulation, and metabolism. This bac-

terial community has been linked to CRC progression advancement and growth because of an imbalance known as microbial dysbiosis microbiome.

Theoretical opinions on cancer development and microbiota

Two fundamental philosophical systems support the study of gut microbiota and CRC growth. The first is the microbiome hypothesis, which claims that several biochemical and immune functions are disrupted by an imbalance in the gut microbiota composition, leading to severe inflammation and cancer. In this hypothesis, the gut's loss of beneficial bacteria, including *Bifidobacterium* and *Faecalibacterium*, is combined with the proliferation of harmful bacteria, such as *F. nucleatum* and *B. fragilis*, providing a favorable environment for carcinogenesis.⁷ The Cyst Micro-environment and Microbiota Interaction Model, the second model, suggests that bacterial communities actively shape the tumor microenvironment, influencing immune responses and cancer cell proliferation. Some bacteria, such as *F. nucleatum*, have been shown to inhibit cluster of differentiation (CD)8+ T cell growth, thereby preventing tumors from evading defense rec-

Table 5. Pathway prediction in each group

Healthy controls pathway analysis	CRC pathway analysis
L-glutamate and L-glutamine	Pyruvate fermentation to acetone

Table 6. EC prediction in each group

Healthy controls EC analysis	CRC pathway EC analysis
Sortase A	Pyruvate fermentation to acetone
Serine-type D-Ala-D-Ala carboxypeptidase	K ⁺ -transporting ATPase
Beta-glucosidase	Ribonucleoside-diphosphate reductase

ognition.⁸ In contrast, certain species, such as *Blautia* from the *Lachnospiraceae* family, lead to tumor suppression by enhancing anti-cancer resistance.⁹

While incorporating findings from our study conducted in Central Taiwan, this literature review summarizes current research on the role of gut microbiota in CRC.

CRC microbial dysbiosis

The findings from this study suggest that gut microbiota composition of patients with CRC and healthy individuals differs considerably. Numerous studies have demonstrated that patients with CRC exhibit a marked increase in microbial diversity, a key sign of colon health. A shift toward infectious bacterial communities, which disrupt normal intestinal functions, contributes to the decline in microbial diversity, a condition known as dysbiosis.¹⁰

According to several studies, patients with CRC exhibit substantially lower alpha diversity, which determines an individual's microbial diversity and diversity level. In patients with CRC, lower Shannon index ratings have constantly been reported, indicating a decline in bacterial diversity. Our study supports these findings, demonstrating a statistically significant ($p < 0.05$) decrease in microbial diversity among patients with CRC in Central Taiwan.

Alpha diversity, which measures how different bacterial compositions differ between people, has also been thoroughly studied. PCoA results have demonstrated that the gut microbiota of patients with CRC forms distinct clusters compared to that of healthy individuals, which indicates divergence. Our investigation further supports these findings. PCoA revealed a clear distinction in gut microbial composition between healthy individuals and patients with CRC, indicating a fundamental shift associated with CRC.

CRC-associated bacteria

Recent research has demonstrated that certain bacterial species are essential for the development of CRC. Furthermore, CRC has been constantly linked

to pathogenic bacteria, contributing to its growth through various mechanisms.

F. nucleatum is one of the most well-known CRC-associated bacteria. This species has been shown to promote tumor development and immune evasion by binding to tumor tissue and preventing immune responses.¹¹ The ability of *F. nucleatum* to suppress CD8⁺ T cell function can diminish the ability of the body to recognize and eliminate carcinogenic cells. In line with our earlier results and supporting its contribution to intestinal carcinoma, our research found a major increase of *F. nucleatum* in the samples from patients with CRC.¹²

B. fragilis is another important bacterial type implicated in CRC. Enterotoxins are produced by some *B. fragilis* strains that are key contributors to CRC growth, both of which can damage DNA and cause severe inflammation.¹³ In intestinal epithelium cells, colibactin, a genotoxin that increases the risk of developing tumors, is produced, similarly to *Escherichia coli*.

Some bacterial species have been suggested to protect against CRC, in contrast to these harmful microbes. Recent research has demonstrated that *Blautia* from the *Lachnospiraceae* family has the ability to maintain colon homeostasis and inhibit tumor growth.⁹ Our research supports this hypothesis, as we found that *Blautia* from the *Lachnospiraceae* family was more abundant in healthy individuals than in patients with CRC, suggesting a potential protective role against cancer.

Microbial metabolites and CRC growth

Various molecules that the gut microbiota produce have various effects on CRC growth. Depending on the biological makeup and the microbial composition of the host, these metabolites have the potential to either inhibit or promote tumor development.

Short-chain fatty acids (SCFAs), which are beneficial microbial metabolites, have gained considerable attention for their role in maintaining gut health. SCFAs, such as butyrate and propionate, have demonstrated anti-inflammatory and anti-carcinogenic properties by supporting apoptosis in cancer cells and

reducing severe inflammation.¹⁴ In this study, we found that the gut microbiota of healthy individuals was associated with higher levels of L-glutamate and L-glutamine biosynthesis, which may help maintain colonic health by maintaining colon barrier integrity and altering immune responses.

On the other hand, tumor-promoting microbial metabolites have also been found. For instance, triglyceride fermentation to acid has been linked to CRC physiological programming, which provides an energy supply for cancer cell development. According to our study, patients with CRC showed a physiological shift that converted triglyceride to acetate, which suggests that this metabolic pathway may be involved in the progression of CRC.¹⁵

Microbiota's immune modulation by the gut microbiota

The immune system plays a vital role in controlling tumor growth, and gut microbiota can significantly affect immune responses in the tumor microenvironment. *F. nucleatum*, a well-known example, has been shown to inhibit CD8+ T cell activity, enabling cancer cells to escape immune surveillance.²

Emerging evidence points to the potential benefits of some beneficial bacteria for improving tumor resistance. According to some studies, members of the *Lachnospiraceae* community might facilitate the detection of tumor-infiltrating CD8+ T cells by promoting immune responses.¹⁶ This hypothesis needs to be validated further, and the potential immunomodulatory effects of *Lachnospiraceae* must be explored.

Research gaps and limitations in existing literature

There are still major gaps in literature despite the significant progress in establishing stomach microbiota's commitment to CRC. A major obstacle is the lack of region-specific information. Although a lot of research has been done in American groups on CRC-associated bacteria, little is known about Asian bacterial versions. Our analysis addresses this issue by uncovering fascinating insight into the gut microbiota of

CRC residents in central Taiwan.

Additionally, protective bacteria benefits are contradictory. While some research links *Lachnospiraceae* family's ability to protect against CRC,⁹ other analyses have contradictory conclusions.¹⁷ Our findings support the protective hypothesis, which suggests that *Lachnospiraceae* *Blautia* might be involved in tumor suppression.

Also, the CRC study's findings regarding microbial metabolites are conflicting. While some research emphasizes the SCFAs' anti-cancer properties, people speculate that certain compounds may promote tumor growth in particular circumstances. Our study adds to this debate by exhibiting various physiological shifts in CRC patients. Our findings support earlier studies on cancer development and gut dysbiosis, and they also show a significant decrease in CRC people's microbial diversity. *Bacteroides fragilis* and *Fusobacterium nucleatum* in CRC users suggest they are involved in tumor-promoting methods, like immune evasion and inflammation. *Bacteroides thetaiotaomicron*'s place impacts immune responses and malignancy survival in making short-chain fatty acids like propionate.¹⁸ Depending on the CRC stage, *Lachnoclostridium* is known to develop butyrate, a potential tumor protein.¹⁹ These biological swings can be understood to aid in creating specific medical and therapeutic plans.

Limitation

This study has several limitations. First, most patients with left-sided colorectal cancer underwent bowel preparations before sample collection. Although biofilm or feces samples were scraped directly from the tumor surface, the potential impact of bowel preparation on microbiota composition remains unclear and requires further investigation. Second, many stage IV patients received systemic therapies, including chemotherapy. These treatments may significantly alter gut microbiota, and their effects are difficult to measure. A separate small-scale analysis excluding patients with prior systemic therapy is planned. Third, dietary data has not been compared between groups, dietary surveys will be used in future studies to allow for proper dietary analysis.

Conclusion

In this study, particular bacterial species that contribute to disease development were identified and insights into the gut microbiota profile of patients with CRC in Central Taiwan were offered. Our results suggest that bacterial imbalance plays a vital role in CRC development, and that certain bacterial taxa may serve as diagnostic markers. Future research will explore the interactions between the lesion environment and microbiome through laboratory-based validation.

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原 著

結直腸癌患者與健康個體腸道菌相差異： 來自台灣中部的初步研究發現

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研究目的 大腸直腸癌在台灣的发生率居第三位。新興證據顯示，腸道菌相在其發病過程中可能扮演關鍵角色。本研究旨在探討台灣地區微生物與結直腸癌之間的關聯，並建立一份區域性腸道菌相圖譜。

材料與方法 本研究分析了 133 位健康成人與 131 位結直腸癌患者的糞便樣本，使用 16S rRNA 定序技術進行菌相分析。透過 Alpha 與 Beta 多樣性分析比較兩組之菌種差異，並進一步進行微生物代謝產物的統計分析。

研究結果 健康族群的腸道菌相多樣性顯著高於結直腸癌患者。特別是 *Collinsella aerofaciens*、*Eubacterium hallii* 與 *Lachnospiraceae* (尤其是 *Blautia*) 在健康組中較為豐富。文獻指出，*Blautia* 可能具有保護作用。代謝分析顯示，健康者較偏向合成 L-麩胺酸與 L-麩醯胺，而癌症患者則傾向於將丙酮酸發酵為丙酮。

結論 本研究確認結直腸癌患者的腸道菌相多樣性明顯降低，顯示菌相失衡可能與癌症發生機制有關。這些發現為未來癌症預防策略的發展提供了新方向，後續仍需擴大樣本數並加強對代謝產物的深入分析。

關鍵詞 大腸直腸癌、腸道菌相、微生物代謝產物、菌相失調、癌症生成。