High occurrence of *Fusobacterium nucleatum* and *Clostridium difficile* in the intestinal microbiota of colorectal carcinoma patients

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Abstract

Colorectal carcinoma is considered the fourth leading cause of cancer deaths worldwide. Several microorganisms have been associated with carcinogenesis, including *Enterococcus* spp., *Helicobacter pylori*, enterotoxigenic *Bacteroides fragilis*, pathogenic *E. coli* strains and oral *Fusobacterium*. Here we qualitatively and quantitatively evaluated the presence of oral and intestinal microorganisms in the fecal microbiota of colorectal cancer patients and healthy controls. Seventeen patients (between 49 and 70 years-old) visiting the Cancer Institute of the Sao Paulo State were selected, 7 of whom were diagnosed with colorectal carcinoma. Bacterial detection was performed by qRT-PCR. Although all of the tested bacteria were detected in the majority of the fecal samples, quantitative differences between the Cancer Group and healthy controls were detected only for *F. nucleatum* and *C. difficile*. The three tested oral microorganisms were frequently observed, suggesting a need for further studies into a potential role for these bacteria during colorectal carcinoma pathogenesis. Despite the small number of patients included in this study, we were able to detect significantly more *F. nucleatum* and *C. difficile* in the Cancer Group patients compared to healthy controls, suggesting a possible role of these bacteria in colon carcinogenesis. This finding should be considered when screening for colorectal cancer.

Key words: oral and intestinal bacteria, colorectal cancer, intestinal microbiota.

Introduction

The human intestinal microbiota is a complex ecological environment that harbors up to 100 trillion bacteria. The collective genome of these intestinal bacteria contains at least 100 times as many genes as there are in the human genome (Ahmed et al., 2007).

It is estimated that the intestinal microbiota comprises 40,000 or more different microbial species (Castellarin et al., 2012), which account for ~50% of the fecal volume (De Cruz et al., 2012). It is known that the intestinal microbiota collaborate with the host in provision of additional metabolic capabilities, protection against pathogens, modulation of the immune system and gastrointestinal development (Frank et al., 2007).

The microbial ecology of the human intestine can be affected by the host environment and dietary habits. Although these effects are not yet completely understood, it has been hypothesized that country-specific dietary habits affect the microbiota development and subsequently host health (Frank et al., 2007).

The human intestinal microbiota has been analyzed using various molecular techniques, such as microarray analysis, quantitative real-time polymerase chain reaction (qRT-PCR), fluorescence *in situ* hybridization (FISH) and metagenomic sequencing as reviewed by Ivanov and Litman (2011). qRT-PCR is advantageous because of its specificity and suitability for quantifying population size (or prevalence) of specific bacterial groups/species. In addition, as a high throughput method qRT-PCR can be used...
to detect specific pathogens in large numbers of clinical samples.

Colorectal carcinoma is considered the fourth leading cause of cancer deaths, estimated to be responsible for approximately 610,000 deaths per year worldwide (WHO, 2011). Although inflammation is a well-established risk factor (McLean et al., 2011), the cause of colorectal carcinoma remains unclear.

Colorectal carcinoma is typically caused by earlier-stage adenomatous lesions or polyps, and analyses for the presence of biological markers (e.g., microbial species) will likely be important for further understanding the development of this inflammatory process. Several risk factors of colon cancer have been identified and include older age (> 50 years-old), personal history of colorectal cancer or polyps, inflammatory intestinal conditions, genetic predisposition, family history, low-fiber and high-fat diet, sedentary lifestyle, diabetes, obesity, smoking, alcohol and cancer radiation therapy (Ponssamy et al., 2011).

In colorectal cancer, several microorganisms have been associated with carcinogenesis, including Enterococcus spp., Helicobacter pylori, enterotoxigenic Bacteroides fragilis and pathogenic E. coli strains (Collins et al., 2010). Oral and intestinal bacteria can alter the intestinal environment and in vivo studies aimed at determining the presence/absence of specific organisms under different host environments and dietary habits, as well as their co-occurrence with specific risk factors and biological markers (e.g., diabetes, obesity, smoking, alcohol, radiation therapy, adenomatous lesions), would likely provide novel insights into the microbiota-carcinoma relationship.

Oral microorganisms are capable of producing infectious diseases, including endocarditis, acute appendicitis, gastrointestinal diseases, lung and brain abscesses and periodontal diseases (Nakano et al., 2007). These anaerobic bacteria are found in subgingival biofilms and have a well-established association with periodontitis (Signat et al., 2011). Among these, Fusobacterium nucleatum is most frequently detected in the oral cavity (presumably because of its role as bridge between early and later colonizers) and is the most common bacteria in both healthy and diseased oral cavities (Castellarin et al., 2012). In addition to F. nucleatum, other periodontal bacteria (e.g., Porphyromonas gingivalis and Prevotella intermedia) are involved in human and animal periodontal diseases and have pro-inflammatory properties (Castellarin et al., 2012).

Recent studies have detected a prevalence of oral fusobacteria (mainly F. nucleatum) in tissues from colorectal cancer patients and shown that strains isolated from inflamed biopsy tissue of intestinal disease patients display a more invasive phenotype (Strauss et al., 2011). Since oral and intestinal microorganisms have been implicated in gastrointestinal disorders, here we qualitatively and quantitatively evaluated the presence of these microorganisms in the fecal microbiota of colorectal cancer patients and healthy controls.

**Material and Methods**

**Cohort and sample collection**

Seventeen patients (13 male, 4 female) between 49 and 70 years-old (mean age: 60 years) visiting the Cancer Institute of the Sao Paulo State (Sao Paulo, SP, Brazil) were included in the study. Among these, 7 patients (5 male, 2 female) displaying polyps, tumors and an inflamed area were diagnosed with colorectal carcinoma (by colonoscopy). The remaining 10 patients (8 male, 2 female) did not present polyps, tumors, abnormal areas or inflammation and were considered healthy. Fecal samples were collected 2 d before colonoscopy. Patients who had taken antibiotics or with any systemic infection were excluded. All patients were asked to participate in this study and provided written informed consent. This study was approved by the Ethic Committee of the Biomedical Science Institute at University of Sao Paulo (CEPSH-1165).

**Bacterial quantitative determination**

Bacterial DNA from feces was obtained using a commercial QIAamp DNA Stool Mini Kit (QIAGEN, Hilden, Germany) according to the manufacturer’s instructions. DNA was stored at -80 °C until use.

The quantitative determination of oral and intestinal microorganisms (F. nucleatum, P. gingivalis, P. intermedia, Clostridium difficile, Clostridium perfringens, B. fragilis, Bacteroides vulgatus, Parabacteroides distasonis, Lactobacillus spp., Bifidobacterium spp., and Escherichia coli) was performed by qRT-PCR (SybrGreen detection system). DNA amplification was performed in final volumes of 20 μL, containing 10 μL of 2X Go Taq qPCR Master Mix (Promega), 5 μM of each primer and ultra-pure water (Table 1) using a Rotor Gene 6000 instrument (Corbett Life Science, Mort lake, New South Wales, Australia). Cycling parameters were as follows: 95 °C for 10 min (initial denaturation); 40 cycles of 95 °C for 15 s and a primer pair-specific annealing temperature (see Table 1) for 60 s. A melting curve was used to evaluate the presence of primers-dimers. All primer sequences were analyzed using the NetPrimer Analysis Software (http://www.premierbiosoft.com/netprimer). The specificities of the primers were predicted by comparison to all available sequences in the BLAST database (www.ncbi.nlm.nih.gov/BLAST).

Standard curves using eight dilution points, in duplicate, were performed with DNA obtained from F. nucleatum ATCC 25586, P. gingivalis ATCC 33277, P. intermedia ATCC 25611, C. difficile VPI 10463, C. perfringens ATCC 13124, B. fragilis ATCC 25285, B. vulgatus ATCC 8482, P. distasonis ATCC 8503, L. acidophilus ATCC 4356, B. bifidum ATCC 1696, and E.
coli ATCC 25922. A no DNA reaction was used as a negative control.

**Statistical Analyses**

The Fischer’s exact test was used to evaluate the influence of sex. Unpaired t-tests were used to assess differences in the bacterial quantification results between the Cancer and Healthy Groups and to test for differences across age groups. A p-value of < 0.05 was considered statistically significant.

**Results**

Patients with cancer were significantly older than patients without cancer (65.4 ± 1.1 vs. 54.8 ± 1.3 years-old, p < 0.0001). Log_{10} values [mean ± standard deviation (SD)] for the copy number per gram of feces were calculated for each microorganism. The number of positive samples and the target copy numbers of each microorganism are shown in Table 2. Most of the evaluated microorganisms were detected in both the Cancer and Healthy Groups.

Statistically significant differences in the qRT-PCR detection limits of *F. nucleatum* and *C. difficile* were detected between the Cancer Group and Healthy Group. For *F. nucleatum* the detection limits were log_{10} 3.5 and 1.0 copies for the Cancer and Healthy Group respectively (p = 0.01). For *C. difficile* the detection limits were log_{10} 1.5 (Cancer Group) and log_{10} 0.4 (Healthy Group) (p = 0.04).

*Clostridium difficile* was more prevalent than *C. perfringens* in cancer patients. We also detected significantly more *C. perfringens* in the Cancer Group than in the Healthy Group (p = 0.04).

*Bacteroides fragilis* was present in both the Cancer (log_{10} 1.4 to log_{10} 8.0) and Healthy Group (log_{10} 0.9 to log_{10} 7.6). *B. vulgatus* was present in all fecal samples, ranging from log_{10} 3.5 to log_{10} 7.6 in the Cancer Group and from log_{10} 0.9 to log_{10} 8.6 in the Healthy Group. *P. distasonis* was detected in all 7 of the cancer patients and in 9/10 healthy patients, with copy numbers ranging from log_{10} 2.1 to 6.6 and log_{10} 3.2 to 7.3, respectively.

*Lactobacillus* (log_{10} 5.3 to 7.8) and *Bifidobacterium* (log_{10} 4.3 to 10.2) species were detected in all 7 cancer patients. *Lactobacillus* was detected in 10/10, and *Bifidobacterium* in 9/10, of the healthy patients, with copy numbers ranging from log_{10} 3.5 to 7.4 and log_{10} 3.9 to 9.3, respectively. *E. coli* was detected in all evaluated patients with values ranging from log_{10} 2.8 to 9.5 (Cancer Group) and log_{10} 1.7 to 9.5 (Healthy Group). We detected no significant difference in the *E. coli* copy number between groups.

### Table 1 - Species-specific oligonucleotides used to the bacterial quantitative detection.

<table>
<thead>
<tr>
<th>Microorganisms</th>
<th>Oligonucleotides</th>
<th>Tm (ºC)</th>
<th>Amplion size (bp)</th>
<th>References</th>
</tr>
</thead>
</table>
| *Fusobacterium nucleatum* | F: CTT AGG AAT GAG ACA GAG ATG  
R: TGA TGG TAA CAT AGC AAA GG | 56      | 120               | Periasamy *et al.* (2009) |
| *Porphyromonas gingivalis* | F: ACC TTA CCC GGG ATT GAA ATG  
R: CAA CCA TGC AGC ACC TAC ATA GAA | 60      | 83                | Nonnenmacher *et al.* (2005) |
| *Prevotella intermedia* | F: CGT GGA CCA AAG ATT CAT CCG TTGA  
R: CCG CTT TAC TCC CCA ACA AA | 55      | 259               | Okamoto *et al.* (1999) |
| *Clostridium difficile* | F: ATT AGG AGG AAC ACC AGT TG  
| *Clostridium perfringens* | F: TCA TCA TTC AAC CAA AGG AGC AAT CC  
R: CCT TGG TAG GCC GTT ACC C | 60      | 105               | Siragusa and Wise (2007) |
| *Bacteroides fragilis* | F: TCR GGA AGA AAG CTT GCT  
R: CAT CCT TTA CCG GAA TCC T | 56      | 162               | Tong *et al.* (2011) |
| *Bacteroides vulgatus* | F: GCA TCA TGA GTC CGC ATG TTC  
R: TCC ATA ATC CCG CAT GTA T | 60      | 287               | Wang *et al.* (1996) |
| *Parabacteroides distasonis* | F: GTC GGA CTA ATA CCG CAT GAA  
R: TTA CCA TCC ATA GAA CCT TCA T | 60      | 273               | Wang *et al.* (1996) |
| *Lactobacillus* spp. * | F: AGC AGT AGG GAA TCT TCC A  
R: ATT YCA CCG CTA CAC ATG | 60      | 380               | Ponnusamy *et al.* (2011) |
| *Bifidobacterium* spp. | F: GCG TGC TTA ACA CAT GCA AGT C  
R: CAC CGG TTT CCA GGA GCT ATT | 60      | 125               | Ponnusamy *et al.* (2011) |
| *Escherichia coli* | F: AGA AGC TTG CTC TTN GCT GA  
R: CTT TGG TCT TGG GAC GTT AT | 57      | 120               | Lee *et al.* (2010) |
Important to verify whether the presence of Porphyromonas gingivalis and Prevotella intermedia in the oral cavity (Signatur et al., 2011) has been associated with several periodontal diseases. This microorganism is considered the most commonly observed microorganism in the subgingival biofilm and is involved in periodontal diseases. Microorganisms are fastidious under atmospheric conditions, however, Porphyromonas gingivalis can produce various fimbriae types that are associated with adherence to different cell surfaces (Sojar et al., 2002). In addition, it is known that Porphyromonas gingivalis and Prevotella intermedia are capable of several adaptive regulatory and metabolic activities that contribute to their pathogenicity (Sojar et al., 2002).

In a study by De Cruz et al. (2012), 6.8% of patients who had undergone colorectal cancer surgery were diagnosed as having C. difficile-associated colitis. Clostridium difficile species (e.g., C. difficile and C. perfringens) in unbalanced ecosystem can produce intestinal inflammatory diseases in humans and animals. Here we report that C. difficile is significantly abundant in both cancer patients and healthy controls (p = 0.04).

Bacteroides fragilis, B. vulgatus and P. distasonis are considered important commensal bacteria in the intestinal resident microbiota of humans and animals. Some species of B. fragilis are able to produce an enterotoxin and these have been detected among strains isolated from colon cancer patients, normal feces and extra-intestinal infections. Due to the low B. fragilis copy number found here, the presence of enterotoxigenic B. fragilis was not evaluated.

Species of Lactobacillus and Bifidobacterium are also commensal bacteria and represent less than 10% of the human oral and intestinal microbiota. These bacteria are considered the most numerous probiotics, and it is suggested that their contribution to the intestinal microbiota might be dependent on age and diet (Zoetendal et al., 2006). Lactobacillus spp. are widely used as probiotics and there is an assumed interaction with the host via the binding of its extracellular pili to human mucus. However, the molecular details of the probiotics signaling mechanisms are not yet understood and it remains to be established whether the effect is direct (e.g., through metabolites or structural components modulating the immune responses of the host) or indirect (via alteration of the intestinal microbiota) (Kankaenen et al., 2009).

Species of Bifidobacterium represent around 3% of the fecal microbiota (approximately 9.4 x 10^6 cells/g of feces).
ces) and are more prominent in the large intestine compared to the terminal ileum. Whereas *Lactobacillus* are more abundant in the distal intestine (proximal region of colon) than in the terminal ileum (Ahmed *et al.*, 2007).

As a commensal microorganism of the human intestinal microbiota, we expected *E. coli* to be present in all clinical samples. Although associations between mucosa-adherent *E. coli* and colorectal cancer have been reported (Arthur *et al.*, 2012), we detected no significant difference in *E. coli* abundance between the patient groups.

Since carcinogenesis is a lengthy and multifactorial process, factors such as diet, habit, ethnicity and environmental exposure might participate in the cancer process (Arthur *et al.*, 2012). Surprisingly, we detected high occurrences of the three evaluated oral microorganisms in our patients. Based on these findings, future studies (i.e., observational and longitudinal studies) should focus on potential roles for these bacteria (especially *F. nucleatum*) during colorectal carcinoma pathogenesis.

Despite the small number of patients evaluated in this study, we detected statistically significant differences in the abundance of *F. nucleatum* and *C. difficile* between healthy and cancer patients, suggesting a possible role of these bacteria in colon carcinogenesis. This finding should be considered when designing screens for colorectal cancer.

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