

# Chapter 11

## Bacterial Infection and Associated Cancers

Caixia Zhu, Yuyan Wang, Cankun Cai, and Qiliang Cai

**Abstract** Bacterial infections were traditionally not considered as major causes of cancer. However, increasing evidence in the past decades has suggested that several cancers are highly associated with bacterial infection. The bacterial infections have evolved some unique strategies including lateral gene transfer, biofilm and microbiome to induce genome instability and chronic inflammation, as well as escape of immune surveillance for carcinogenesis. Here we summarize and highlight the recent progress on understanding of how bacterial infection plays a role in tumor formation and malignancy.

**Keywords** Bacterial infection • Cancer

### 11.1 Introduction

Although viral infection is the main agent of infection-causing cancers in humans, and a number of bacterial pathogens have also been shown to make a significant contribution to cancer [1], research on effects of bacterial infection was left far behind than viral infection. The role of bacterial infection in inducing cancer is still a highly debated subject; in fact, several parameters must be met to be infectious cause of cancer. While the evidence of antibiotics such as aspirin could reduce risks of breast cancer for some time [2, 3], indicating that appropriate bacteria may contribute to the development and progress of particular cancer.

Early observations in 1772, *Mycobacterium tuberculosis* was the first bacterium thought to cause lung cancer, due to active tuberculosis in the lung cancer patient which was more frequently than the general population [4]. However, the *Mycobacterium tuberculosis*-cancer theory failed to stand in many cases test and

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**Table 11.1** The association of bacterial infection with various cancers

Bacterium	Related cancers	References
<i>Helicobacter pylori</i>	Gastric adenocarcinoma	[13]
	Mucosa-associated lymphoid tissue (MALT) lymphoma	
<i>Fusobacterium nucleatum</i>	Colorectal cancer	[23, 34, 35]
	Oral squamous cell carcinoma	
	Pancreatic cancer	
<i>Porphyromonas</i> ssp. ( <i>asaccharolytica</i> , <i>gingivalis</i> )	Colorectal cancer	[23, 34, 35]
	Oral squamous cell carcinoma	
	Pancreatic cancer	
<i>Staphylococci aureus</i>	Mortality of patients with pneumonia?	[39]
<i>Streptococci</i>		
<i>S. VGS</i>	Pediatric acute myeloid leukemia	[41, 42]
<i>S. GBS</i>	Breast cancer	[43]
<i>S. pneumoniae</i>	Leukemia, lymphoma, or myeloma	[44]
<i>S. bovis</i>	Colorectal cancer	[50]
<i>Enterococci faecium</i>	Hematologic malignancies	[52]
<i>Salmonella typhimurium</i>	Gallbladder cancer	[53, 54]

appear to be the results of the malignancy instead of the cause. Despite the early mistake, the possible association of bacterial infection with carcinogenesis continues to be promulgated. A significant breakthrough was made when the chronic infection of *Helicobacter pylori* was identified to cause stomach ulcers followed by onset of gastric carcinomas or MALT (mucosa-associated lymphoid tissue) lymphomas [5, 6]. After the substantial progress in understanding the role of *H. pylori* on carcinogenesis, it has been estimated that bacteria account for at least half of organism infections in patients with malignancy [7]. Here we will address and highlight the relevance of *H. pylori*, oral bacteria, and some gram-positive bacteria with cancers (Table 11.1).

## 11.2 *Helicobacter pylori* and Cancers

*Helicobacter* is spiral-shaped, gram-negative bacterium [8, 9] and was firstly isolated and cultured from a human gastric biopsy by Marshall and Warren in 1982 [10]. The seminal discovery of this bacterium and its role in gastritis and peptic ulcer disease led to award of Nobel Prize of Medicine in 2005 for Marshall and Warren. Unlike other viruses and bacteria, *H. pylori* has the ability to colonize in highly acidic environment within the stomach [11]. The majority of *H. pylori* strains have expressed several virulence factors that have evolved to affect host cell signaling pathways, which included CagA (cytotoxin-associated gene A antigen), VacA (vacuolating cytotoxin), BabA (blood group antigen-binding adhesion), OipA (outer inflammatory protein), and IceA.

It has been estimated that nearly half of the world's population is infected with *H. pylori*, and the majority of colonized individuals could develop chronic inflammation. Despite that *H. pylori* colonization does not absolutely cause symptoms [12], long-term carriage of *H. pylori* will significantly increase the risk of developing site-specific diseases. For example, around 10% of the infected individuals will develop peptic ulcer disease, 3% of them will develop gastric adenocarcinoma, and 0.1% of them will develop mucosa-associated lymphoid tissue (MALT) lymphoma [13]. However, due to the fact that individuals infected with *H. pylori* do not necessarily have antibodies against bacteria, or may not be detectable in blood, the number of cancer patients seropositive for *H. pylori* may be underestimated. It has been found that gastric MALT lymphoma can be completely cured by eradication of *H. pylori* at early stage and therefore is considered the first clonal lesion which can be eliminated by treatment with antibiotics [14].

The relationship between *H. pylori* infection and gastric cancer has been widely studied for over four decades. Several studies have now provided clear notion that *H. pylori* infection is significantly associated with gastric cancer and eradication of *H. pylori* could significantly decrease the risk of gastric cancer in infected individuals without premalignant lesions [15–17]. Gastric cancer as the third most common cause of cancer deaths in the world; gastric adenocarcinoma accounts for over 95% of malignant neoplasms of the stomach, followed by gastrointestinal stromal tumors and mucosa-associated lymphoid tissue (MALT) lymphoma [18]. *H. pylori* infection is more prevalent (some up to 80%) in the developing countries where poor hygiene enhances person-to-person transmission through domestic contacts at an early age [8]. A recent prospective and population-based study in China showed that higher education, lifestyle changes, and sanitation habits could influence the rate of infection [9]. Although gastric cancer is relatively rare in United States, the incidence varies in many developed countries, for example, Korea, Mongolia, and Japan are the highest (29.9–41.8 per 100,000 persons), while Canada, Western Europe, and Australia are much lower [8, 19].

### 11.3 Oral Bacteria and Cancers

Many bacteria including *Bacteroides fragilis*, *Enterococcus faecalis*, *Escherichia coli*, *Fusobacterium nucleatum*, and *Porphyromonas asaccharolytica* have been shown to modulate tumorigenesis in colorectal cancer (CRC) [20, 21]. A recent review has summarized well how oral bacteria potentially induce colorectal cancer [22]; here we will address the key progress on the association between oral bacteria and cancer.

Although *B. fragilis*, *E. faecalis*, and *E. coli* present weak pathogenic features, two oral bacteria *F. nucleatum* and *P. asaccharolytica* were consistently identified in CRC patients and often synergistically promote oral and colon cancer progression [23]. In addition to *F. nucleatum* and *P. asaccharolytica*, other oral strains including *Peptostreptococcus*, *Prevotella*, *Parvimonas*, and *Gemella* were effectively used as

biomarkers to detect CRC [24, 25]. Given the fact of the consistent co-occurrence of these oral bacteria in CRC, their potential roles in tumorigenesis were proposed to be synergistic activities of biofilm formation and anaerobic asaccharolytic metabolism. A “driver-passenger” model, namely, a “driver” organism such as *P. gingivalis* and *F. nucleatum* can produce virulence factors to help a “passenger” bacterial load and growth, has been proposed to induce this cancer-associated biofilm formation. The consistence of high abundance of *F. nucleatum* in many CRC and adenoma instead of healthy colon biofilm samples indicates that this oral organism plays an essential role in carcinogenesis [26, 27]. Besides *F. nucleatum*, other oral anaerobic bacteria such as *Leptotrichia* and *Campylobacter* have also been revealed by deep sequencing and pairwise correlation analysis of CRC and normal tissues [28].

Because there are so many anaerobic organisms that exist in colon tissue, it has been proposed that the asaccharolytic metabolism of these oral bacteria may play a role in carcinogenesis. Due to these bacteria usually that digest peptides and amino acids instead of sugar or carbon, they become typically proteolytic. The coordinated metabolism will promote growth of a diverse and cooperative polymicrobial ecosystem and continue the breakdown of host proteins to inhibit immune response [29]. A similar effect was observed when these oral organisms inhabit the colon [30]. Recent studies have shown that *F. nucleatum* can disrupt epithelial junctions through E-cadherin to alter mucosal environment where it facilitates growth of other anaerobic microbes once it localizes in colon tissue [31]. In addition, *F. nucleatum*-mediated degradation of host protein in the mouth and gut will build up a chronic inflammatory microenvironment to promote the development of CRC [32]. Another outcome of these metabolites was found to cause DNA damage in colon tissues by inducing polyamines and genotoxic ROS production, which will facilitate biofilm formation and promote cancer cell proliferation [33].

Given the recent advances in the integrated view of the oral microbiome in colorectal tumorigenesis, it has been accepted that all polymicrobes coordinate in concert rather than just a specific pathogen nor virulence factors to create an inflammatory microenvironment that leads to bacteria-associated cancers. In regard to how the microbe disseminates from the oral cavity to the colon, two hypotheses have been proposed. One possible hypothesis is that the microbe could disseminate from ulcerated gingival tissues into the bloodstream and then is located at colon tissue. The other possible hypothesis is that the oral bacteria are swallowed and colonized at colon tissue. However, these two routes remain to be further studied, and inflamed colon or perturbed community may contribute to colonization of oral microbes.

In addition to colorectal cancer, the oral bacteria including *Porphyromonas* and *Fusobacterium* have also been found to strikingly associate with oral squamous cell carcinoma (OSCC is one of the most common cancers worldwide) and pancreatic cancer [34, 35]. In the epithelial and OSCC cell model, it has been found that *P. gingivalis* infection not only can upregulate the expression of B7-H1 and B7-DC receptors, which contribute to chronic inflammation [36], but also promote cellular invasion of OSCC cells through inducing metalloproteinase MMP-9 expression [37]. Further studies revealed that gingipains, a cysteine proteinase produced by *P. gingivalis*, plays a critical role in this process [37]. Similarly, *F. nucleatum* can also enhance tumor cell proliferation and migration through MMP-9 and MMP-13 [38].

## 11.4 Gram-Positive Bacteria and Cancer

Several lines of evidence have shown that many gram-positive microbes can cause serious infections and invasive bacterial disease in cancer patients. They include *Staphylococci*, *Streptococci*, and *Enterococci*. To understand the impact of these bacteria in patients with malignancy will help develop cancer therapeutic strategy and improve the survival of the cancer patient. We will describe the most recent progress on these three types of bacteria and their associated cancers below.

*Staphylococcus aureus*—Whether *S. aureus* is a cause of infection in cancer patients remains to be further demonstrated; it has a high relevance with the mortality of patients with pneumonia [39]. Cancer patients treated with antistaphylococcal antibiotics (i.e., daptomycin or ceftaroline) have shown a generally favorable outcome [40].

*Streptococci*—Among the *Streptococci*, *viridans group streptococci (VGS)* is the prominent member of the oral microbiome and is often found to correlate with high mortality of patients with pediatric acute myeloid leukemia [41, 42].  $\beta$ -hemolytic streptococci GBS is found to associate with breast cancer [43], and *S. pneumoniae* affects the malignancy of patients with leukemia, lymphoma, or myeloma [44]. It has been shown that VGS is multidrug resistant including  $\beta$ -lactams, while GBS remains susceptible to  $\beta$ -lactams and could be treated with penicillins or cephalosporins, and *S. pneumoniae* is susceptible to levofloxacin and vancomycin [45–47]. In addition, *Streptococcus bovis* in gastrointestinal microflora was found in blood and caused infective endocarditis [48, 49], which has been previously shown to associate with colorectal cancer [50], albeit no *S. bovis* DNA was identified in colorectal neoplastic tissues by using the PCR technique [51].

*Enterococci*—Although *Enterococci* is generally considered as low-virulence bacteria, *E. faecium* is found to associate with increased risk of mortality of patients with hematologic malignancies [52]. It is known that *E. faecium* is penicillin susceptible, while  $\beta$ -lactam or vancomycin is resistant for therapy of cancer patients.

Another example is *Salmonella typhimurium (S. typhi)* and gallbladder cancer (GBC), due to patients who are infected with this bacterium developed GBC more frequently [53, 54]. However, the causative links between this bacterial infection and cancer remain to be further demonstrated.

## 11.5 Potential Mechanisms of Bacterium-Associated Carcinogenesis

Chromosome instability is a common feature of cancer cells. Despite evidence of epidemiological studies of bacteria-associated cancer is persuasive, the molecular mechanisms of bacterial infection-causing genome instability still remain largely unclear. However, recent studies have shown that bacteria—their eukaryotic endosymbionts lateral gene transfer (LGT)—are a mean of causing genome instability [55]. Although the link between the LGT and tumor-causing ability has not been

established, it is speculated that LGT may cause tumorigenesis. For example, in vitro experiments demonstrated that *Bartonella henselae* (a bacterium causing bacillary angiomatosis-peliosis tumor in humans [56]) is able to integrate their plasmid DNA into the human host genome [57]. Bioinformatics analysis revealed high incidence of LGT from *Acinetobacter* and *Pseudomonas* like DNA in the mitochondrial DNA of patients with acute myeloid leukemia [58]. In contrast, very few evidence of integration of *H. pylori* DNA was reported, despite the fact that infection with this bacterium is highly associated with gastric cancer.

Given chronic inflammation which is also a common physiological response of host immunity to microbe infections, and is involved in generation of several mediators such as free radicals, prostaglandins, and cytokines, deregulation of these mediators by bacteria will lead to cell proliferation, angiogenesis, and oncogenic activation. Therefore, the specific modification of the inflammatory response by bacteria will lead to persistent infections and eventually development of cancer cells. For instance, ROS and IL-1 $\beta$ , as products of chronic inflammation, are shown to be upregulated by *H. pylori* in gastric epithelial cells for cell proliferation and angiogenesis [59, 60]. Epithelial cell infection with *Pseudomonas aeruginosa* or *H. pylori* is able to induce VEGF expression and trigger angiogenesis [61, 62]. In addition, *H. pylori* also plays a key role in activation of NF- $\kappa$ B through increasing the expression of IL-8 and TNF- $\alpha$  [63, 64]. Further studies have revealed that Toll-like receptors TLR4-mediated activation of NF- $\kappa$ B signaling facilitate the *H. pylori* colonization [65].

Deregulation of host cell proliferation and apoptosis is another common mechanism targeted by viral infection [66]. Emerging evidence has shown that bacteria could also evolve several strategies to control cell progression. For example, *H. pylori*-encoded CagE could promote the activation of Cyclin D1 in cell cycle [67]. The toxin CNF released by *E. coli* could not only induce G1-S transition and DNA replication but also inhibit cell apoptosis to stimulate cell progression [68, 69]. To block cell apoptosis, *H. pylori*-encoded Cag antigen also induces COX-2 expression to activate Bcl-2 and suppress apoptosis [70].

The evasion of the immune system is another key mechanism utilized by bacteria to promote cell malignancy. It has been demonstrated that bacteria have evolved multiple mechanisms to evade host immune response, including the modulation of bacteria surface, subversion of phagocytes, and blockade of innate immunity. To avoid surface signal recognition by immune system, many bacteria form carbohydrate-rich capsules or incorporate host proteins into capsules to mask their surface antigens from host receptors [71]. Since phagocytosis is one of the main ways used by host to counter bacterial infection, it is not surprising for bacteria to employ different strategies to escape. For example, *Streptococcus pneumoniae* and *Staphylococcus aureus* produced immunoglobulin proteases to preclude the capture of antigens [72] or antibody-binding proteins to scavenge opsonizing antibodies [73]. To avoid the acquired immune response, *H. pylori* produce a vacuolating toxin VacA to block T cell proliferation and in turn inhibit the receptor-IL-2 signaling pathway and decrease of activated T cells [74, 75].

## 11.6 Future Perspective

Although it has been demonstrated that some bacterial infections associate with development of cancer, very few studies demonstrate the genomic instability of cells which was directly caused by bacteria or exposed to bacterial components through blood. More details about the molecular pathways involved in the induction of genomic instability in response to bacterial infection remain to be further explored. It still needs to answer why the causative relationship between the bacterial infection and cancers is only limited for a few cancers and whether the bacterial infection process is required to cause cancer. The association of oral organisms with colorectal cancer indicates that relocation of bacteria in inappropriate tissues and polymicrobial interactions together could be the key for bacteria to cause carcinogenesis. Along with the development of next-generation deep sequencing technology and bioinformatics analysis, it will provide a clear scenario about how bacterial infection contributes to cancer, which will facilitate to develop effective diagnostic and therapeutic strategies against infection-causing cancers.

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