



Antioxidant Role of Probiotics in Inflammation-Induced Colorectal Cancer

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Abstract: Colorectal cancer (CRC) continues to be a significant contributor to global morbidity and mortality. Emerging evidence indicates that disturbances in gut microbial composition, the formation of reactive oxygen species (ROS), and the resulting inflammation can lead to DNA damage, driving the pathogenesis and progression of CRC. Notably, bacterial metabolites can either protect against or contribute to oxidative stress by modulating the activity of antioxidant enzymes and influencing signaling pathways that govern ROS-induced inflammation. Additionally, microbiota byproducts, when supplemented through probiotics, can affect tumor microenvironments to enhance treatment efficacy and selectively mediate the ROS-induced destruction of CRC cells. This review aims to discuss the mechanisms by which taxonomical shifts in gut microbiota and related metabolites such as short-chain fatty acids, secondary bile acids, and trimethylamine-N-oxide influence ROS concentrations to safeguard or promote the onset of inflammation-mediated CRC. Additionally, we focus on the role of probiotic species in modulating ROS-mediated signaling pathways that influence both oxidative status and inflammation, such as Nrf2-Keap1, NF-κB, and NLRP3 to mitigate carcinogenesis. Overall, a deeper understanding of the role of gut microbiota on oxidative stress may aid in delaying or preventing the onset of CRC and offer new avenues for adjunct, CRC-specific therapeutic interventions such as cancer immunotherapy.



1. Introduction

Colorectal cancer (CRC) consistently contributes to global mortality, ranking as the second leading cause of cancer-related deaths and the third most diagnosed cancer worldwide [1]. A recent study by GLOBOCAN, the Global Cancer Observatory, which included data on 36 various cancers from 185 countries, estimates that CRC accounted for 9.6% of new cancer cases and 9.3% of new cancer deaths in 2022 [2]. GLOBOCAN also projects that the yearly incidence of CRC will increase from 1.9 million new cases in 2020 to 3.6 million new cases by 2040, with CRC-related deaths rising from 930,000 to 1.6 million during the same period [3]. Although the majority of CRC diagnoses occur in individuals over the age of 70 [4], the incidence of CRC in those under 50 has been rising in recent years, prompting the American Cancer Society to recommend earlier screening [5]. Due to the global burden of the disease and its high mortality rate, significant research has been directed towards understanding the factors driving CRC pathogenesis and improving preventative measures [6,7]. Currently, the non-modifiable risk factors for CRC development include sex, race, genetics, and the presence of inflammatory bowel disease [7], while the modifiable risk factors include dietary habits, physical inactivity, obesity, and smoking [6]. Emerging evidence has shown that the composition of intestinal bacteria, collectively termed the gut microbiota, can influence or protect against CRC pathogenesis



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Copyright: © 2024 by the authors. Licensee MDPI, Basel, Switzerland. This article is an open access article distributed under the terms and conditions of the Creative Commons Attribution (CC BY) license (https:// creativecommons.org/licenses/by/ 4.0/). by acting as a key intermediary of these modifiable risk factors [8–10]. For example, the introduction of a high-fat diet in animal models has been shown to induce tumorigenesis through significant shifts in microbial composition, including increasing pathogenic and inflammatory microbial species such as *Alistipes* while reducing probiotic bacteria like *Parabacteroides* [11]. Cigarette smoking has a similar, unfavorable effect on gut microbiota, enriching species like *Eggerthella lenta* and depleting *Parabacteroides* and *Lactobacillus* to activate oncogenic signaling in the colonic epithelium [9]. There are multiple proposed mechanisms by which these shifts in microbial composition promote CRC development including, but not limited to, inflammatory signaling [12], direct or indirect DNA damage through the production of harmful metabolites [13,14], histone modification [15], upregulating oncogenic genes [11], inducing tumor resistance to treatment [16], and promoting the formation of reactive oxygen species (ROS) [17].

Of particular interest, sustained increases in ROS play a central role in activating carcinogenic signaling pathways by acting as secondary messengers to induce tumorigenesis and cancer progression [18]. Interestingly, microbiota are critical modulators of ROS and oxygen free radical generation, particularly in states of dysbiosis [19]. As such, it has been demonstrated that commensal bacterial species can suppress inflammatory signaling through antioxidant properties, whereas pathogenic bacterial species exert the opposite effect [20]. Additionally, the gut microbial composition has also been shown to be influenced by states of increased oxidative stress with colorectal cancer-associated bacteria adapting their transcriptomes to defend against microenvironment pressures, leading to the pervasiveness of inflammatory gut microbiota [17]. For example, Escherichia coli from cancerous microenvironments with increased oxidative stress displayed greater activation of genes that induce virulence, host colonization, metabolite uptake, and survivability compared to their non-cancerous counterparts [17]. Given this reciprocal influence between the gut microbiota and oxygen free radicals, probiotics have emerged as an adjuvant therapeutic method with antioxidant properties. They can mitigate oxidative stress by augmenting antioxidant and anti-inflammatory signaling pathways, promoting the production of antioxidant microbiota-derived metabolites, and enhancing the activity of antioxidases [21]. To date, studies have strongly supported the role of probiotic administration in inflammatory gut conditions [22,23] and accumulating evidence demonstrated their anti-proliferative and anti-inflammatory efficacy in inflammation-driven CRC [24-28].

In this review, we present emerging evidence demonstrating the mechanisms by which unfavorable taxonomical shifts in the gut microbiota generate sustained increases in reactive oxygen species to initiate inflammatory signaling and resulting carcinogenesis. First, we briefly describe the role of ROS and oxygen free radicals in tumorigenesis as it pertains to CRC. In the process, we identify key gut microbial species and important microbiota-derived metabolites that contribute to ROS formation and modulate oxidative status in CRC models. Lastly, we discuss the role of probiotics in reducing oxidative stress by enhancing antioxidase concentrations and mitigating ROS-mediated inflammatory signaling, thereby aiding in the prevention and treatment of inflammation-driven CRC.

2. Reactive Oxygen Species, Oxidative Stress, and Colorectal Cancer (CRC)

Under basal conditions, ROS serve as essential signaling molecules, controlling multiple aspects of cellular physiology including the mediation of growth factors, transcription, and immunomodulation [29]. Endogenously, the majority of ROS are produced via oxidative phosphorylation and the mitochondrial electron transport chain with additional contributions from pro-oxidative enzymes such as nicotinamide adenine dinucleotide phosphate oxidase (NOX), nitric oxide synthase (NOS), xanthine oxidases (XO), cyclooxygenases (COX), and lipoxygenases [30,31]. Exogenous factors such as air pollution, radiation, diet, smoking, and drugs also significantly contribute to the total amount of cellular ROS [32]. When in excess, the accumulation of ROS and resulting imbalance between oxygen free radicals and antioxidants lead to a pathological disruption of normal cellular physiology [33,34]. Specifically, oxidative stress is shown to confer cell damage, DNA mutations,

inflammatory stress, and the dysregulation of growth factors, which in combination can lead to tumorigenesis [29].

As it pertains to CRC, studies have elucidated potential mechanisms by which tumorigenesis may occur in direct association with the accumulation of ROS [35,36]. Importantly, ROS-mediated pathways have been shown to induce DNA damage and the subsequent tumorigenic mutations commonly seen in CRC pathology including *p53*, *APC*, and *BRAF* [37]. It is estimated that over 50% of human colorectal tumors are derived from *p53* mutations [38], with the oxidation of DNA bases contributing to the mispairing of guanine and cytosine with adenine and thymine bases [39]. Specifically, the DNA oxidation of guanine and cytosine bases results in the formation of 8-oxoguanine and 5-hydroxycytosine, respectively, leading to mispairing during DNA replication and high mutation rates [35]. Interestingly, it has been reported that 8-oxoguanine concentrations are higher in the urine of CRC patients compared to healthy controls, likely due to the enhanced DNA excision rates of mismatched bases and the subsequent excretion [40].

In addition, lipid peroxidation is also a potent inducer of CRC development [36,41]. Byproducts of lipid peroxidation pathways are among the most significantly elevated in colitis-associated CRC [36]. For example, the administration of low doses of epoxyketooctadecenoic acid (EKODE) has been found to exacerbate intestinal barrier dysfunction, lipopolysaccharide, and bacterial translocation along with CRC development via inflammatory signaling pathways such as NF-κB and c-Jun N-terminal kinases (JNK) [36]. Similar results have been observed with other lipid peroxidation byproducts including 4-hydroxynonenal (4-HNE) and 12,13-epoxyocyadecenoic acid (EpOME), both of which augmented inflammation and contributed to colorectal tumorigenesis [42,43]. Proteins are also affected by oxidative stress and confirmational changes in their structure can contribute to CRC development. Sulfur-containing amino acids (cysteine and methionine) are easily oxidized, leading to the formation of undegradable protein aggregates, notably of important enzymes, structural proteins, and receptors [44]. A comparative study identified 31 proteins containing oxidation-sensitive cysteines that are associated with tumorigenesis, with cysteine oxidation found to be correlated with CRC-associated changes [45]. Therefore, dysregulated protein degradation systems are a hallmark of CRC, and targeting these pathways has become of recent interest in cancer treatment [46].

Though the accumulation of ROS is shown to confer carcinogenic changes in colorectal cancer cells, researchers have harnessed the apoptotic and senescence-inducing capabilities of ROS as an anti-cancer therapeutic modality [47]. Within their tumor microenvironments, uncontrolled proliferation in cancer cells increases ATP requirements and concurrently upregulates oxidative phosphorylation and ROS concentrations. However, intrinsic antioxidant activation is also upregulated in cancer cells, reducing oxidative stress to levels comparable to non-cancerous counterparts. It is important to note the duality of ROS generation within cancer cells, as moderate ROS levels may induce cancer survival and proliferation, while the overload of ROS induces apoptosis and preferential destruction of tumor cells [48]. Toxic accumulation of ROS leads to endoplasmic reticulum stress, triggering apoptotic pathways, most notably via inositol requiring enzyme-1 (IRE1) signaling to induce autophagy and senescence [49]. Taken together, these findings highlight the versatility of ROS and the importance of redox balance in CRC cell physiology.

2.1. Antioxidants, Nrf2-Keap1, and Carcinogenesis

Given the pro-carcinogenic influence of ROS accumulation on CRC pathogenesis, cellular antioxidant defense mechanisms serve an important role in alleviating oxidative stress [50]. A recent large-scale study suggests that higher exposure to antioxidants and corresponding oxidative balance correlates negatively with the onset of CRC [51].

To further defend against oxidative and electrophilic stress, eukaryotic cells utilize the Nrf2-Keap1 pathway to activate an antioxidant response element (ARE) and related gene network to promote the production of antioxidant enzymes [52]. In an unstressed oxidative environment, Kelch-like ECH-associated protein 1 (Keap1) binds to and inhibits nuclear

factor erythroid2-related factor (Nrf2). Alternatively, states of oxidative stress induce a conformational change in Keap1, releasing Nrf2, which then translocates to the nucleus to activate ARE [52]. The activation of ARE initiates the transcription of antioxidant enzymes such as superoxide dismutase (SOD), catalase (CAT), glutathione peroxidase (GPx), glutathione-S-transferase (GST), and heme-oxygenase 1 (HO-1), which mitigate redox imbalance and free radical damage [53] (Figure 1).



Figure 1. Visualization of the Nrf2-Keap1 pathway and antioxidant enzyme transcription. Under oxidative stress, Nrf2 is phosphorylated and dissociates from Keap1. Phosphorylated Nrf2 then translocates to the nucleus where it binds to small musculoaponeurotic fibrosarcoma (sMAF), activating the antioxidant response element (ARE). This initiates antioxidant enzyme gene transcription including superoxide dismutase, catalase, glutathione peroxidase, glutathione-S-transferase, and heme-oxygenase 1. Conversely, under physiological conditions, Keap1 targets Nrf2 for proteasomal degradation, and antioxidant enzymatic transcription is not upregulated. Abbreviations: Nrf2, nuclear factor erythroid 2; Keap1, Kelch-like ECH-associated protein 1; ROS, reactive oxygen species; p-Nrf2; phosphorylated Nrf2; ARE, antioxidant response element; sMAF, small musculoaponeurotic fibrosarcoma.

The importance of the Nrf2-keap1 antioxidant pathway in carcinogenesis is demonstrated through studies with Nrf2 knockout mice which exhibit oxidative toxicity and significant inflammation compared to controls [54,55]. More specifically, in an Azoxymethane/Dextran Sulfate Sodium model of colitis-associated CRC, Nrf2 knockout was associated with higher tumor incidence, indicating a critical role of Nrf2-dependent inflammatory suppression in mitigating CRC development [54]. Increased inflammatory and oxidative markers in Nrf2 deficient mice promoted the proliferation of intestinal crypt cells, increasing the risk and presence of mutations leading to carcinogenesis [54]. Similarly, another study with Nrf2 deficient mice showed a higher incidence of tumor cells and identified 23 novel Nrf2-related genes that indicated poorer prognosis in CRC tumor samples [55]. Aging also dysregulates Nrf2 activity, increasing tumorigenesis via ROS-mediated DNA damage and mutations [56], which may also play a role in CRC development and higher prevalence in

older generations. Telomeres, the protective caps of eukaryotic chromosomes, are highly susceptible to oxidative damage [57], and in combination with Nrf2 dysregulation and unbalanced redox status, oxidative stress can lead to mutations, genomic instability, and carcinogenesis [56].

Although the Nrf2 pathway is necessary for mitigating oxidative stress to prevent the onset of colorectal carcinogenesis, fully malignant cells exhibit an opposite fate in response to excessive Nrf2 signaling [58]. Specifically, Nrf-2 activity may induce cancer resistance to chemotherapy and enhance tumor growth by protecting against ROS-mediated cancer cell destruction [58,59]. A recent study using alpha-hederin as an anti-CRC therapy observed that lower activation of the Nrf2-Keap1 pathway conferred better treatment outcomes, notably due to its role in modulating tumor microenvironments [60]. Interestingly, the tumor to normal tissue ratio of Nrf2-Keap1 pathway activation has also been linked to lymphovascular invasion in colorectal cancer [61]. It is hypothesized that oncogenic factors promote conformational changes in the Nrf2-Keap1 complex to prevent Nrf2 degradation [62,63]. Therefore, colorectal cancer cells induce the aberrant activation of Nrf2 to reduce oxidative stress within the tumor microenvironment, enhancing their survival [64]. Excess Nrf2 activity worsens chemotherapy resistance and confers poorer prognosis indicating that Nrf2 inhibitors may play an anti-cancer role in this setting [63].

2.2. Inflammatory Signaling, Oxidative Stress, and Carcinogenesis

Inflammation is a significant risk factor for CRC development as those with inflammatory bowel disease (IBD) experience up to a three-fold increased incidence of the condition [65]. IBD is a condition that is characterized by chronic relapsing and remitting intestinal inflammation, which is believed to result from persistent immune responses triggered by multiple factors including genetic predisposition and interactions with gut microbial components [66]. The two primary subtypes of IBD are Crohn's disease (CD) and Ulcerative colitis (UC) [66]. CD is known to cause transmural inflammation, affecting the entire gastrointestinal tract, particularly the terminal ileum, and is marked by skip lesions [67]. In contrast, UC typically begins in the rectum and causes continuous inflammation that extends proximally, almost exclusively affecting the colon [68]. When uncontrolled, both subtypes can lead to carcinogenic progression, with UC having a slightly higher tendency to induce CRC due to localized inflammatory changes to the colon [69].

Recent research has identified oxidative stress-related genetic risk loci associated with the onset of IBD and its subsequent carcinogenic progression [70]. Genome-wide associated studies have revealed polymorphisms within the *NADPH quinone oxidoreductase* (*NQO1*) and *superoxidase dismutase* 2 (*SOD2*) genes. *NQO1* polymorphisms have been linked to anti-inflammatory therapeutic resistance, while mutations in *SOD2* correlate with an earlier age of onset in UC patients [71]. Additionally, meta-analyses have shown that *GST M1* null genotype mutations increase susceptibility to IBD in certain populations [72,73], but not in others [74]. Another genetic locus linked to both the susceptibility and progression of UC involves the Nrf2 transcription factor encoded by the *nuclear factor erythroid-derived* 2-*like* 2 (*Nfe2L2*) gene, which can induce inflammation through the uncontrolled production of ROS [75]. Furthermore, the *paraoxonase* (*PON*) genetic loci within chromosome 7 have been associated with IBD development, with a single amino acid mutation (arginine to glutamine) at position 192 showing a statistically significant difference in susceptibility to or protection against the condition [76].

Chronic inflammation in IBD induces carcinogenesis through multiple mechanisms including intestinal epithelial cell dysplasia via p53 or APC pathways initiated by chromosomal instability, microsatellite instability, and hypermethylation [77]. Oxidative stress induces pro-inflammatory signaling pathways like nucleotide-binding domain, leucinerich containing family 3 (NLRP3), and nuclear factor kappa beta (NF- κ B), which constitutively damage the intestinal barrier and indirectly contribute to colorectal carcinogenesis through increasing susceptibility to dysplastic transformation [78,79]. More specifically, the influence of oxidase stress on NLRP3 inflammasome activation stems from increased mitochondrial NADPH oxidase activity and endoplasmic reticulum stress [80,81]. For example, in colitis-induced CRC mice, a high-cholesterol diet increased tumorigenesis through the mitochondrial ROS-mediated upregulation of the NLRP3 inflammasome [82]. Specifically, NLRP3-ASC assembly increased IL-1 β concentrations, augmenting chronic inflammation and inducing dysplasia [82]. Interestingly, mitochondrial ROS directly contributes to NLRP3 relocation to endoplasmic structures, initiating interactions with its adaptor molecule, ASC, and activating the inflammasome [83]. In turn, the overactivation of NLRP3 induces colitis through the upregulation of pro-inflammatory cytokines within intestinal epithelial cells, sustained macrophage activity, and recruitment of effector T cells [84]. This strongly influences carcinogenesis as CRC tumors are densely surrounded by macrophages with strong NLRP3 expression which contributes to greater cell migration, invasion, and metastasis, leading to a poorer prognosis [85].

Understanding the pro-inflammatory and immunoregulatory role of NF-KB is also crucial in CRC pathogenesis [86]. Oxidative stress modulates NF-κB activity as ROS, notably hydrogen peroxide, and phosphorylates the inhibitor of nuclear factor kappa B (IkB), leading to NF- κ B release and translocation to the nucleus [87]. The subsequent activation of NF-kB regulates key components of innate and adaptive immune responses including cytokine transcription and inflammasome activation and is a hallmark of inflammatory bowel conditions when dysregulated [88]. More specifically, the byproducts of NF- κ B activation encompass a wide range of cellular processes including but not limited to the induction of pro-inflammatory cytokines such as tumor necrosis factor- α and interleukin-1, the release of chemokines like CXCL12 and CXCL13, the activation of multiple transcription factors involved in angiogenesis and inflammation, the alteration of adhesive molecule expression like cadherins, and the secretion of antimicrobial peptides [89,90]. Interestingly, the expression of NF- κ B is found to be comparatively elevated in patients with colorectal cancer when compared with IBD, supporting its role in adenoma to carcinoma transformation [91]. The NF-kB signaling pathway has been associated with oncogenic mutation notably those in the p53, BRAF, and APC genes, which comprise a large percent of colorectal cancers [92]. NF- κ B signaling is also implicated in cell cycle progression and dysregulation induces constitutive expression of proliferative genes [93]. Suppressing NF-KB activation has been shown to induce cell cycle arrest at the G0/G1 stage, reducing colorectal cancer growth [94]. NF-κB inhibitors also suppress the IL-1-induced proliferation of CRC cells in inflammatory microenvironments by inhibiting IkB phosphorylation [95]. Therefore, targeting the NF-κB pathway to elicit anti-inflammatory and anti-proliferative effects on inflammation-derived CRC development is warranted [96].

Nrf2-mediated pathways may also disrupt NF-κB activation, helping mitigate the development of inflammation-induced CRC [97]. Specifically, Nrf2 activation in response to oxidative stresses induces HO-1 activity, responsible for degrading heme, a potent oxidant, into iron, biliverdin, and carbon dioxide [98]. Concurrently, degradation into these byproducts, particularly carbon dioxide, negatively influences NF-κB translocation into the nucleus, resulting in the downregulation of the pathway and inflammatory effects [99]. Thus, Nrf2-mediated antioxidant signaling plays a crucial role in mitigating the extent of NF-κB-induced inflammation and related inflammatory damage in the onset of colorectal carcinogenesis.

3. Gut Microbiota and Colorectal Cancer (CRC)

It is estimated that trillions (10¹³–10¹⁴) of commensal microbes reside within the human gastrointestinal tract [100]. This collection of intestinal microbes is termed as the gut microbiota while their total genomic composition is referred to as the gut microbiome [100]. When a healthy or favorable gut microbial composition is maintained, gut microbiota confers a myriad of beneficial effects on host physiology including immunomodulation, energy homeostasis, protection from gut bacterial pathogen overgrowth, and reduced gut intestinal barrier permeability [101–103]. Gut microbial composition is influenced by both environmental and genetic factors throughout an individual's lifetime, with diet, antibiotic use, mode of delivery during birth, geographical location, age, and family genetics playing a significant role [104]. Given the multifactorial influence on the compositional makeup of the gut microbiota, perturbations are common and have been linked to multiple disease states, including obesity, dyslipidemia, type 2 diabetes mellitus, neuropsychiatric disorders, inflammatory bowel disease, and even cancers [105–108]. Over the last few decades, significant data have linked states of dysbiosis to CRC, with the identification of specific taxonomical shifts and trends in microbiota species that may act as biomarkers of CRC as well as species that are associated with CRC diagnosis and progression [11,109]. These trends include increased relative abundances of *Fusobacterium nucleatum*, *Porphyromonas gingivalis*, *Megamonas funiformis*, *Bacteroides vulgatus*, *Bacteroides stercoris*, *Ruminococcus gnavus*, *Dorea longicatena*, *Escherichia coli*, *Clostridium*, *Atopobium parvulum*, and *Actinomyces odontolyticus* [109–113] with generally decreased abundances of protective species such as *Lacticaseibacillus paracasei*, *Clostridium butyricum*, *Streptococcus thermophilus* and *Faecalibacterium prausnitzii*, *Roseburia intestinalis*, and *Eubacterium rectale* [114–117].

Of the listed perturbations in microbial composition, the most supported evidence exists for Fusobacterium nucleatum [118], which is consistently elevated in the fecal samples of affected patients with early to late stages of CRC [110]. For example, the introduction of Fusobacterium nucleatum into mice containing the APC gene mutation accelerated tumorigenesis through myeloid cell infiltration and pro-inflammatory signaling in CRC [119]. Mechanistically, Fusobacterium nucleatum has been described to exert tumorigenic effects through multiple modalities, including altering the gene expression of microRNAs associated with CRC [120], production of harmful metabolites to disrupt autophagy [121], and activating inflammatory signaling via the NF-kB pathway [122]. In addition to supporting tumorigenesis, Fusobacterium nucleatum contributes to tumor metastasis through NF-κB dependent mechanisms including the upregulation of cancer migration genes, methylation of mRNA, and inducing macrophage infiltration into tumor cells [123–125]. Similarly, Fusobacterium nucleatum concentration is shown to modulate cancer immunotherapy targeting immune checkpoint inhibitors, with a direct correlation between the relative abundance of the bacterium and PD-L1 blockade in mouse models [126]. Recent data have also shown that the bacterium can induce chemoresistance through inhibition of ferroptosis, pyroptosis, and apoptosis [127–129], making the species crucial to our understanding of both the pathogenesis and augmentation of therapeutic modalities.

In addition to *Fusobacterium nucleatum*, other microbial species are found to have significant association with various stages of CRC. For example, studies suggest that Atopobium parvulum and Actinomyces odontolyticus co-occur and increase in abundance in intramucosal and multiple polypoid adenomas [110]. Atopobium parvulum, a bacterium with cysteine desulfarase activity, promotes hydrogen sulfide formation within the gut, which can be toxic to colonocytes [130]. The elevation of *Atopobium parvulum* in early-stage CRC and the related overproduction of hydrogen sulfide also lead to further disruption of the gut microbiome and CRC progression in conjunction with other hydrogen sulfide-producing species such as Fusobacterium nucleatum [121,130]. Additionally, the analysis of culprit species in CRC pathogenesis has identified multiple species that may serve as potential biomarkers for CRC development including Fusobacterium nucleatum, Peptostreptococcus anaerobius, Bacteroides fragilis, Parvimonas micra, Xanthomonas perforans and Clostridium symbiosum [112,131]. Similarly, Bacteroides massiliensis, Bifidobacterium pseudocatenulatum, Corynebacterium appendicis, and Alistipes onderdonkii have been identified as biomarkers that may help differentiate non-cancerous tissue from CRC tissue [132]. Furthermore, species such as Porphyromomnas gingivalis are not only linked to CRC pathogenesis, but also provide insight into patient prognosis [111,133]. Porphyromomnas gingivalis induces carcinogenesis through activation of the NLRP3 inflammasome, promoting the development of inflammation-driven CRC [111]. In relation to prognosis, studies show that patients with significantly elevated *Porphyro*momnas gingivalis in fecal samples have decreased cancer-specific survivability [133]. Taken together, there is strong evidence for the intricate interplay between the gut microbiota and CRC pathogenesis, treatment, identification, and prognosis.

3.1. Microbiota, Reactive Oxygen Species, and Colorectal Cancer

As previously described, the presence of ROS and oxidative stress creates a protumorigenic intestinal environment serving as an important risk factor for CRC development [134] through direct oxidative damage to the intestinal epithelium [135]. Microbiota serve as important modulators of redox status, both positively and negatively depending on the relative abundances of various species and the intestinal microenvironment [136,137]. The disruption of the intestinal barrier via oxidative damage increases permeability, allowing for the translocation of pathogenic microbiota and metabolites, which may drive inflammation-associated CRC [138]. Additionally, damage to the intestinal barrier increases the susceptibility of intestinal stem cells to genotoxic or environmental mutagens which can contribute to uncontrolled inflammatory bowel states [139].

Certain gut microbiota influence carcinogenesis through their oxidative potential and redox properties, including Peptostreptococcus anaerobius, Enterococcus faecalis, and Bacteroides fragilis [140–142]. Peptostreptococcus anaerobius modulates the tumor microenvironment by increasing ROS levels to induce intestinal dysplasia through pro-inflammatory pathways [141]. Specifically, cholesterol biosynthesis pathways and cell proliferation are upregulated in response to *Peptostreptococcus anaerobius* metabolite binding of Toll-like Receptor 2 (TLR-2) and Toll-like Receptor 4 (TLR-4), promoting ROS formation [141]. Reactive oxygen species were identified as an intermediate of these processes, as the introduction of antioxidants or knockdown of TLR-2 or TLR-4 ameliorates both cell proliferation and cholesterol biosynthesis [141]. Furthermore, Enterotoxigenic Bacteroides fragilis (ETBF) secretes a zinc-dependent metalloprotease toxin, known as *Bacteroides fragilis* toxin (BFT), which is strongly associated with colon epithelial cell proliferation through the induction of intestinal inflammation [143]. Specifically, BFT binds to receptors on the colonic epithelial cell, triggering carcinogenesis-associated changes such as the cleavage of E-cadherin, enhancing Wingless-related integration site (Wnt) signaling, and the release of pro-inflammatory cytokines [143]. E-cadherin, in particular, is implicated in CRC and other cancers, as it serves as an adhesion molecule on epithelial cells, facilitating cell-to-cell interactions. The loss of its functionality is correlated with the formation of colorectal adenomas [144]. Concurrently, the collection of changes induced by BFT exacerbates colonic barrier permeability, induces DNA damage, and enhances the metastatic potential of CRC [143]. In addition, ETBF drives inflammatory stimuli to induce tumorigenesis through the enzyme spermine oxidase (SMO) [140]. SMO oxidizes spermine to catabolize polyamines with inflammatory stimuli serving as the primary stimulus in its enzymatic activity [145]. Its oxidative byproducts are cytotoxic in excess, yielding significant DNA damage and resulting carcinogenesis including those of breast, gastric, and colorectal origin [146–148]. In a murine model, the *Bacteroides fragilis* toxin upregulate SMO to induce DNA damage via its ROS byproducts [140]. Further, given its enzymatic association with carcinogenesis, novel SMO inhibitors have been studied with great efficacy in suppressing cell proliferation and migration [149]. Similarly, Enterococcus faecalis is thought to be a driver of CRC development through its oxidative capacity [142]. This bacterium is a well-documented producer of extracellular superoxide and induces chromosomal instability, such as an euploidy, tetraploidy, and cell cycle arrest, in murine colonic epithelial cells [150].

In addition to contributing to the formation of oxidative environments, CRC-associated species also protect themselves against oxidative stress through intrinsic adaptation mechanisms to improve survivability [17,151]. *Fusobacterium nucleatum* is an obligate anaerobe that withstands oxidative stress microenvironments allowing for the sustained survivability, attachment, and invasion of target tissues [151]. Until recently, it was known that the bacterium can cope with excess ROS [152], though the mechanisms by which it can do so had not been elucidated. A recent study has identified a five-gene locus in *Fusobacterium nucleatum*, encoding *methionine sulfoxide reductase* (*MsrAB*), a two-component signal transduction system known as *ModR*, and distinct proteins [151]. The significance of this multigene locus is shown through *ModR*-directed regulation of *MsrAB*, conferring resistance to ROS-mediated destruction and increased virulence pertaining to the adherence

or invasion of the bacterium to CRC epithelial cells [151]. In addition to *Fusobacterium nucleatum, Escherichia coli* also adapts to oxidative environments with different regulatory and resistance responses observed in cancerous and non-cancerous bacteria [17]. This is demonstrated through the upregulation of the inherent arginine decarboxylase (AdiA) enzyme of *Escherichia coli* with oxidative stress induction [17]. AdiA is described as an important enzyme in withstanding oxidative pressure in bacterial species to enhance survivability [153]. Taken together, these studies provide strong evidence supporting the influence of gut microbiota trends on oxidative environments seen in CRC and vice versa.

Antibiotics, Redox Balance, and Colorectal Cancer

Similar to the taxonomical trends observed in CRC pathogenesis, it is important to briefly discuss the effects of microbiota depletion through antibiotic use and its relationship with carcinogenesis, particularly in the context of redox imbalance. Notably, findings from a large cohort study suggest that early-life antibiotic use is significantly associated with an increased risk for colon cancer development across all ages, particularly in individuals under the age of 50 [154]. Additionally, a recent meta-analysis of six studies concluded that individuals with the highest levels of antibiotic exposure had a 10% higher risk of developing colorectal neoplasia compared to those with the lowest antibiotic exposure [155]. This increased risk is thought to be in part secondary to the antibiotic-mediated selection of pro-carcinogenic, resistant bacterial species as well as stress-resistant cancerous cells that lack effective DNA repair mechanisms [156].

In the post-antibiotic period, these resistant bacteria and DNA mutations permeate, as evidenced by studies showing resistance of Fusobacterium nucleatum and Escherichia coli subtypes to multiple antibiotic classes [157,158]. In addition to allowing for the overgrowth of carcinogenesis-associated gut microbial species, studies in rodent models have shown that antibiotic use can potentiate the effect of unfavorable gut microbiota [159]. For example, various antibiotic classes were shown to increase the abundance of heightened adherent invasive Escherichia coli (AIEC) while also promoting its further expansion in chronically infected mice [159]. Importantly, inflammation induced by antibiotic use upregulates reactive nitrogen species leading to the production of oxidized metabolites that provide a fitness advantage to these pathogenic bacteria, facilitating their expansion [159]. However, not all antibiotics contribute to carcinogenic changes. For instance, erythromycin, a macrolide antibiotic with unique anti-inflammatory and antioxidative properties has demonstrated chemopreventative effects [160]. Studies have shown that erythromycin suppresses pro-inflammatory signaling by inhibiting NF-kB activation, which in turn reduces the expression of downstream targets such as interleukin-6 and COX2 in colorectal cancer cell lines [160]. Given that COX is an inducer of oxidative stress [161], the significant decrease in its expression suggests reduced oxidative stress in proximal intestinal polyps, which were also reduced by up to 70.9% compared to controls [160].

While excessive antibiotic use generally tends to initiate carcinogenic changes, targeted antibiotic therapy may have therapeutic value once colorectal carcinogenesis has occurred, particularly when used against pathogenic, CRC-associated microbial species such as *Fusobacterium nucleatum*, ETBF, and AIEC [162,163]. For example, Metronidazole, an antibiotic that provides enteric anaerobic coverage, has proven effective against *Fusobacterium nucleatum* [164]. Studies involving rodent CRC xenografts abundant in *Fusobacterium nucleatum* derived from humans showed that Metronidazole treatment reduced *Fusobacterium* load, cancer cell proliferation, and overall tumor growth [164]. Additionally, studies in murine models have demonstrated the efficacy of Cefoxitin, a second-generation cephalosporin, in eradicating ETBF while reducing colonic adenoma formation and median colon tumor numbers [165]. Notably, ETBL is associated with the development of interleukin 17A (IL-17A) dependent, inflammation-induced tumors that require persistent colonization of this *Bacteroides fragilis* subtype for tumorigenesis [165]. Cefoxitin was found to effectively decrease mucosal IL-17A expression in this study [165]. In summary, this subsection underscores the importance of antibiotic stewardship as broad-spectrum or prolonged antibiotic

use can contribute to the overgrowth of pathogenic bacterial species and the subsequent onset of CRC. At the same time, there is growing evidence that once CRC has developed, selected antibiotics targeting these CRC-associated bacteria may play a role in treatment alongside chemotherapeutic agents.

3.2. Microbiota Metabolites, Reactive Oxygen Species, and Colorectal Cancer

Many of the beneficial and pathogenic effects exerted by gut microbiota on cancer development, progression, and treatment are mediated by the metabolites they produce [166]. Just as taxonomical shifts in gut microbiota have been observed in the literature, their metabolites also display unique and conserved changes in those affected with CRC [131,167,168]. For example, CRC-associated metabolites include elevated concentrations of branched-chain amino acids (BCAAs), secondary bile acids, polyamines, and Trimethylamine-N-Oxide (TMAO), while short-chain fatty acids (SCFAs) are characteristically decreased in affected patients [131,169,170]. Of particular interest to this review, there is substantial evidence linking SCFA, secondary bile acids, and TMAO to pre-cancerous and cancerous oxidative environments as they pertain to CRC. These microbiota metabolites will be further discussed in the following subsections.

3.2.1. Short Chain Fatty Acids (SCFAs), Reactive Oxygen Species, and Colorectal Cancer

SCFAs are the catabolic end products of dietary fermentation reactions catalyzed by gut microbiota-related enzymes providing numerous benefits to the human host. These include promoting intestinal barrier integrity, energy regulation, anti-inflammatory, and antioxidant effects [171]. Human enzymes cannot metabolize certain dietary fibers and resistant starches; therefore, gut microbiota serve a symbiotic benefit in producing these SCFAs, which consist mostly of acetate, propionate, and butyrate [172]. In states of dysbiosis and systemic disease, the concentrations of SCFA are notably altered, often significantly reduced [173]. This pattern is observed in patients with CRC, with affected patients having lower serum and fecal SCFA concentrations than unaffected individuals [167,174,175]. A meta-analysis study showed that lower fecal concentrations of acetate, propionate, and butyrate are associated with a higher risk of developing CRC [174]. As previously mentioned, butyrate-producing genera including *Faecalibacterium*, Eubacterium, and *Roseburia*, are significantly reduced in CRC patients. Interestingly, CRC-associated bacteria, such as *Fusobacterium nucleatum*, contribute to this imbalance by outcompeting butyrate-producing bacteria, thereby decreasing its concentration [175].

The mechanisms through which SCFA contribute to the prevention of carcinogenesis and tumor progression are multi-fold, including influencing cell cycle regulation, inflammatory signaling, and cancer signaling pathways as well as suppressing tumor proliferation and metastasis [176]. These metabolic byproducts are known to regulate cancer cell growth through modulating ROS production [175]. Two proposed mechanisms by which SCFA can influence oxidative stress include the activation of its G-coupled protein receptor (GPR41 or GPR43) or its histone deacetylase inhibitor (HDACi) activity [177]. At physiologic levels, butyrate increases the activity of antioxidant enzymes such as glutathione-S-transferase and superoxide dismutase to mitigate oxidative stress [178,179]. SCFA introduction as well as other GPR43 agonists exert similar antioxidant effects and reduce ROS formation [179] (Figure 2). Moreover, GPR43 agonism exerts beneficial effects on inflammatory pathways by improving oxidative stress [180]. For example, in a sepsis-induced inflammatory murine model, the upregulation of the GPR43 gene correlated with reduced ROS-mediated mitochondrial damage while inhibiting NLRP3 inflammasome activity to reduce inflammation, an effect not seen in GPR43 knockout mice [180]. Similarly, GPR43-deficient mice have exacerbated colonic inflammatory responses with elevated pro-inflammatory cytokine concentrations such as TNF- α and IL-17, which is refractory to SCFA treatment [181]. Further, resistant starch diets, rich in SCFA, induced GPR43 mRNA reducing inflammation and decreasing tumor multiplicity and colonic adenocarcinoma formation in a rodent model [182]. Therefore, the SCFA receptor GPR43 plays an important role in reducing oxidative stress and inflammation that could lead to inflammation-driven CRC.



Figure 2. Short chain fatty acids (SCFAs) and antioxidant roles against CRC development. SCFA improves CRC through a reduction in oxidative stress, which enhances antioxidase release and attenuates inflammation. SCFA binding to its receptor, GPR43, and activates the Nrf2-Keap1 pathway. Keap1 dissociates from Nrf2, allowing Nrf2 to enter the nucleus and upregulate the transcription of antioxidant enzymes. This, in turn, reduces ROS concentrations to attenuate the onset of inflammation-induced CRC. On the right, butyrate is shown to enhance HDAC inhibitor activity, which reduces ROS production. Decreased ROS production leads to less activation of the NF-KB signaling pathway and NLRP3 inflammasome, again lessening the development of inflammation-induced CRC. Abbreviations: GPR43, G-coupled Receptor 43; Nrf2, nuclear erythroid factor 2; Keap1, Kelch-like ECH associated protein 1; GST, glutathione-S-transferase; SOD, superoxide dismutase; GPx, glutathione peroxidase; CAT, catalase; ROS, reactive oxygen species; CRC, colorectal cancer; HDACi, histone deacetylase inhibitors; NF-κB, nuclear factor kappa beta; NLRP3, NLR family pyrin domain containing 3.

Histone deacetylase (HDAC) removes acetyl groups on histones, allowing DNA to wrap more tightly, making them more resistant to gene transcription, activation of signaling pathways, and epigenetic modification [183]. Butyrate, the most potent HDACi of the three common SCFAs, assists in inhibiting the removal of acetyl groups [184]. This inherent HDACi capability of SCFA helps suppress the NF- κ B signaling pathway [185] and NLRP3 inflammasome activity [186] to protect the intestinal barrier from inflammatory DNA damage induced by ROS production (Figure 1). Importantly, butyrate-mediated histone deacetylation allows for the transcriptional upregulation of antioxidative enzymes such as glutathione-S-transferases (GST) to inhibit the phosphorylation of *extracellular*

signal-regulated kinase (ERK) and *mitogen-activation protein kinase (MAPK)* signaling in colon cancer cells [187]. *ERK* and *MAPK* overexpression is commonly observed in CRC, as their dysregulation promotes the uncontrolled proliferation of cells [187]. In support of these findings, the accumulation of butyrate has been shown to play an anti-proliferative role by halting cell cycle progression in intestinal epithelial cells, thereby protecting against colonic neoplasia [188]. Research points to histone modification, specifically histone 3 hyperacetylation, as a key factor in the upregulation of cell cycle proteins such as cyclin D1 and p21 [189,190]. Further, through epigenetic modification via HDACi activity, butyrate acts on the Nrf2 promoter to exert potent antioxidant effects [191] (Figure 2). Butyrate administration synergistically promotes Nrf2 accumulation and inhibits histone acetylation through the induction of the AMPK signaling pathway [191]. As such, antioxidant enzymes are upregulated to promote redox balance and attenuate oxidative damage to the intestinal barrier.

However, it should be noted that balanced concentrations of Nrf2 are important, as elevations may also contribute to CRC progression. Significant upregulation of Nrf2 in chemo-resistant cancer cells may make adequate treatment difficult [192-194]. Similarly, colonocytes utilize SCFA as a primary energy source under normal circumstances [195]. With cancer being both a genetic and metabolic disease, cancer cells shift their main source of energy to glucose rather than butyrate [196]. As such, inefficiently metabolized butyrate by cancer cells accumulates in the nucleus of cancer-affected cells, functioning as an HDACi [196]. This phenomenon, known as the Warburg effect, works against cancer cells; in the setting of high butyrate, therefore, probiotics that enhance SCFA concentrations, notably butyrate, are beneficial [197]. Further, in CRC cells treated with acetate, propionate, or butyrate, ROS levels become significantly elevated, contributing to cancer cell death and anti-cancer activity [198]. For example, sodium butyrate introduction directly into colorectal cancer cells induced mitochondria-mediated apoptosis and associated ROS generation [199]. It is shown that the ROS production following direct SCFA treatment into colorectal cancer cells also occurs through the reprogramming of metabolic profiles including alterations in macromolecule transport and metabolism, mitochondrial transport, and respiratory chain complex along with elevated ROS production [198]. This excess ROS production further contributes to cancer cell death, making butyrate a potential therapeutic option when directly administered to colorectal cancer cells [200]. Taken together, these studies demonstrate the importance of redox balance and the multifocal contributions of SCFA in modulating oxidative stress as preventative and therapeutic measures in CRC.

3.2.2. Secondary Bile Acids, Reactive Oxygen Species, and Colorectal Cancer

Bile acids are produced in the liver, stored by the gallbladder, and eventually excreted into the upper intestinal tract to facilitate the digestion of lipids and other fat-soluble molecules [201]. Before excretion, primary bile acids are conjugated with taurine and glycine to prevent passive reabsorption in the upper small intestine [202]. Most primary bile acids undergo enterohepatic cycling, where they are reabsorbed in the distal ileum and returned to the liver via the portal blood system [203]. About 5% of primary bile acids reach the colon, where gut microbiota-derived enzymes convert them into secondary bile acids [204]. Bile salt hydrolase (BSH) is a major enzyme in this process liberating glycine and taurine from primary bile acids. BSH-containing bacterial genera include *Clostridium*, *Enterococcus*, *Listeria*, *Bacteroides*, *Bifidobacterium*, and *Lactobacillus* [205]. Similarly, certain gut microbiota have hydroxysteroid dehydrogenase (HSDH) activity which oxidizes hydroxy groups in primary bile acids to diversify the bile acid pool [206]. Interestingly, these reactions, particularly with HSDH, are highly dependent on the redox potential and oxidative status of the microenvironment [207].

In colon cancer, secondary bile acids are characteristically elevated and have been associated with pathogenesis and tumor progression through multiple mechanisms, including the modulation of oxidative status within the tumor environment [208–211]. Secondary bile acids primarily consist of lithocholic acid (LCA) and deoxycholic acid (DCA) with LCA

being the most toxic secondary bile acid in relation to CRC, and DCA a close second [212]. LCA and DCA produce ROS through the activation of membrane-bound NADH/NADPH oxidases and phospholipase A2 (PLA2) [213,214]. Excess ROS production can activate cellular signaling pathways, including pro-inflammatory NF- κ B, causing sustained inflammation and oxidative DNA damage contributing to CRC pathogenesis [209,211,215]. At the same time, bile acid-induced oxidative stress promotes apoptosis through mitochondrial disruption, resulting in cytochrome C release into the cytosol and activation of caspases [211,216]. However, these cytotoxic effects can affect normal and cancerous cells, with a propensity to have a greater impact on normal cellular physiology. Specifically, these cytotoxic pathways alter the genetic stability of normal colonic cells, while resistant mutant cells may proliferate through the activation of multiple cellular signaling pathways inducing carcinogenesis [213,217]. For example, DCA-mediated ROS production can constitutively activate NF- κ B and promote apoptosis resistance in CRC cells [218] (Figure 3).



Secondary Bile Acids

Figure 3. Secondary bile acids and their oxidative role in development or protection against CRC. Lithocholic acid and deoxycholic acid increase oxidative stress through the activation of membranebound NADPH oxidases. In turn, this increases NF- κ B inflammatory signaling, thereby worsening intestinal tract inflammation. At the same time, ROS production induced from these secondary bile acids can damage DNA, induce cytochrome C release, and initiate apoptosis. These mechanisms influence CRC development. Conversely, ursodeoxycholic acid is a more favorable secondary bile acid that improves microbial composition and decreases ROS production. The stimulation of *ERK1/2* in colon cancer cell lines via UDCA-induced ROS reduction influences cell cycle arrest by preventing cell cycle progression in colon cancer cell lines. This anti-proliferative effect through modulation of oxidative status is beneficial in preventing against progression into CRC. Abbreviations: LCA, lithocholic acid; DCA, deoxycholic acid; UDCA, ursodeoxycholic acid; NOX, NADPH oxidase; ROS, reactive oxygen species; NF- κ B, nuclear factor kappa beta; Cyt C, cytochrome C; CRC, colorectal cancer; *ERK1/2, extracellular signal-regulated kinase*.

While most microbial-synthesized secondary bile acids are tumorigenic, the microbial and synthetically produced secondary bile acid, ursodeoxycholic acid (UDCA), may have anti-cancer properties [219-221]. Interestingly, UDCA introduction can shift the gut microbial composition towards more favorable bacteria, such as increases in Faecalibacterium prausnitzii and Akkermansia muciniphila, while decreasing pro-inflammatory Ruminococcus gnavus [222,223]. Additionally, UDCA competitively displaces toxic bile acid and can accelerate bile acid enterohepatic circulation [224,225]. Though these favorable effects are well-documented, UDCA naturally comprises about 5% of the total bile acid pool; therefore, the effects of DCA and LCA, particularly in pre-cancerous microenvironments and microbial dysbiosis, may predominate [226]. Further, UDCA inhibits the formation of colon cancer progenitor cells by modulating the oxidative environment [221]. For example, UDCA decreased the total colon cancer cell count without increasing apoptosis. More specifically, UDCA treatment-induced reduction in intracellular ROS to enhance ERK1/2 phosphorylation in colon cancer cell lines [221]. ERK1/2 phosphorylation is correlated with cell cycle arrest through G1/S and G2/M transition regulation; therefore, UDCA has anti-proliferative effects through the regulation of cellular oxidative status [221] (Figure 3). These studies highlight the multifactorial influence of secondary bile acids in tumorigenesis and anti-cancer properties, with DCA and LCA having generally harmful effects through ROS production and UCDA having a therapeutic role due to its antioxidant potential.

3.3. Trimethylamine-N-Oxide, Oxidative Stress, and Colorectal Cancer

Trimethylamine (TMA) is a byproduct of gut microbiota metabolism of dietary precursors including carnitine, choline, and betaine [227]. TMA-producing bacteria include those that are elevated in CRC such as *Escherichia* and are generally not abundant in individuals with a healthy composition of gut flora [228]. *Escherichia*, specifically, has intrinsic carnitine oxygenase activity, catalyzing the conversion of carnitine to TMA, a reaction dependent on oxygen availability [228,229]. Alternatively, the phylum Firmicutes has choline-TMA lyase and betaine reductase activity which help convert choline and betaine to TMA, respectively [228]. Once produced, TMA is oxidized to Trimethylamine-N-Oxide (TMAO) in the liver by hepatic flavin monooxygenase [230].

TMAO concentrations are elevated in individuals with CRC and have been correlated with carcinogenesis through mechanisms including oxidative stress-driven inflammation, leading to DNA damage [231,232]. Studies have shown that elevated TMAO levels induce oxidative stress, activating the NLRP3 inflammasome pathway to produce proinflammatory cytokines in a dose-dependent manner [232]. Another study also noted NLRP3 inflammasome activity following increases in TMAO [233]. Interestingly, treatment with N-acetylcysteine, an ROS inhibitor, reversed these TMAO-mediated effects, further supporting the role of TMAO-induced oxidative stress and related inflammation [232] (Figure 4). Additionally, a recent meta-analysis of 363 manuscripts confirmed associations between TMAO and inflammation in humans, demonstrating sustained and dose-dependent increases in C-reactive protein, an important inflammatory marker [234].

While the influence of TMAO on oxidative stress and inflammation is well-documented, the exact mechanisms conferring CRC pathogenesis require further elucidation. In colon epithelial cells, TMAO induces oxidative stress and apoptosis, inducing NLRP3 activity [235]. However, as mentioned throughout this review, sustained levels of ROS and inflammation are known to confer DNA damage and protein misfolding, leading to carcinogenesis. In other cancers, such as hepatocellular carcinoma and pancreatic cancer, TMAO induces carcinogenesis by upregulating inflammatory signaling pathways and superoxide dismutase activity, promoting inflammation-induced cancers [231,236]. Thus, targeting TMAO has been studied as immunotherapy in treating these cancers [237,238]. TMAO may also serve as a future therapeutic target for inflammation-induced CRC in the context of oxidative stress, though more research is necessary to confirm these findings.



Figure 4. Pro-oxidative role of gut etabolite, Trimethylamine-N-Oxide (TMAO) on CRC development. TMAO increases ROS production to initiate inflammatory signaling, mediating the activation of the NLRP3 inflammasome. NLRP3 activity increases pro-inflammatory cytokines, leading to inflammatory gut pathology leading to the onset of inflammation-induced CRC. The administration of N-acetylcysteine, an ROS inhibitor, attenuates TMAO-induced oxidative stress and related inflammation. Abbreviations: ROS, reactive oxygen species; NLRP3, NLRP3, NLR family pyrin domain containing 3; IL-1, interleukin-1; TNF, tumor necrosis factor; IL-6, Interleukin 6; CRC, colorectal cancer.

4. Probiotics, Antioxidant Properties, and Colorectal Cancer

While harmful gut microbial species have been documented to induce ROS-mediated carcinogenesis, beneficial bacteria with probiotic effects can combat colorectal cancer development and progression through their antioxidant properties [21,239,240]. In conditions of bowel inflammation and elevated ROS, probiotics have been shown to reduce ROS concentrations to non-pathological levels [241]. For example, the daily consumption of a probiotic mixture containing *Lactobacillus acidophilus*, *Lactobacillus rhamnosus*, and *Bifidobacterium bifidum* reduced the mean number of tumors by 40% in an inflammation-induced rodent model of CRC [242]. The influence of probiotic bacteria on preventing carcinogenesis through the modulation of oxidative status is multi-faceted. This includes the

microbiota-dependent activation of antioxidative enzymes, regulation of inflammatory signaling pathway, and alteration of circulating microbiota-derived metabolites [243–245]. Probiotic microbial genera include first-generation probiotics such as Bifidobacterium, and Lactobacillus as well as Next-Generation Probiotics (NGPs) like Akkermansia muciniphila, Faecalibacterium prausnitzii, Bacteroides fragilis, Blautia producta, and Clostridium butyricum. First-generation probiotics are well described to have anti-cancer and anti-inflammatory effects related to CRC, partly by regulating oxidative status through oxidative and inflammatory pathways, such as Nrf2-keap1 and NF- κ B signaling, respectively [246–248]. The antioxidant role of NGPs in relation to CRC is less extensively studied, but these probiotics have been documented to have beneficial roles in inflammatory bowel states by exerting antioxidant effects [114,249]. Recent studies have clarified the multifaceted impact of NGPs in mitigating oxidative stress to prevent CRC carcinogenesis [114]. For example, *Faecalibacterium prausnitzii* inhibits NF-κB activation to attenuate the proliferation of CRC cell lines, likely due to its strong butyrate-producing capacity [114]. Additionally, treatment with Faecalibacterium prausnitzii reduced lipid peroxidation and oxidative stress in an azoxymethane-induced CRC rodent model [114]. Azoxymethane is a toxin that induces CRC by depleting GSH and impairing antioxidant response in colon cells [250]. Aberrant crypt foci, precursors to colorectal polyps, were also reduced in this study, indicating that Faecalibacterium may be indicated in CRC prevention.

The following subsections will discuss in detail the mechanisms by which probiotics confer positive changes in combatting oxidative stress and how this influences CRC carcinogenesis and progression, which are also summarized in Table 1. Additionally, probiotics and gut microbiota have also been shown to assist in cancer chemotherapy and immunotherapy [126,237,238,251].

4.1. Probiotics, Antioxidant Enzymes, and Colorectal Cancer

Probiotics exert beneficial antioxidant effects through the modulation of antioxidant enzymes, such as superoxide dismutase, catalase, glutathione peroxidase, and glutathione-S transferase [21]. Generally, lactic acid bacteria are well documented for having intrinsic oxidative defense enzymes such as NADH oxidase and pyruvate oxidase, which help to maintain redox balance [244,252,253]. For example, a recent study demonstrated that introducing *Lactobacillus bulgaricus* into an animal model increased levels of superoxide dismutase, catalase, and glutathione peroxidase, thereby mitigating oxidative stress [254].

Importantly, the positive antioxidant enzymatic changes in probiotics are shown to play a protective role in the onset of CRC-specific tumorigenesis [27,255,256]. Interestingly, the oral administration of Lactococcus lactis, a catalase-producing bacterium, prevented 1,2 dimethylhydrazine (DMH)-induced colon cancer [255] (Table 1). This was evidenced by increased catalase activity which led to significantly less ROS-mediated, inflammatory colonic damage and tumor appearance compared to a non-catalase-producing bacterium counterpart in murine models [255]. Further support for these findings comes from studies involving Lactobacillus plantarum administered in vitro to DMH-induced colon cancer cells, which similarly increased antioxidant enzyme activity, including SOD, CAT, and GST. This led to a reduction in mean tumor volume and total number of tumors [27]. DMH is a procarcinogen that induces colorectal cancer through a series of metabolic reactions producing ROS that alkylate DNA and induce carcinogenesis [257]. Further, a more recent study found that exopolysaccharides (EPS) derived from the probiotic Lactobacillus acidophilus increase the antioxidant enzymes (SOD, CAT, and GPx) concentrations in DMHinduced colon cancer model [256]. EPS-producing bacteria, particularly the Lactobacillus delbruecki strain, also reduced lipid peroxidation via increased antioxidant enzyme activity (GSH, SOD, CAT, and GPx), thereby ameliorating inflammatory mucosal damage [258]. EPS from Lactobacillus and Bifidobacterium have gained attention for their potent antiinflammatory and antioxidant properties including their inherent antioxidant enzyme capabilities [259,260].

Table 1. Effects of probiotics on antioxidant enzymes, antioxidant regulatory pathways, ROSmediated inflammatory signaling pathways in CRC pathogenesis, and augmentation of current Immunotherapy. Abbreviations: ROS, reactive oxygen species; DMH, 1,2 dimethylhydrazine; SOD, superoxide dismutase; CAT, catalase; GST, glutathione-S-transferase; GPx, glutathione peroxidase; EPS, exopolysaccharides; Nrf2, nuclear factor erythroid related factor 2; Keap1, Kelch-like ECHassociated protein 1; NF-κB, nuclear factor kappa beta; DSS, Dextran Sulfate Sodium; CRC, colorectal cancer; IL, interleukin; CRISPR, clustered regularly interspaced short palindromic repeats; NLRP3; nucleotide-binding domain leucin rich containing family pyrin domain containing 3; PD-1, programmed cell death protein 1.

	Probiotic	Results/Implications	Reference
Antioxidant Enzymes	Lactococcus lactis	Increased catalase activity resulting in significantly decreased ROS-mediated inflammatory damage and tumor appearance	[255]
	Lactobacillus plantarum	Administration into DMH-induced colon cancer cells, increased antioxidant enzymes (SOD, CAT, and GST) to reduce mean tumor volume and size	[27]
	Lactobacillus acidophilus	Produced metabolic derivative, EPS, which increased antioxidant enzymes (SOD, CAT, and GPx) to mitigate DMH-induced colon cancer	[256]
	Lactobacillus delbruecki	EPS reduced lipid peroxidation with concurrent increases in antioxidant enzyme activity (SOD, CAT, GPx, and GSH) Ameliorated Inflammatory damage to colonic epithelium	[258]
Nrf2-Keap1	Lactobacillus casei	Reduces oxidative and inflammatory stress in enterocytes by activating the Nrf2-Keap1 and NF-KB pathways Nrf2 activation reduced ROS accumulation through the upregulation of GPx	[248]
	Bifidobacterium bifidum, Lactobacillus gasseri	Activating effects on Nrf2 in combination with vitamin D3 to increase GST and inhibit the onset of colorectal carcinogenesis	[261]
NF-ĸB	Faecalibacterium prausnatzii	Inhibited NF-κB activation to attenuate the proliferation of CRC cell lines Reduced lipid peroxidation and oxidative stress	[114]
	Lactobacillus fermentum	Attenuated NF-кB signaling in DSS-induced colorectal cancer Decreased pro-oxidant cyclo-oxygenase 2	[262]
	Lactiplantibacillus plantarum-12	EPS production alleviated inflammation through inhibition of NF-κB signaling pathway Related reduction in pro-inflammatory cytokines to inhibit inflammation-induced CRC development	[263]
	Clostridium butyricum	Decreases the phosphorylation of NF-ĸB to decrease cytokine activation, ultimately reducing tumor incidence and size in a colitis-induced CRC model Improves microbial composition in the same CRC model	[264]
	Bifidobacterium longum	Diminished NF-KB induction in CRC cells to attenuate development of aberrant crypt foci	[265]
VSL#3	Lactobacillus acidophilus, Lactobacillus plantarum, Lactobacillus casei, Lactobacillus bulgaricus, Bifidobacterium breve, Bifidobacterium longum, Bifidobacterium infantis, Streptococcus thermophilus	Reduced the expression of pro-oxidant enzymes such as cyclo-oxygenase 2 in DSS-induced mice Attenuate IL-6, IL-1β and increased concentrations of regulatory IL-10	[266]
		Attenuated ROS concentrations to reduce pro-inflammatory chemokines and colitis symptoms Reduced barrier permeability	[267]
		Promotes butyrate production, which is found to increase the expression of antioxidants in colitis-associated CRC models	[268]

	Probiotic	Results/Implications	Reference
Immuno-therapy Augmentation	Lactobacillus rhamnosus GG	Incorporated as part of a probiotic-CRISPR cancer immunotherapy system that can penetrate hypoxic tumor environments Allowed CRISPR system to reach tumor microenvironment to enhance ROS release and promote cell death	[269]
	Lactobacillus reuteri	Metabolite, reuterin, alters tumor microenvironment oxidative status Selectively enhances ROS expression within colorectal cancer cells to suppress tumor growth	[244]
	Enterococcus faecalis	Reduced NLRP3 inflammasome activity through attenuation of phagocytosis, which is necessary for activation Prevented the onset of CRC development	[270]
	Enterococcus durans	Nanoparticle treatment of probiotic cultures increased folate concentrations ROS-producing capabilities of the treated probiotic decreased CRC viability by 19%	[271]
	Roseburia intestinalis	Induction of CD8+ T-cell mediated cytotoxicity through metabolite, butyrate Augmented PD-1 therapy against CRC	[251]
Radiotherapy Augmentation	Roseburia intestinalis	Sensitized inflammation-induced CRC cells to radiotherapy treatment through butyrate production Butyrate facilitated autophagy in irradiated cells to induce cell death	[272]

Table 1. Cont.

4.2. Probiotics, Antioxidant Signaling Pathways, and Colorectal Cancer

As discussed throughout this review, the Nrf-2 antioxidant pathway plays a crucial role in regulating oxidative stress by modulating a broad spectrum of antioxidant enzymes, contributing to the detoxification and elimination of oxygen free radicals [248]. The gut microbiota and their metabolites significantly influence the maintenance of intestinal barrier integrity, partly through the Nrf2-dependent upregulation of epithelial tight junction proteins [273]. Similarly, natural products that improve inflammatory disease and colitis-associated CRC are shown to inhibit inflammatory responses, oxidative stress, and mucosal injury by enhancing gut microbial composition and signaling via the Nrf2/HO-1 pathway.

The probiotic-mediated activation of Nrf-2 is shown to mediate significant antioxidant and anti-inflammatory effects, thus suppressing the onset of inflammation-induced CRC [248,274]. For example, a recent comparative study on the antioxidant and antiinflammatory efficacy of probiotic administration in colitis-induced mice showed the down-regulation of Nrf2 and NF-kB related genes and alleviated colitis [274]. Interestingly, the probiotic, containing 88 strains of *Lactobacillus* and *Bifidobacterium spp.*, improved antioxidant enzymatic activity (SOD, CAT, GPX, and GSH), while reducing the concentrations of pro-inflammatory cytokines such as TNF- α [274]. Lactobacillus casei, a lactic acid-producing bacterium, has demonstrated a redox role against oxidative and inflammatory stress in enterocytes through activation of both Nrf-2 and NF-κB signaling [248]. In this study, Nrf2 activation by Lactobacillus casei reduced ROS accumulation in enterocytes by upregulating glutathione peroxidase [248]. Similarly, Bifidobacterium bifidum and Lactobacillus gasseri supplementation in conjunction with vitamin D3 also activated Nrf2, with concomitant increases in GST to inhibit the onset of colorectal carcinogenesis in a rodent model [261]. Overall, Lactobacillus spp. and their metabolites are well documented to confer potent antioxidant effects through activation of Nrf2 mediated pathways throughout the body, providing further insight into the role of these bacteria in redox balance and treatment of inflammatory disease [275–277]. These findings suggest that probiotic supplementation can reduce ROS-mediated damage and inflammatory stress to enterocytes helping delay or prevent the onset of CRC [248,261]. However, it is important to note that the effects of probiotics

on Nrf2-keap1 activity in malignant cells are not well studied and the highlighted studies mainly focus on the preventative effects of probiotics on inflammation-induced CRC.

4.3. Probiotics, ROS-Mediated Inflammatory Signaling Pathways, and Colorectal Cancer

Probiotics have significant positive implications in preventing inflammation-induced CRC through mediating ROS-mediated, inflammatory, and cancer-related signaling pathways such as NF-κB [278]. Enhanced oxidative stress can initiate constitutive signaling through the NF-KB pathway, promoting inflammatory damage and related carcinogenesis in the colon [86,279]. Lactic acid bacteria are implicated in mitigating the NF-κB signaling pathway and protecting against carcinogenesis [262,263]. For example, Lactobacillus fermentum supplementation in Dextran Sulfate Sodium (DSS)-induced colorectal cancer rodent models attenuated NF- κ B signaling pathway signaling by decreasing key proteins I κ B α and p65 and target protein cyclooxygenase-2, a known pro-oxidant [262]. DSS induces CRC by causing colonic epithelial inflammatory damage [280], suggesting that probiotics can mitigate inflammatory signaling pathways to delay carcinogenesis [262]. Similarly, Lactiplantibacillus plantarum-12-derived EPS significantly alleviated inflammation by inhibiting the NF-κB signaling pathway and reducing pro-inflammatory cytokines in a murine model of inflammation-induced colon cancer [263]. This bacterium also enhances gut microbial composition by promoting the survival of beneficial gut microbiota and reducing the relative contributions of inflammatory species [263]. Additionally, the butyrate-producing Clostridium butyricum decreases the phosphorylation of NF-KB and improves microbial composition in a colitis-associated colon cancer rodent model [264]. Inhibition of NF- κ B signaling was a catalyst for the observed decreased cytokine activity, increased apoptosis, and reduced tumor incidence and size. Similarly, Bifidobacterium longum reduced NF-KB signaling in CRC cells while attenuating the development of aberrant crypt foci in this murine model [265]. Taken together, these studies provide strong evidence linking the NF- κ B pathway, a byproduct of increased oxidative stress, to CRC pathogenesis, with probiotics serving as an efficient therapeutic intervention to attenuate signaling.

Further, VSL#3, a probiotic mixture consisting of microbial species from three bacterial genera (Lactobacillus, Bifidobacterium, and Streptococcus) mitigates inflammation-induced colorectal adenocarcinoma development through the modulation of ROS and inflammatory markers [266,267,281]. Specifically, colonic inflammation scores and incidence of colonic dysplastic lesions were significantly reduced following administration, with concurrent reductions in IL-6, IL-1β, and increased concentrations of regulatory IL-10 [266]. Similarly, the expression of pro-oxidative enzymes such as cyclooxygenase-2 was reduced in these DSS-induced mice, corresponding with decreased ROS activity [266]. Follow-up studies also supported the anti-inflammatory role of VSL#3 through observed suppression of IL-6/STAT3 promoting preventative effects on CRC development [281]. The anti-inflammatory effect of this probiotic mixture is elucidated through its influence on enhancing intestinal barrier function in MUC2-deficient mice [267]. MUC2 serves multiple important roles in maintaining intestinal barrier integrity, with the glycoprotein serving as a protective mucin layer and an important food source for beneficial bacteria [282]. In MUC2-deficient mice, VSL#3 alone reduced barrier permeability, while attenuating pro-inflammatory chemokines and colitis symptoms, partly through the attenuation of ROS [267]. Interestingly, these effects were mediated by the gut metabolite, acetate. However, butyrate production from the introduction of VSL#3 has also demonstrated increased expression of antioxidant enzymes in a colitis-associated CRC model [268]. Taken together, VSL#3 and other probiotic formulations play integral roles in inflammatory pathways, often involving mediation of oxidative stress and ROS, to mitigate the progression or development of inflammationinduced CRC.

4.4. Probiotics, Antioxidants and Colorectal Cancer Immunotherapy, and Treatment

There is compelling evidence showing that probiotics protect against CRC pathogenesis and progression, in part, by modulating oxidative stress and related inflammatory processes. In recent years, it has been shown that probiotics can influence oxidative microenvironments to enhance cancer immunotherapy in the treatment of colorectal cancer [269,283]. For example, in antibiotic-treated rodent models, cancer immunotherapy via CpG oligonucleotide treatment diminished both cytokine production and ROS-mediated cytotoxicity in cancer-specific cells, indicating poorer therapeutic responses [283]. Further, recent studies have elucidated a probiotic-CRISPR cancer immunotherapy system consisting of *Lactobacillus rhamnosus GG*. This *Lactobacillus* spp. acts as a vector that can penetrate hypoxic tumor environments allowing CRISPR-derived cancer immunotherapy to reach the tumor microenvironment, enhance ROS release, and induce cell death [269]. Additionally, *Lactobacillus reuteri*, a commonly used probiotic, has been shown to reduce the survivability and proliferation of CRC cells by alternating the oxidative status of the tumor microenvironment [244]. Interestingly, its metabolite, reuterin, mediates these positive effects through protein oxidation, selectively enhancing ROS expression within tumor cells to suppress cancer growth [244]. The observed dose-dependent effects of reuterin were observed in colon cancer cells, but not in reuterin-resistant counterpart cells.

Enterococcus spp. have also emerged as probiotics with anti-neoplastic properties [270]. While *Enterococcus faecalis* was previously implicated in pro-carcinogenic effects due to colonic epithelial DNA damage via extracellular superoxide and hydrogen peroxide production [284], recent studies have shown the opposite. Heat-killed *Enterococcus faecalis* treatment has been shown to mitigate intestinal inflammation and prevent inflammation-induced CRC [270], by reducing NLRP3 inflammasome activity. This effect was not observed in NLRP3 knockout mice [270], highlighting the importance of the inflammasome in the efficacy of *Enterococcus faecalis* on CRC treatment. Further, a recent study aimed to harness the ROS-producing capabilities to selectively destroy colorectal cancer cells through nanoparticle therapy [271]. Nanoparticle treatment of *Enterococcus durans* cultures increased extracellular folate concentrations, interacting with metabolic pathways involving amino acids, SCFAs, and energy metabolites [271]. The subsequent introduction of this nanoparticle-treated *Enterococcus durans* cell line into HCT 116 colorectal cancer cell lines decreased cell viability by 19%, indicating a novel anti-neoplastic role of the bacterium.

In the inflammation-induced CRC model, recent findings have shown that *Roseburia intestinalis* enhances immunotherapy, specifically anti-PD-1 therapy in CRC via butyrate production [251]. CRC patients exhibited significantly reduced *Roseburia* concentrations, while supplementation induced CD8+ T-cell mediated cytotoxicity through butyrate binding to Toll-like receptor 5 and activation of NF- κ B signaling [251]. Similarly, *Roseburia intestinalis* has also been shown to sensitize inflammation-induced CRC to radiotherapy treatment, again through the production of butyrate [272]. In this rodent model, butyrate facilitated autophagy in irradiated cells, inducing cell death [272]. These findings suggest that *Roseburia intestinalis* may play an important role in augmenting immunotherapy through the modulation of oxidative and related immunological factors.

5. Conclusions and Perspectives

There is substantial evidence linking the gut microbiota to oxidative status in CRC models. The intricate interplay between microbiota metabolites, ROS production, and tumorigenesis provides valuable insight into colorectal carcinogenesis. ROS play a dual role in CRC, acting as signaling molecules under normal conditions but contributing to tumorigenesis when in excess. ROS can induce DNA damage, lipid peroxidation, and protein modifications, leading to mutations and carcinogenesis. Oxidative stress also promotes inflammatory signaling pathways, such as NF-kB and NLRP3, further contributing to CRC development. The gut microbiota significantly impacts oxidative status and CRC pathogenesis. Certain bacterial species, such as *Fusobacterium nucleatum* and *Escherichia coli*, can enhance ROS production and inflammatory signaling, promoting tumor growth and metastasis. Conversely, beneficial bacteria like *Faecalibacterium prausnitzii* and *Lactobacillus* spp. exhibit antioxidant properties, mitigating ROS-mediated damage and reducing inflammation. Probiotics have shown promise in preventing and treating inflammation-induced

CRC. They can modulate oxidative stress, enhance antioxidant enzyme activity, and influence inflammatory pathways. Specific probiotics, such as *Lactobacillus* and *Bifidobacterium*, have demonstrated efficacy in reducing tumor incidence, enhancing immune responses, and improving the efficacy of cancer immunotherapy. The findings reviewed underscore the complex interplay between gut microbiota, ROS, and CRC. Future research should focus on (i) elucidating the precise mechanisms by which specific gut bacteria influence ROS production and inflammatory pathways; (ii) investigating the role of probiotics in different stages of CRC and their potential in combination therapies with the existing treatments; (iii) exploring the impact of diet and lifestyle modifications on gut microbiota composition and CRC risk; (iv) developing targeted probiotic therapies to enhance the antioxidant and anti-inflammatory responses in CRC patients. Incorporating probiotics and other microbiota-targeted therapies into clinical practice could offer a novel approach to CRC prevention and treatment, potentially improving patient outcomes and reducing the global burden of this disease.

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