

Interaction Between Local Superfoods and The Microbiome: The Role of The Indonesian Traditional Diet In Mitigating Colorectal Carcinogenesis

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Abstract.

This study examines the interaction between local superfoods and the gut microbiome in mitigating colorectal carcinogenesis through the Indonesian traditional dietary pattern. The central problem lies in the increasing prevalence of intestinal dysbiosis driven by modern dietary transitions, which contributes to colorectal cancer risk. The study aims to analyze the role of the Indonesian traditional diet in maintaining microbial balance as a preventive strategy against colorectal cancer. A narrative literature review approach was employed, thematically synthesizing peer-reviewed publications addressing gut dysbiosis, colorectal carcinoma, and tempeh as Indonesian fermented soybean food, consistent with standard narrative review reporting practice rather than a PRISMA-based systematic protocol. The findings indicate that local superfood consumption promotes eubiosis, reduces chronic inflammation, and supports colonic health. The study concludes that the Indonesian traditional diet represents a strategic microbiome-based nutritional prevention approach.

Keywords: Gut Dysbiosis; Colorectal Carcinoma; Tempe (Indonesian Fermented Foods); Traditional Diet and Microbiome.

I. INTRODUCTION

Colorectal cancer represents one of the leading causes of global mortality and is increasingly understood not merely as a genetic disorder but as an ecological disease closely associated with the balance of the human gut microbiome (Wang & Li, 2022). Advances in microbiome research demonstrate that intestinal bacterial communities actively maintain colonic epithelial homeostasis through immune regulation, nutrient metabolism, and the production of bioactive metabolites that exert protective effects against tumorigenesis (Singh et al., 2023). Disruption of this balance, commonly referred to as intestinal dysbiosis, leads to the dominance of pathogenic bacteria that produce proinflammatory and genotoxic metabolites, thereby accelerating colorectal carcinogenesis (Singh et al., 2023). Within this context, dietary patterns emerge as a primary determinant because diet directly shapes both the structure and metabolic function of gut microbiota through dynamic diet microbiome interactions (Wang & Li, 2022). Traditional diets based on plant foods and natural fermentation have been shown to increase the production of short-chain fatty acids, particularly butyrate, which supports colonic mucosal integrity and suppresses cancer cell proliferation (Wang & Li, 2022). Indonesia possesses a wide range of local superfoods such as tempeh, traditional spices, and high-fiber foods whose bioactive compounds have recently been catalogued as preventive agents against degenerative disease (Tambunan, 2025), yet remain insufficiently examined within a microbiome-based cancer mitigation framework. Therefore, understanding the interaction between local superfoods and the microbiome becomes a critical scientific issue for evaluating the preventive potential of the Indonesian traditional diet against colorectal carcinogenesis.

Recent literature emphasizes that the relationship between diet and colorectal cancer has largely been explained through the Western diet theory, which highlights high consumption of animal fats, refined sugars, and ultra-processed foods as major risk factors for cancer development; however, this approach primarily focuses on risk exposure rather than clarifying the specific protective mechanisms embedded within traditional local diets (Singh et al., 2023). Contemporary microbiome studies reveal that dietary modification can rapidly alter gut bacterial composition, yet most investigations remain centered on Western populations, limiting representation of Southeast Asian dietary diversity, particularly the Indonesian context. A recent systematic review on dietary interventions and microbiota among individuals at risk for colorectal cancer indicates that dietary modification significantly reshapes microbiome profiles, although findings remain

heterogeneous due to variations in food types, cultural consumption patterns, and environmental determinants that have not been comprehensively integrated. Furthermore, functional food and prebiotic theories have not fully linked traditional fermented food consumption with microbiota derived anti carcinogenic metabolic mechanisms in depth. This gap suggests that the dysbiosis inflammation carcinogenesis framework has yet to adequately explain how the Indonesian traditional diet functions as a restorative agent toward intestinal eubiosis. Consequently, a systematic synthesis of literature that connects diet--microbiome theory with Indonesian local superfoods is necessary to provide a more integrated biological explanation for colorectal cancer mitigation mechanisms.

This study aims to conduct a narrative literature review to analyze the interaction between Indonesian local superfoods and the gut microbiome in mitigating colorectal carcinogenesis through a multidisciplinary integration of nutrition science, microbiology, and molecular oncology. The narrative review approach was selected because it enables integrative synthesis of empirical evidence derived from experimental, clinical, and epidemiological studies across disciplines, thereby generating a richer conceptual understanding than a single-study analysis (Sukhera, 2022). The research focuses on the relationship between the consumption of locally fermented soybean foods such as tempeh and modulation of microbiota communities that produce protective metabolites, including short-chain fatty acids with anti inflammatory and antitumor properties (Wang & Li, 2022). The study further evaluates how bioactive compounds derived from local plants, particularly polyphenols, operate through the polyphenol microbiota interplay mechanism in which phenolic compounds are transformed by colonic bacteria into smaller bioactive metabolites possessing antioxidant and anti-carcinogenic effects (Singh et al., 2023). Through this narrative review framework, the study seeks to identify consistent patterns explaining how Indonesian traditional dietary practices contribute to gut microbiome ecosystem stability and reduce colorectal cancer risk. Thus, the research objective extends beyond literature synthesis toward constructing a scientific conceptual framework positioning traditional diet as a microbiome based preventive strategy.

The importance of this research is grounded in the argument that the increasing incidence of colorectal cancer in developing countries cannot be explained solely by genetic factors but is strongly associated with dietary transitions driven by westernization, which shift consumption patterns away from traditional foods toward low-fiber and high processed fat diets (Singh et al., 2023). Such dietary changes contribute to intestinal dysbiosis characterized by chronic inflammation, epithelial damage, and activation of pro carcinogenic molecular pathways mediated by harmful microbial metabolites (Wang & Li, 2022). Recent scientific evidence suggests that microbiome-based dietary intervention holds significant potential as a safe and sustainable non-pharmacological preventive strategy compared with approaches relying exclusively on curative treatment. Nevertheless, the limited number of studies positioning the Indonesian traditional diet as a central scientific object has restricted the optimal utilization of local superfoods within preventive health policy development. This study therefore hypothesizes that integrating consumption of fermented soybean foods and traditional plant-based dietary components can restore microbiome balance toward eubiosis, thereby biologically suppressing colorectal carcinogenesis processes. Based on empirical evidence and research objectives, this study becomes highly relevant for strengthening the scientific foundation of culturally grounded precision nutrition strategies in Indonesia.

II. METHODS

Study Design and Reporting Guideline

This study was conducted as a systematic literature review structured according to the general reporting principles of the PRISMA 2020 Statement (Page et al., 2021), adapted to the scope and resources available for this review; deviations from full PRISMA methodology are stated explicitly below and in the Limitations. Because this review synthesizes previously published literature, ethical approval and informed consent were not required.

This research is grounded in five major theoretical frameworks that serve as conceptual foundations for understanding the relationship between traditional Indonesian diets and colorectal carcinogenesis mitigation, encompassing the gut microbiome-cancer axis, dietary fermentation science, short-chain fatty acid metabolism, dysbiosis theory, and the traditional-versus-Western diet paradigm.

Eligibility Criteria

Criteria To strengthen the empirical grounding of the thematic synthesis, a supplementary targeted search of primary empirical studies was additionally conducted using the Consensus academic search database, covering tempeh/fermented soy-gut microbiota studies, dietary fiber-short-chain fatty acid-colorectal cancer studies, and Indonesian/Asian traditional diet-gut microbiota studies. Screening was performed at the title/abstract level; full-text verification of the identified primary studies is recommended prior to final reliance on specific quantitative findings reported herein.

Studies were considered eligible if they: (1) constituted original empirical research (human intervention, human observational, or animal/model studies); (2) examined an exposure involving Indonesian or Asian traditional/local foods, fermented soy-based foods (particularly tempeh), dietary fiber, or polyphenol-rich plant foods; and (3) reported an outcome related to gut microbiota composition or function and/or a colorectal-cancer-relevant endpoint (e.g., short-chain fatty acid production, precancerous lesion risk, colorectal cancer risk). Narrative reviews, systematic reviews, and meta-analyses were excluded from the primary evidence base but several were retained as contextual and mechanistic background references cited elsewhere in this review.

Information Sources and Search Strategy

Literature was identified using Consensus (consensus.app), an AI-assisted academic search platform indexing peer-reviewed publications. Four topic-based searches were conducted in July 2026 using keyword combinations addressing: (1) tempeh or fermented soybean consumption and gut microbiota; (2) dietary fiber, short-chain fatty acids, and colorectal cancer risk; (3) polyphenol-rich spices and gut microbiota-colorectal cancer interactions; and (4) Indonesian traditional diet and gut microbiota composition. For each query, the top-ranked results returned by the platform were retrieved for screening (10 per query; 40 records in total). This single-platform, top-ranked retrieval approach is narrower in scope than a conventional multi-database systematic search (e.g., PubMed, Scopus, ScienceDirect, Google Scholar) and should be regarded as a preliminary, resource-constrained systematic search; expansion to additional databases and more exhaustive retrieval is recommended before final submission.

Study Selection

Retrieved records were screened at the title and abstract level against the eligibility criteria above. Duplicate records ($n = 2$) were removed, leaving 38 unique records. Of these, 25 were excluded, primarily because they were reviews or meta-analyses rather than primary empirical studies ($n = 23$), or because the exposure or outcome fell outside the defined scope ($n = 2$). The remaining 13 records were assessed for eligibility using the abstract content available through the search platform; full-text screening was not performed due to resource constraints and is recommended as a verification step by the author team prior to submission.

Data Extraction and Quality Assessment

Data extracted from each included study comprised the study design, population or model, dietary exposure, and principal finding relevant to gut microbiota or colorectal-cancer-related outcomes (Table 2). Because full-text access was not obtained for all included studies, formal risk-of-bias or methodological quality scoring (e.g., Newcastle-Ottawa Scale) was not performed; instead, study design and sample size are reported transparently in Table 2 so readers can weigh the strength of each source. Two included studies were flagged as carrying comparatively lower evidentiary weight due to a very small sample size (Hitipeuw et al., 2025; $n = 2$ infants) or an outcome only indirectly related to the review question (Surono et al., 2021; nutritional stunting rather than a microbiota-colorectal cancer endpoint directly).

Data Synthesis

Given substantial heterogeneity in study design, population, exposure operationalization, and outcome measures across the 13 included studies, a quantitative meta-analysis was not undertaken. Findings were synthesized narratively and organized thematically according to the type of local superfood or dietary exposure examined, supplemented by mechanistic and review literature cited throughout the Discussion. Data analysis followed a content-analysis approach for interpreting textual and quantitative information drawn from the included literature (Krippendorff, 2018; Hsieh & Shannon, 2005).

III. RESULTS

Intestinal Dysbiosis as a Precursor to Colorectal Carcinogenesis

The reviewed literature demonstrates that intestinal dysbiosis is consistently defined as alterations in the composition, metabolic function, and stability of human gut microbial communities that deviate from biological homeostasis. The analyzed literature indicates that contemporary microbiome research positions dysbiosis as an early indicator of gastrointestinal health disturbance preceding clinical manifestations of chronic disease (Human Microbiome Project Consortium, 2012; Hou et al., 2023; Shreiner et al., 2022). Evidence gathered from scientific databases shows increased abundance of pathobiont bacteria such as *Fusobacterium nucleatum* and pathogenic *Escherichia coli*, accompanied by reduced populations of butyrate-producing bacteria including *Faecalibacterium prausnitzii* and *Roseburia* species in individuals experiencing metabolic and intestinal inflammatory disorders (Chen et al., 2024; Garrett, 2015). The literature further describes that microbial imbalance correlates with decreased production of short-chain fatty acids responsible for maintaining colon mucosal integrity (Louis & Flint, 2017; Valdes et al., 2018). Several studies emphasize diet as a primary determinant influencing microbiota structure, often exceeding genetic factors in explanatory power (Wong et al., 2023; Sonnenburg & Bäckhed, 2016; Zmora et al., 2019). Data synthesized in this review consistently associate low-fiber and high animal-fat dietary patterns with increased dysbiosis across diverse global populations (O'Keefe, 2016). Overall findings indicate that intestinal dysbiosis represents not merely a microbiological phenomenon but a systemic biological condition linked to metabolic dysfunction, chronic inflammation, and alterations within the colon microenvironment (Tilg et al., 2022; Thakur et al., 2026).

Interpretation of the literature data reveals that intestinal dysbiosis develops through alterations in nutrient substrates available to gut microbiota. Studies demonstrate that low dietary fiber intake reduces fermentation of complex carbohydrates, depriving commensal bacteria of essential energy sources required to produce protective metabolites (Sreenesh et al., 2025; Louis & Flint, 2017; Valdes et al., 2018). The analyzed literature shows that under these conditions, opportunistic microorganisms shift toward metabolizing proteins and lipids, generating proinflammatory compounds such as ammonia, hydrogen sulfide, and secondary bile acid derivatives (O'Keefe, 2016; Sonnenburg & Bäckhed, 2016; Zmora et al., 2019). Several studies associate these metabolites with epithelial barrier disruption and increased intestinal permeability (Garrett, 2015; Tilg et al., 2022; Hou et al., 2023). Additional evidence indicates that dysbiosis-induced environmental changes activate mucosal immune responses characterized by elevated inflammatory cytokine production (Shreiner et al., 2022; Tilg et al., 2022). The literature also highlights the dynamic nature of dysbiosis, showing that microbial composition changes according to long-term dietary patterns (Wong et al., 2023). Studies consistently report that plant-based diets and traditional fermented foods increase microbial diversity and restore anti-inflammatory metabolite production (Astuti et al., 2023; Lee et al., 2024; Leeuwendaal et al., 2022; Nout & Kiers, 2022; Lippolis et al., 2023). These findings position nutritional factors as central mechanisms explaining the biological processes underlying intestinal dysbiosis (Wang & Li, 2022; Chen et al., 2024).

The relationship between descriptive and explanatory findings on intestinal dysbiosis aligns with the research problem addressing increasing colon health disturbances associated with modern dietary transitions. Literature analysis demonstrates that populations consuming highly processed diets experience reduced

microbiota diversity compared with communities maintaining plant-based traditional dietary patterns (Sonnenburg & Bäckhed, 2016; Zmora et al., 2019). The data illustrate a clear association between modern dietary transitions and growing gut microbiome imbalance (Wong et al., 2023). Several studies further report that dysbiosis frequently appears before clinical diagnosis of colorectal cancer, positioning dysbiosis as a biological precursor to disease development (Chen et al., 2024; Garrett, 2015; Wang & Li, 2022). Population-based studies included in the review identify correlations among urbanization, lifestyle change, and increased microbiota disruption in Asian populations experiencing rapid dietary shifts (Nguyen et al., 2024; Xi & Xu, 2023; Arnold et al., 2017). The collected evidence suggests that colon health challenges are closely linked to broader food system transformations rather than isolated medical factors (Dekker et al., 2022; Siegel et al., 2020). These relationships reinforce the relevance of investigating traditional Indonesian dietary practices as nutrition-based mitigation strategies targeting microbiome imbalance (Lee et al., 2024; Nout & Kiers, 2022).

Colorectal Cancer as a Multifactorial, Diet-Associated Disease

Literature findings on colorectal cancer describe the disease as a malignancy of colon epithelial tissue developing through multistage carcinogenesis (Dekker et al., 2022; Biller & Schrag, 2021). Scientific studies explain that colorectal cancer progresses through sequential molecular alterations beginning with adenomatous lesions and advancing toward invasive carcinoma (Dekker et al., 2022; Siegel et al., 2020). The reviewed literature identifies genetic mutations involving APC, KRAS, and TP53 genes as common characteristics in tumor development (Dekker et al., 2022; Chen et al., 2024). Beyond genetic factors, analyzed studies emphasize environmental determinants including dietary patterns, chronic inflammation, and microbiota alterations as critical contributors to disease progression (Garrett, 2015; O'Keefe, 2016; Chen et al., 2024). Epidemiological evidence demonstrates increasing global incidence of colorectal cancer, including rising cases among younger populations (Arnold et al., 2017; Nguyen et al., 2024; Xi & Xu, 2023). The literature also describes biological differences between proximal colon, distal colon, and rectal tumors (Dekker et al., 2022). Lifestyle factors such as excessive red meat consumption, obesity, and physical inactivity consistently appear alongside increased disease risk (Nguyen et al., 2024; O'Keefe, 2016; Singh et al., 2023). Collectively, the literature portrays colorectal cancer as a multifactorial disease shaped by complex interactions among genetic susceptibility, environmental exposure, and microbiome dynamics (Garrett, 2015; Hou et al., 2023; Chen et al., 2024).

Explanation of colorectal cancer literature reveals that tumor development results from long-term interaction among multiple biological mechanisms (Garrett, 2015; Chen et al., 2024). Studies indicate that chronic inflammation within the colon mucosa creates a microenvironment conducive to abnormal cell proliferation (Tilg et al., 2022; Garrett, 2015). Several analyzed investigations show that specific microbial metabolites can induce DNA damage and alter gene expression pathways regulating cell growth (O'Keefe, 2016; Chen et al., 2024; Wang & Li, 2022). The literature also describes how disrupted bile acid metabolism caused by high-fat dietary patterns produces carcinogenic compounds that increase oxidative stress in colon epithelial cells (O'Keefe et al., 2015; O'Keefe, 2016). Additional research links reduced butyrate production by gut microbiota with impaired apoptosis regulation in colon cells (Louis & Flint, 2017; Wang & Li, 2022; Chen et al., 2024). These findings demonstrate that colorectal cancer evolves through progressive interaction between genetic alterations and environmental pressures within the colon microenvironment (Garrett, 2015; Hou et al., 2023; Chen et al., 2024). The literature consistently identifies diet as a significant factor influencing inflammatory pathways and microbiota metabolism associated with tumor development (Sonnenburg & Bäckhed, 2016; Zmora et al., 2019; Singh et al., 2023).

The relationship between descriptive and explanatory data on colorectal cancer strongly corresponds with the research problem concerning changes in modern consumption patterns (Nguyen et al., 2024; Xi & Xu, 2023). The analyzed literature indicates that increased colorectal cancer incidence frequently accompanies adoption of Western dietary patterns characterized by high consumption of ultra-processed foods (O'Keefe, 2016; Nguyen et al., 2024). Synthesized epidemiological evidence shows that regions

experiencing reduced intake of traditional plant-based foods also demonstrate increased metabolic and inflammatory risk factors affecting colon health (O'Keefe et al., 2015; Sonnenburg & Bäckhed, 2016). The literature further shows that microbiota alterations induced by modern dietary habits correlate with biological mechanisms involved in colon carcinogenesis (Garrett, 2015; Chen et al., 2024; Wang & Li, 2022). Several studies report that populations maintaining traditional dietary practices exhibit greater microbiome diversity than urban populations with high processed food intake (O'Keefe et al., 2015; Sonnenburg & Bäckhed, 2016; Zmora et al., 2019). These relationships confirm alignment between rising colorectal cancer trends and the research focus on traditional Indonesian diets as preventive approaches (Astuti et al., 2023; Lee et al., 2024; Nout & Kiers, 2022). Consequently, epidemiological realities strengthen the urgency of examining interactions between local foods and gut microbiota (Astuti et al., 2023; Lee et al., 2024; Hou et al., 2023).

Tempe and Local Fermented Foods as Functional Modulators of the Gut Microbiome

Literature findings concerning local soybean fermentation indicate that tempe is classified as a traditional Indonesian functional food with distinct nutritional and microbiological characteristics (Astuti et al., 2023; Nout & Kiers, 2022; Teoh et al., 2024). The analyzed literature explains that fermentation by *Rhizopus* species modifies soybean protein structures into more digestible forms (Astuti et al., 2023; Nout & Kiers, 2022). Research data show increased levels of bioactive peptides, aglycone isoflavones, B-complex vitamins, and antioxidant compounds following fermentation (Astuti et al., 2023; Leeuwendaal et al., 2022). Several studies report that tempe fermentation produces viable microorganisms alongside prebiotic substrates supporting beneficial gut bacteria growth (Leeuwendaal et al., 2022; Lee et al., 2024). The literature associates tempe consumption with enhanced antioxidant activity and improved lipid metabolism across experimental models (Astuti et al., 2023; Lippolis et al., 2023). Additional studies indicate that fermented soybean foods contain dietary fiber and phenolic compounds capable of interacting with colon microbiota (Lee et al., 2024; Lippolis et al., 2023). Overall findings demonstrate that tempe functions not only as a plant protein source but also as a traditional dietary component with biological relevance for gut microbiome health (Astuti et al., 2023; Leeuwendaal et al., 2022; Hou et al., 2023).

Interpretation of fermented soybean literature shows that fermentation enhances bioavailability of active compounds previously bound within raw soybean matrices (Nout & Kiers, 2022; Astuti et al. (Seo et al., 2025), 2023). Studies explain that fermentative microorganisms produce protease and phytase enzymes that break complex compounds into metabolically accessible bioactive components (Nout & Kiers, 2022). Evidence indicates that fermentation-derived metabolites serve as substrates for commensal gut bacteria, promoting increased microbial diversity (Lee et al., 2024; Leeuwendaal et al., 2022; Hou et al., 2023). The literature also reports transformation of isoflavones into aglycone forms exhibiting stronger anti-inflammatory activity than glycoside forms (Astuti et al., 2023; Lippolis et al., 2023). Several studies demonstrate associations between fermented food consumption and increased production of short-chain fatty acids supporting colon epithelial homeostasis (Louis & Flint, 2017; Lee et al., 2024; Leeuwendaal et al., 2022). These findings indicate that local soybean fermentation generates simultaneous probiotic and prebiotic effects (Leeuwendaal et al., 2022; Lee et al., 2024). The biological mechanism of tempe fermentation can therefore be explained through interaction among nutrient transformation, microbial fermentation activity, and metabolic responses of gut microbiota (Hou et al., 2023; Shreiner et al., 2022; Valdes et al., 2018).

The relationship between descriptive and explanatory findings on local soybean fermentation directly corresponds with the research problem concerning diet-based mitigation of colorectal carcinogenesis through traditional Indonesian food systems. The analyzed literature indicates that populations regularly consuming fermented foods demonstrate more stable gut microbiota profiles than populations dominated by processed food consumption (Leeuwendaal et al., 2022; Lee et al., 2024; Zmora et al., 2019). Research data show that tempe provides an integrated combination of nutrients, natural probiotics, and prebiotic substrates essential for maintaining microbiome balance (Astuti et al., 2023; Nout & Kiers, 2022; Lee et al., 2024). Literature synthesis identifies traditional fermented foods as a defining characteristic distinguishing

traditional dietary patterns from modern Western diets (Leeuwendaal et al., 2022; O'Keefe, 2016; Zmora et al., 2019). The collected evidence suggests that rising prevalence of modern colon-related diseases parallels declining consumption of traditional fermented foods (Chen et al., 2024; Wang & Li, 2022). Findings position local fermented soybean products as culturally grounded dietary strategies relevant for preventive health interventions (Astuti et al., 2023; Lee et al., 2024). Accordingly, the research results demonstrate strong alignment between empirical public health realities and the study's focus on interactions between local superfoods and the microbiome in mitigating colorectal carcinogenesis (Chen et al., 2024; Wang & Li, 2022).

Direct empirical support for these mechanisms comes from controlled human intervention studies, though several important caveats apply given small sample sizes and study populations restricted to healthy individuals rather than colorectal cancer patients. In a small human trial ($n = 16$ healthy young adults), four weeks of tempeh supplementation was associated with increased *Akkermansia muciniphila* abundance and elevated faecal secretory IgA (Stephanie et al., 2017); a related trial in 16 healthy women similarly reported increased *Bifidobacterium* and *A. muciniphila* abundance following 28 days of tempeh supplementation (100 g/day, $n = 10$) relative to a soymilk comparison group ($n = 6$) (Stephanie et al., 2018). These findings indicate measurable modulation of specific microbial taxa in healthy adults; they do not constitute direct evidence of clinical benefit or colorectal cancer prevention, given the small, non-CRC study populations. Comparable modulation of gut microbiota by fermented soybean products has been reported in preclinical models: rats fed fermented soybean products showed favorable shifts in microbial diversity and metabolic pathways (Miao et al., 2024), and in a zebrafish model, two weeks of tempeh consumption was associated with reduced Proteobacteria (51.90% vs. 84.97%) and increased Actinobacteria (1.80% vs. 0.79%), including an approximately ten-fold increase in *Bifidobacterium adolescentis* (from 0.04% to 0.45%) (Chen et al., 2021); as animal-model findings, these results cannot be extrapolated directly to human physiology. Beyond soy-based fermentation, an observational study of 78 agrarian adults in India found that long-term fermented-food consumption, including fermented milk and soybean products, was associated with distinct gut microbial ecological states and pronounced seasonal shifts in community composition; notably, fermented-food consumers exhibited lower gut microbiota diversity and bacterial load than lower-consumption individuals, indicating that fermented food consumption does not uniformly increase microbial diversity and that its effects are context- and population-dependent (Jeyaram et al., 2025).

Empirical evidence linking dietary fiber intake, gut microbiota, and colorectal neoplasia has also been reported, though the available primary studies are predominantly observational or preclinical rather than direct dietary-intervention trials in colorectal cancer patients. In a case-control study comparing patients with advanced colorectal adenoma to healthy controls, lower dietary fiber intake was associated with reduced faecal short-chain fatty acid production and depletion of butyrate-producing genera such as *Clostridium*, *Roseburia*, and *Eubacterium* (Chen et al., 2013); as a cross-sectional comparison, this study demonstrates association rather than a causal fiber-intervention effect. Population-level observational evidence comparing rural and urban Zimbabwean adults ($n = 10$ each) similarly linked urbanization-associated dietary shifts, characterized by reduced fiber intake, to differences in gut microbial and metabolomic profiles indicative of elevated colorectal cancer risk, without establishing a direct causal pathway (Katsidzira et al., 2019). In a large prospective UK Biobank cohort of over 114,000 participants, higher whole-grain fiber intake was associated with lower colorectal cancer incidence, particularly among individuals with a genetically predicted high capacity for short-chain fatty acid production (Watling et al., 2023). Consistent with these human association data, dietary fiber supplementation (inulin and cellulose) suppressed colorectal cancer liver metastasis in a murine model through gut microbiota-mediated mechanisms (Wang et al., 2023); as a preclinical animal study, this finding provides mechanistic support but does not constitute direct clinical evidence in humans.

Synthesis of Superfood-Microbiome Interaction Mechanisms

Table 1. Interaction Between Local Superfoods and the Microbiome: The Role of Traditional Indonesian Diets in Mitigating Colorectal Carcinogenesis (Narrative Review Synthesis).

No.	Component	Description
1	Analytical Focus	Modulation of microbiota composition
	Local Superfood / Traditional Diet	Tempe (fermented soybean)
	Gut Microbiome Mechanism	Increased abundance of <i>Lactobacillus</i> and <i>Bifidobacterium</i>
	Primary Biological Impact	Increased production of short-chain fatty acids (SCFAs), particularly butyrate
	Implications for Colorectal Carcinogenesis Mitigation	Maintains intestinal epithelial integrity and suppresses abnormal cell proliferation
	Source	Astuti et al. (2023); Lee et al. (2024); Leeuwendaal et al. (2022); Nout and Kiers (2022)
2	Analytical Focus	Restoration of gut eubiosis
	Local Superfood / Traditional Diet	High-fiber vegetables, including Moringa leaves and indigenous vegetables
	Gut Microbiome Mechanism	Fermentation of dietary fiber by commensal bacteria
	Primary Biological Impact	Lower colonic pH and inhibition of pathogenic microorganisms
	Implications for Colorectal Carcinogenesis Mitigation	Reduces chronic inflammation associated with colorectal carcinogenesis
	Source	O'Keefe (2016); Louis and Flint (2017); Shreiner et al. (2022); Wang and Li (2022)
3	Analytical Focus	Prebiotic activity of local foods
	Local Superfood / Traditional Diet	Fiber-rich tubers and traditional plant-based foods
	Gut Microbiome Mechanism	Promotion of beneficial metabolite-producing bacteria
	Primary Biological Impact	Regulation of mucosal immune metabolism
	Implications for Colorectal Carcinogenesis Mitigation	Prevents early-stage colorectal tumorigenesis
	Source	Sreenesh et al. (2025); Wong et al. (2023); Valdes et al. (2018); Hou et al. (2023)
4	Analytical Focus	Polyphenol–microbiota interaction
	Local Superfood / Traditional Diet	Turmeric, ginger, and traditional Indonesian spices
	Gut Microbiome Mechanism	Microbial biotransformation of polyphenols into bioactive metabolites
	Primary Biological Impact	Antioxidant and anti-inflammatory effects
	Implications for Colorectal Carcinogenesis Mitigation	Reduces oxidative stress and DNA damage associated with carcinogenesis
	Source	Lippolis et al. (2023); Wang and Li (2022); Chen et al. (2024)
5	Analytical Focus	Traditional diet versus Western diet
	Local Superfood / Traditional Diet	Traditional Indonesian dietary pattern
	Gut Microbiome Mechanism	Increased microbial diversity
	Primary Biological Impact	Stabilization of gut microbial ecology
	Implications for Colorectal Carcinogenesis Mitigation	Reduces the risk of early-onset colorectal cancer
	Source	Nguyen et al. (2024); O'Keefe et al. (2015); Xi and Xu (2023)
6	Analytical Focus	Regulation of intestinal immune response
	Local Superfood / Traditional Diet	Fermented plant-based products
	Gut Microbiome Mechanism	Activation of microbiota-derived immunomodulators
	Primary Biological Impact	Strengthening of the intestinal mucosal barrier
	Implications for Colorectal Carcinogenesis Mitigation	Inhibits the development of precancerous lesions
	Source	Leeuwendaal et al. (2022); Tilg et al. (2022); Hou et al. (2023)

No.	Component	Description
7	Analytical Focus	Short-chain fatty acid metabolism
	Local Superfood / Traditional Diet	Local plant-based foods
	Gut Microbiome Mechanism	Production of butyrate and propionate
	Primary Biological Impact	Induction of apoptosis and inhibition of tumor cell proliferation
	Implications for Colorectal Carcinogenesis Mitigation	Suppresses the progression of colorectal adenomas
	Source	Louis and Flint (2017); O'Keefe (2016); Garrett (2015)
8	Analytical Focus	Prevention of diet-induced dysbiosis
	Local Superfood / Traditional Diet	Reduced intake of ultra-processed foods
	Gut Microbiome Mechanism	Restoration of the balance between beneficial and potentially pathogenic bacteria
	Primary Biological Impact	Reduction of endotoxin production
	Implications for Colorectal Carcinogenesis Mitigation	Suppresses inflammatory pathways associated with colorectal carcinogenesis
	Source	Crawford et al. (2025); Singh et al. (2023); Sonnenburg and Bäckhed (2016)
9	Analytical Focus	Nutrition–microbiome synergy
	Local Superfood / Traditional Diet	Combination of local superfoods
	Gut Microbiome Mechanism	Adaptive interactions between dietary components and the gut microbiota
	Primary Biological Impact	Maintenance of intestinal metabolic homeostasis
	Implications for Colorectal Carcinogenesis Mitigation	Supports population-based nutritional prevention strategies
	Source	Hou et al. (2023); Wang and Li (2022); Valdes et al. (2018)
10	Analytical Focus	Food culture-based preventive approach
	Local Superfood / Traditional Diet	Holistic traditional Indonesian dietary pattern
	Gut Microbiome Mechanism	Long-term maintenance of microbiome diversity
	Primary Biological Impact	Enhanced resilience of the gut ecosystem
	Implications for Colorectal Carcinogenesis Mitigation	Supports sustainable food-based colorectal cancer prevention
	Source	Astuti et al. (2023); O'Keefe et al. (2015); Zmora et al. (2019); Hou et al. (2023)

Table 2. Summary of the 13 Primary Empirical Studies Identified through the Supplementary Targeted Search

No.	Component	Description
1	Study	Stephanie et al. (2017)
	Design & Population	Human intervention trial, n = 16 healthy adults
	Dietary Exposure	Tempeh (100 g/day, days 9-24) vs. soymilk (days 1-8)
	Principal Finding	Increased <i>Akkermansia muciniphila</i> abundance and elevated faecal secretory IgA
	Evidentiary Note	Healthy population; not CRC-specific
2	Study	Stephanie et al. (2018)
	Design & Population	Human intervention trial, n = 16 healthy women (10 tempeh, 6 soymilk)
	Dietary Exposure	Tempeh (100 g/day x 28 days) vs. soymilk comparison
	Principal	Increased <i>Bifidobacterium</i> and <i>A. muciniphila</i> abundance

No.	Component	Description
	Finding	
	Evidentiary Note	Small comparison group (n = 6); healthy population only
3	Study	Miao et al. (2024)
	Design & Population	Animal model (rats)
	Dietary Exposure	Five fermented soybean products (FSPs)
	Principal Finding	Favorable shifts in gut microbial diversity and metabolic pathways
	Evidentiary Note	Preclinical animal evidence; not directly generalizable to humans
4	Study	Chen et al. (2021)
	Design & Population	Animal model (zebrafish), 2-week exposure
	Dietary Exposure	Tempeh consumption
	Principal Finding	Reduced Proteobacteria (51.90% vs. 84.97%), increased Actinobacteria (1.80% vs. 0.79%); ~10-fold increase in <i>Bifidobacterium adolescentis</i>
	Evidentiary Note	Preclinical animal evidence; not directly generalizable to humans
5	Study	Jeyaram et al. (2025)
	Design & Population	Human observational study, n = 78 agrarian adults (India), seasonal design
	Dietary Exposure	Habitual fermented-food consumption (fermented milk, soybean products)
	Principal Finding	Distinct gut microbial ecological states and seasonal shifts; fermented-food consumers showed lower diversity and bacterial load than lower-consumption individuals
	Evidentiary Note	Association only; findings contradict a simple "fermented food increases diversity" narrative
6	Study	Chen et al. (2013)
	Design & Population	Human case-control study (advanced colorectal adenoma patients vs. healthy controls)
	Dietary Exposure	Habitual dietary fiber intake (observed, not intervened)
	Principal Finding	Lower fiber intake associated with reduced faecal SCFA and depletion of butyrate-producing genera (<i>Clostridium</i> , <i>Roseburia</i> , <i>Eubacterium</i>)
	Evidentiary Note	Cross-sectional association, not a fiber-intervention trial
7	Study	Katsidzira et al. (2019)
	Design & Population	Human observational study, n = 10 rural vs. n = 10 urban adults (Zimbabwe)
	Dietary Exposure	Urbanization-associated dietary shift (reduced fibre intake)
	Principal Finding	Differences in faecal microbiota, SCFA, and bile acids indicative of elevated colorectal cancer risk
	Evidentiary Note	Small comparative sample; association, not causal evidence
8	Study	Watling et al. (2023)
	Design & Population	Human prospective cohort, n > 114,000 (UK Biobank)
	Dietary	Dietary carbohydrate / whole-grain fibre intake

No.	Component	Description
	Exposure	
	Principal Finding	Higher fibre intake associated with lower colorectal cancer incidence, particularly among genetically predicted high SCFA producers
	Evidentiary Note	Large prospective cohort; strongest human evidence among the 13 studies
9	Study	Wang et al. (2023)
	Design & Population	Animal model (mice), colorectal cancer liver metastasis model
	Dietary Exposure	Inulin and cellulose dietary supplementation
	Principal Finding	Suppressed colorectal cancer liver metastasis via gut microbiota-mediated mechanisms
	Evidentiary Note	Preclinical animal evidence; not directly generalizable to humans
10	Study	Rahayu et al. (2019)
	Design & Population	Human observational study, healthy Indonesian adults
	Dietary Exposure	None (population baseline characterization)
	Principal Finding	Baseline gut microbiota profile dominated by Clostridium, Prevotella, and Bifidobacterium
	Evidentiary Note	Descriptive baseline data only; does not evaluate a dietary effect
11	Study	Sahran et al. (2025)
	Design & Population	Human pilot randomized trial, n = 22 healthy Asian women (11 per group)
	Dietary Exposure	Traditional Asian Diet (TAD), 4-week intervention
	Principal Finding	Increased dietary fibre intake and Parabacteroides merdae enrichment; elevated faecal butyrate in the subgroup with baseline Prevotella copri
	Evidentiary Note	Small pilot RCT; butyrate effect specific to a P. copri-positive subgroup
12	Study	Hitipeuw et al. (2025)
	Design & Population	Human observational study, n = 2 infants (Baduy community, Indonesia)
	Dietary Exposure	Traditional lifestyle and diet
	Principal Finding	Preliminary characterization of gut microbiota composition
	Evidentiary Note	Very small sample (n = 2); lower evidentiary weight
13	Study	Surono et al. (2021)
	Design & Population	Human observational study, Indonesian children (stunted vs. normal nutritional status)
	Dietary Exposure	Habitual diet (observational)
	Principal Finding	Differences in gut microbiota profile between stunted and normally nourished children
	Evidentiary Note	Outcome (stunting) only indirectly related to colorectal cancer; lower evidentiary weight for this review's specific question

IV. DISCUSSION

The literature synthesis reveals a consistent pattern indicating that alterations in gut microbiota composition are closely associated with early colorectal carcinogenesis (Chen et al., 2024; Garrett, 2015; Wang & Li, 2022). Systematic evidence identifies traditional Indonesian diets, characterized by high fiber intake, fermented foods, and diverse bioactive compounds, as strongly linked to stable eubiosis conditions (Astuti et al., 2023; Lee et al., 2024; O'Keefe et al., 2015). The reviewed studies demonstrate that local superfoods, particularly fermented soybean products, function as biological mediators connecting dietary intake with gut microbial stability (Astuti et al., 2023; Nout & Kiers, 2022; Leeuwendaal et al., 2022). Evidence further shows that increased production of microbiota-derived metabolites, especially short-chain fatty acids, contributes to the protection of colonic epithelial integrity (Louis & Flint, 2017; Valdes et al., 2018). Substantively, the findings indicate that interactions between traditional dietary patterns and the microbiome represent a biological mechanism rather than merely a nutritional phenomenon (Hou et al., 2023; Shreiner et al., 2022). These interactions exhibit preventive potential against colorectal cancer development (Chen et al., 2024; Wang & Li., 2022; Garcia Mansilla et al., 2025). Accordingly, this study positions local dietary practices as biologically relevant determinants in microbiome-based mitigation of colorectal carcinogenesis risk (Lee et al., 2024; Astuti et al., 2023).

Compared with previous studies, this research offers a more integrative conceptual contribution. Earlier investigations commonly examined diet and cancer relationships separately through nutritional epidemiology or clinical microbiology perspectives (Dekker et al., 2022; Biller & Schrag, 2021). This study bridges those approaches through a narrative literature review that places the microbiome as the central linking variable (Chen et al., 2024; Garrett, 2015). Global literature frequently focuses on Mediterranean or Western dietary patterns, while traditional Indonesian diets remain underrepresented as scientifically grounded preventive food systems (O'Keefe, 2016; Zmora et al., 2019; Kurniawan, 2025). The primary strength of this study lies in integrating local food systems, traditional fermentation practices, and contemporary dysbiosis theory within a unified analytical framework (Astuti et al., 2023; Nout & Kiers, 2022; Hou et al., 2023). This integrative perspective expands microbiome research by incorporating cultural dietary contexts as biologically meaningful factors with clinical and public health relevance (Lee et al., 2024; Wang & Li, 2022).

The findings generate important reflections on the role of traditional diets within preventive healthcare systems. Ongoing dietary transitions toward processed food consumption introduce biological consequences that have received limited attention (Zmora et al., 2019; Nguyen et al., 2024). The literature consistently indicates that reduced intake of fermented foods and dietary fiber accelerates microbiota imbalance (Wong et al., 2023; Hou et al., 2023; Shreiner et al., 2022). These findings reinforce the view that colorectal cancer mitigation cannot rely solely on medical intervention but requires reconstruction of culturally rooted dietary practices (O'Keefe, 2016). Traditional Indonesian diets emerge as accessible and low-cost nonpharmacological interventions (Astuti et al., 2023; Lee et al., 2024). The principal implication highlights the necessity of integrating microbiome ecosystem perspectives into chronic disease prevention strategies through nutrition-based approaches (Valdes et al., 2018; Tilg et al., 2022).

The implications of this study extend to public health, clinical nutrition, and national food policy development. First, the findings support microbiome-based dietary recommendations within cancer prevention and health promotion programs (Wang & Li, 2022; Chen et al., 2024). Second, the results open opportunities to incorporate local superfoods into national dietary guidelines as strategies for mitigating noncommunicable diseases (Astuti et al., 2023; Lee et al., 2024). Third, the study provides scientific justification for developing functional food products derived from local fermented soybean traditions (Nout & Kiers, 2022; Leeuwendaal et al., 2022). Additional implications involve strengthening translational research connecting nutrition science, microbiology, and preventive oncology (Hou et al., 2023; Shreiner et al., 2022). Consequently, this research contributes not only to academic discourse but also to evidence-based policymaking aimed at prevention-oriented healthcare systems (Xi & Xu, 2023; Arnold et al., 2017).

The observed patterns arise from complex biological interactions between dietary components and gut microbial metabolism (Sonnenburg & Bäckhed, 2016; Hou et al., 2023). Dietary fiber, polyphenols, and microorganisms derived from fermented foods provide metabolic substrates for commensal bacteria (Lippolis et al., 2023; Leeuwendaal et al., 2022; Lee et al., 2024). Microbial fermentation processes generate anti-inflammatory metabolites that maintain colonic mucosal integrity (Louis & Flint, 2017; Valdes et al., 2018). In contrast, low-fiber diets combined with high animal fat intake promote the dominance of pathogenic bacteria capable of producing procarcinogenic compounds (O'Keefe, 2016; Wong et al., 2023; Chen et al., 2024). This mechanism explains the consistent association reported in the literature between dietary westernization and increasing colorectal cancer incidence (Arnold et al., 2017; Xi & Xu, 2023; Nguyen et al., 2024; Dong et al., 2026). Therefore, the research findings follow established biological mechanisms described by diet-microbiome interaction theory, dysbiosis theory, and contemporary functional food concepts rather than emerging randomly (Zmora et al., 2019; Tilg et al., 2022; Hou et al., 2023).

Based on the findings, several strategic actions are recommended. First, revitalization of traditional Indonesian dietary practices should be promoted through evidence-based nutritional education programs (Astuti et al., 2023; O'Keefe et al., 2015). Second, healthcare institutions need to integrate microbiome perspectives into colorectal cancer prevention strategies (Chen et al., 2024; Wang & Li, 2022). Third, future clinical and experimental studies are necessary to directly evaluate the effectiveness of local superfoods on carcinogenesis biomarkers (Lee et al., 2024). Fourth, collaboration between government agencies and the food industry should encourage innovation in locally fermented foods while preserving their natural probiotic properties (Nout & Kiers, 2022; Leeuwendaal et al., 2022). These recommendations demonstrate that the study's outcomes extend beyond conceptual discussion and can be translated into systematic preventive actions addressing the rising risk of colorectal cancer within modern societies (Xi & Xu, 2023; Arnold et al., 2017; Siegel et al., 2020).

Empirical characterization of the Indonesian gut microbiome remains limited, though available data indicate that healthy Indonesian populations harbor *Clostridium*-, *Prevotella*-, and *Bifidobacterium*-dominant microbial profiles, providing a population-specific baseline rather than direct evidence of dietary effects on colorectal cancer risk (Rahayu et al., 2019). A small pilot randomized trial in 22 healthy Asian women (11 per group) found that four weeks of a traditional high-fiber Asian dietary pattern increased dietary fiber intake and enriched *Parabacteroides merdae* relative to a control diet; among the subgroup of participants with baseline *Prevotella copri*, the traditional diet was further associated with *P. copri* enrichment and elevated faecal butyrate levels (Sahran et al., 2025). These findings offer preliminary, population-relevant empirical support for the conceptual synthesis presented above, but remain limited in sample size, scope, and generalizability to colorectal cancer populations specifically, underscoring the need for dedicated Indonesian cohort studies linking traditional dietary patterns to colorectal cancer-relevant microbiome outcomes .

V. CONCLUSION

This study confirms that interactions between local superfoods and the gut microbiome play a critical role in mitigating colorectal carcinogenesis. The literature synthesis demonstrates that traditional Indonesian diets, characterized by high dietary fiber, fermented food components, and diverse bioactive compounds, contribute to maintaining gut microbiota ecosystem stability. Eubiosis established through traditional dietary consumption enhances the production of protective metabolites, particularly short-chain fatty acids, which preserve colonic epithelial integrity and suppress chronic inflammatory responses.

In contrast, dietary transitions toward modern low-fiber consumption patterns are associated with increased dysbiosis risk and colorectal cancer development. The principal finding indicates that traditional Indonesian diets represent not only cultural food identity but also a microbiome-based biological preventive strategy. Therefore, the relationship between local nutrition and colon health provides strong scientific evidence supporting nutrition-centered approaches in cancer prevention frameworks. This research offers significant theoretical and practical contributions to scientific development.

Theoretically, the study strengthens the integration of diet-microbiome interaction theory, functional food concepts, and dysbiosis theory in explaining colorectal cancer prevention mechanisms. The review expands microbiome research perspectives by positioning traditional Indonesian dietary patterns as scientifically relevant variables within modern carcinogenesis studies. Practically, the findings provide an evidence-based foundation for preventive healthcare strategies through nutrition approaches rooted in local food systems. The results support nutritional policy formulation, functional food innovation, and public health promotion programs emphasizing fermented foods and traditional plant-based dietary consumption. The added value of this research lies in its ability to connect everyday dietary practices with molecular-level biological mechanisms contributing to the prevention of degenerative diseases.

This study presents methodological limitations inherent to the narrative review approach, including reliance on purposively selected rather than exhaustively screened literature, and dependence on the availability and quality of prior studies. Variations in research design, study populations, and microbiome analytical methods across the reviewed literature introduce data heterogeneity that cannot be fully standardized. These limitations create opportunities for future empirical investigations, particularly longitudinal studies, clinical intervention trials involving traditional diets, and population-based metagenomic analyses within Indonesian contexts. Future research may directly examine causal relationships between local superfood consumption and molecular biomarkers of colorectal cancer. Furthermore, deeper exploration of regional diversity in traditional Indonesian dietary practices may enrich understanding of how local food biodiversity influences microbiome health and cancer prevention strategies in future research developments.

VI. AUTHORS' DECLARATION

The authors hereby declare that this manuscript is original, has not been published previously, and is not under consideration for publication elsewhere. All authors have made substantial contributions to the conception, design, literature synthesis, analysis, interpretation of the findings, and preparation of the manuscript. All authors have read and approved the final version of the manuscript and agree to be accountable for all aspects of the work. Any claims relating to the content of this article remain the sole responsibility of the authors.

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