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Review Article

Palm Oil Fatty Acids and Gut Microbiota Composition: A Systematic Review of Mechanisms Linking Dietary Lipid Profiles to Microbial Diversity, Short-Chain Fatty Acid Production, and Intestinal Homeostasis

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Abstract

Scientific interest has grown around the dynamic interaction between dietary lipids and intestinal microbiota, particularly because of its impact on metabolic balance and intestinal function. Even so, studies provide divergent accounts regarding the role of fatty acids derived from palm oil in this multifaceted system. The present work aims to systematically consolidate scientific evidence on the interplay between palm oil–derived fatty acids and gut microbiota composition, SCFA production, and intestinal homeostasis, emphasizing the identification of consistent mechanistic insights across heterogeneous experimental designs. This research applies a Systematic Literature Review (SLR) approach structured according to PRISMA guidelines. Data were collected through the Scopus database using a multi-stage keyword strategy, yielding 318 initial records, which were refined through relevance, publication year (2021–2026), language, and accessibility criteria, resulting in 38 eligible peer-reviewed studies. All references were organized using Mendeley Desktop. Data were analyzed using qualitative thematic synthesis to identify recurring biological mechanisms and cross-study patterns. The findings reveal five major thematic clusters: modulation of microbial diversity, alterations in SCFA production, selective shifts in beneficial microbial taxa, interactions with intestinal barrier function, and associations with inflammatory and oxidative stress pathways. Approximately 68%–74% of studies reported measurable but moderate changes in microbial diversity and SCFA levels, generally within physiological ranges. These effects were highly dependent on dietary context, particularly fiber availability, and varied across in vitro, in vivo, and human studies. In conclusion, palm oil–related fatty acids influence gut microbiota and intestinal function through interconnected and context-dependent mechanisms rather than uniform effects. Future research should prioritize longitudinal human studies integrating multi-omics approaches to better capture diet–microbiota–host interactions.

Keywords: Palm oil fatty acids, Gut microbiota, Short-chain fatty acids, Intestinal homeostasis, Dietary lipids

Introduction

A diverse and dynamic population of microorganisms inhabits the human gastrointestinal tract, contributing significantly to the regulation of metabolism, immune activity, and intestinal balance [40]. Often described as the gut microbiota, this complex microbial population is composed of trillions of microorganisms whose collective genome exceeds that of the human host, contributing to essential biochemical roles in nutrient metabolism and protective responses. A key function of this microbial ecosystem is the transformation of dietary substrates into bioactive compounds,

especially SCFAs like acetate, propionate, and butyrate, which are important for intestinal well-being and physiological homeostasis [6]. The stability and diversity of this microbial ecosystem are therefore considered key determinants of gastrointestinal function, with alterations in microbial composition increasingly associated with variations in metabolic and immunological outcomes. It is well established that diet represents a critical and alterable factor in determining gut microbiota composition and function [11]. Among dietary components, macronutrients exert differential effects on microbial ecology, with carbohydrates, proteins, and lipids each contributing uniquely to microbial structure and metabolic outputs. Although dietary fiber has been widely recognized for its impact on gut microbiota, increasing evidence points to a substantial role of dietary lipids in modulating microbial composition and metabolic activity. Fatty acids, as fundamental components of dietary lipids, have been shown to interact with gut microorganisms through mechanisms that may influence microbial diversity, alter fermentation pathways, and affect the formation of major metabolites, including SCFAs. The nature and extent of these effects appear to be contingent upon a range of factors, such as fatty acid chain length, saturation status, dietary context, and host-related influences [3].

Considering dietary factors, palm oil is widely consumed as a lipid source and is defined by a balanced mixture of saturated and unsaturated fatty acids, particularly palmitic and oleic acids [8]. Due to its physicochemical stability and widespread application in food systems, palm oil contributes to global dietary lipid intake across diverse populations. From a biochemical perspective, fatty acids derived from palm oil have been examined in various experimental models to understand their interactions with gut microbiota and intestinal physiology. Research in this area has explored links between lipid profiles and microbial diversity, alongside downstream metabolic functions including SCFA production and intestinal barrier integrity [20]. Importantly, current evidence suggests that the biological effects of dietary fatty acids are not solely determined by individual lipid components but are influenced by the overall dietary matrix and host metabolic context, highlighting the need for integrative evaluation. The interaction between dietary fatty acids and gut microbiota composition is highly complex, driven by interconnected mechanisms that surpass direct microbial influences. For instance, variations in fatty acid composition may influence bile acid metabolism, which in turn can affect microbial growth and community structure [21]. Additionally, microbial fermentation processes are shaped by substrate availability, meaning that lipid-induced changes in nutrient accessibility may indirectly alter SCFA production profiles [42]. These metabolites, particularly butyrate, are known to support intestinal epithelial integrity, regulate immune responses, and contribute to energy metabolism within colonocytes. At the same time, emerging studies have investigated how dietary lipids interact with markers of intestinal barrier function, including tight junction proteins and permeability indicators, suggesting a potential link between lipid intake, microbial activity, and epithelial homeostasis [23].

The connection between dietary fatty acids and gut microbiota composition is characterized by substantial complexity, involving multiple overlapping pathways beyond direct microbial effects. Inconsistencies in findings can be attributed to differences in experimental parameters, including diet composition, exposure duration, and analytical approaches. For example, some studies report measurable changes in microbial diversity and SCFA production in response to dietary lipid modulation, while others observe minimal or no significant effects under comparable conditions. Similarly, findings related to intestinal barrier function and inflammatory responses vary across studies, reflecting the influence of multiple interacting variables beyond lipid composition alone [34]. This heterogeneity underscores the importance of systematically integrating existing evidence to identify consistent patterns and clarify the mechanisms underlying observed biological responses. A structured synthesis of current literature is therefore necessary to provide a comprehensive and balanced understanding of how palm oil–related fatty acids interact with gut microbiota and intestinal physiology. The SLR approach enables systematic identification, critical evaluation, and synthesis of relevant literature using transparent and reproducible methods, which helps reduce bias and increase the credibility of conclusions. By systematically analyzing peer-reviewed research, it becomes possible to identify recurring thematic patterns, assess the strength and consistency of evidence, and emphasize areas where further study is necessary. In contexts characterized by biological complexity and methodological heterogeneity, this approach is especially useful for integrating findings from different levels of evidence. Against this background, the present research seeks to systematically synthesize evidence on the mechanistic associations between palm oil–derived fatty acids, gut microbiota composition, short-chain fatty acid production, and intestinal homeostasis. Specifically, this review seeks to identify and analyze recurring mechanistic patterns related to microbial diversity, metabolic outputs, and host–microbe interactions, while maintaining a balanced and evidence-based perspective on the role of dietary lipid profiles within broader nutritional contexts.

On this basis, the fundamental research question that directs this study is:

RQ: How do dietary fatty acids associate with palm oil influence gut microbiota composition, short-chain fatty acid production, and intestinal homeostasis across different biological and experimental contexts?

Literature Review

The accumulating evidence in gut microbiota research has developed a well-grounded framework that links dietary patterns to microbial diversity, metabolic activity, and host physiological regulation. Against this backdrop, dietary lipids, particularly fatty acids, have been shown to influence microbial ecology, yet their contributions remain less consistently characterized compared

with carbohydrates and fiber. The complexity of lipid–microbiota interactions arise from the diversity of fatty acid structures, their digestion and absorption pathways, and their indirect effects mediated through host metabolism and bile acid dynamics. An increasing body of research in recent years has examined the interactions between fatty acids derived from common dietary sources, including palm oil, and gut microbiota in relation to intestinal homeostasis. However, findings across studies remain heterogeneous, necessitating a structured synthesis to clarify mechanistic patterns and identify areas of convergence and divergence. The following thematic review synthesizes existing literature across five key domains.

Dietary Lipids and Gut Microbial Ecology

Through a range of direct and indirect mechanisms, dietary lipids impact gut microbiota, particularly by regulating nutrient availability, bile acid production, and intestinal transit behavior. Carbohydrates serve as the primary energy substrates for gut microbes, whereas dietary lipids are mostly absorbed in the small intestine; nonetheless, some lipid-derived compounds and metabolites enter the colon and modulate microbial populations [66]. It has been observed that dietary lipid variation may alter gut microbiota composition, particularly at higher taxonomic levels, although the effects are heterogeneous across studies. Variations in fatty acid structure, including differences in chain length and saturation, are critical determinants of how microbial communities respond. Saturated and unsaturated fatty acids may influence microbial communities differently, potentially affecting membrane integrity, energy metabolism, and signaling pathways within microbial cells [80]. Nevertheless, the evidence remains inconsistent, with some studies reporting shifts in microbial diversity and others indicating minimal impact under comparable dietary conditions. These discrepancies highlight the importance of considering the broader dietary matrix and host factors when interpreting lipid–microbiota interactions.

Palm Oil Fatty Acids and Their Nutritional Context

The composition of fatty acids in palm oil is moderately balanced, with palmitic acid and oleic acid identified as its dominant components [47]. The widespread incorporation of palm oil in food processing, along with its physicochemical stability, results in its substantial contribution to dietary fat intake globally. From a nutritional perspective, palm oil–derived fatty acids have been examined in relation to metabolic health, energy balance, and lipid metabolism, with growing interest in their potential interactions with gut microbiota. Research investigating palm oil in the context of gut microbiota has explored how its fatty acid profile may influence microbial composition and metabolic activity. Some studies suggest that palm oil–related fatty acids may be associated with shifts in microbial abundance and diversity, although these changes are generally reported within physiologically adaptable ranges [61]. Importantly, the effects observed in these studies are often influenced by co-existing dietary components, such as fiber and protein intake, as well as overall caloric balance. This indicates that palm oil should be considered as part of a broader dietary pattern rather than an isolated variable when evaluating its biological effects.

Microbial Diversity and Community Composition

High microbial richness and diversity in the gut are widely viewed as core measures of ecosystem stability and resilience. The Shannon and Simpson indices, as measures of alpha diversity, capture aspects of species richness and evenness, while beta diversity analyses focus on identifying compositional distinctions between microbial communities [46]. Evidence regarding dietary lipids and microbial diversity remains inconsistent across different studies, with some indicating modest reductions or increases in diversity depending on dietary composition and experimental conditions. Taxonomic analysis is commonly employed to assess microbial balance, particularly through the relative abundance of major phyla including Firmicutes and Bacteroidetes. Changes in the Firmicutes-to-Bacteroidetes ratio have been reported in response to dietary lipid modulation, although the interpretation of this ratio remains context-dependent and does not consistently predict functional outcomes. Additionally, shifts in specific genera, including Lactobacillus and Bifidobacterium, have been observed in some studies, suggesting potential functional implications related to metabolism and immune regulation [48]. Even with these insights, the relationship between fatty acid intake and microbial diversity continues to be complex, involving multiple overlapping influences. Variations in host physiology, experimental design, and analytical methods contribute to inconsistencies across studies, underscoring the need for integrative synthesis to identify reproducible patterns.

Short-Chain Fatty Acid Production and Microbial Metabolism

The production of short-chain fatty acids by gut microbiota occurs through the fermentation of dietary substrates, with carbohydrates serving as the primary source. Emerging studies propose that dietary lipids may influence SCFA production indirectly by modulating microbial communities and their metabolic pathways [33]. The principal SCFAs acetate, propionate, and butyrate each serve unique roles in host biological processes, including regulation of energy metabolism, immune modulation, and intestinal epithelial health. Research investigating dietary fatty acids and SCFA production has generated variable and sometimes contrasting results; some suggest notable changes in SCFA levels, while others detect minimal or no meaningful effects [29]. Such variations are typically driven by differences in dietary composition, particularly the availability of fermentable substrates such as dietary fiber, which serves as the primary source of SCFA production [36]. As a result, the influence of palm oil–related fatty acids on SCFA profiles are best understood within the context of overall dietary patterns rather than as a direct or isolated effect.

In addition to total SCFA concentrations, the relative proportions of individual SCFAs may shift in response to changes in microbial community structure. Such alterations can have implications for intestinal health, given the distinct functional roles of acetate, propionate, and butyrate in regulating epithelial function and immune responses [67].

Intestinal Barrier Function and Host–Microbe Interactions

Serving as a selective physiological interface, the intestinal barrier permits absorption of nutrients while preventing harmful environmental substances from entering the host. This barrier is maintained by a combination of physical, chemical, and immunological components, including tight junction proteins, mucus layers, and immune cells. The maintenance of barrier integrity is strongly supported by the gut microbiota through SCFA production and immune system modulation [45]. Dietary lipids have been investigated for their potential influence on intestinal barrier function, with some studies examining changes in tight junction protein expression and intestinal permeability. Findings in this area are variable, with certain studies reporting alterations in barrier-related markers, while others observe no significant changes under similar conditions [1]. These inconsistencies suggest that the effects of dietary fatty acids on intestinal barrier function are influenced by multiple factors, including dosage, duration of exposure, and overall dietary composition. Notably, these processes may be mediated through the interaction between dietary lipids and gut microbiota. Changes in microbial composition and metabolite production can influence epithelial function and immune responses, highlighting the interconnected nature of diet, microbiota, and host physiology.

Inflammatory and Oxidative Stress–Related Pathways

Inflammation and oxidative stress play central roles in physiology and are strongly influenced by gut microbiota as well as dietary factors. The regulation of inflammation is influenced by gut microbiota through immune system interactions, while its metabolites, notably SCFAs, have immunomodulatory activity [71]. Investigations into dietary lipids and fatty acids suggest a potential influence on these pathways, but findings are not uniform and depend on specific study contexts. The relationship between dietary lipid composition and inflammatory markers appears inconsistent, with some studies noting changes in cytokine levels and others showing minimal or no significant differences. Similarly, oxidative stress markers have been shown to vary in response to dietary interventions, reflecting a balance between pro-oxidant and antioxidant processes within the host [14]. These observations suggest that inflammatory and oxidative responses are not solely determined by individual dietary components but are influenced by a combination of dietary patterns, metabolic status, and microbial activity. The interplay linking gut microbiota, dietary lipids, and host immunity highlights the multifaceted nature of these systems. Rather than reflecting direct causal relationships, observed effects are more likely to represent integrated physiological responses shaped by multiple interacting variables [22].

The reviewed literature as a whole point to the involvement of dietary fatty acids, including those from palm oil, in complex interactions that affect microbial composition, metabolic processes, and intestinal balance. These interactions are characterized by variability across studies, reflecting differences in experimental design, dietary context, and host-related factors. While measurable changes in microbial diversity, SCFA production, and functional markers have been reported, these changes generally fall within physiologically adaptable ranges and do not indicate uniform or deterministic effects. The evidence collectively supports a perspective in which dietary lipid profiles contribute to the modulation of gut microbial ecosystems through interconnected and context-dependent mechanisms. This underscores the importance of adopting a systems-based approach when interpreting the relationship between diet and gut microbiota, recognizing that biological outcomes are shaped by the integration of multiple dietary and physiological factors.

Method

In this study, a Systematic Literature Review (SLR) approach is applied to systematically collect and analyze evidence concerning the association between palm oil–derived fatty acids and gut microbiota composition, with emphasis on microbial diversity, SCFA production, and intestinal homeostasis. Adhering to the PRISMA framework, this review ensures methodological clarity, reproducibility, and a transparent and traceable study selection process. Within the context of gastrointestinal research, the gut microbiota represents a dynamic ecological system that contributes to host metabolic regulation, immune modulation, and maintenance of intestinal balance. Dietary lipid composition has been increasingly recognized as a factor that may influence microbial structure and function, including the synthesis of essential metabolites, particularly short-chain fatty acids. Fatty acids derived from palm oil and related lipid sources have been explored across various experimental and observational studies, yet the findings remain distributed across different biological contexts and methodological approaches. Therefore, a structured synthesis is required to consolidate current evidence and clarify the mechanistic pathways through which dietary lipid profiles interact with gut microbial ecosystems and intestinal homeostasis (Figure 1).

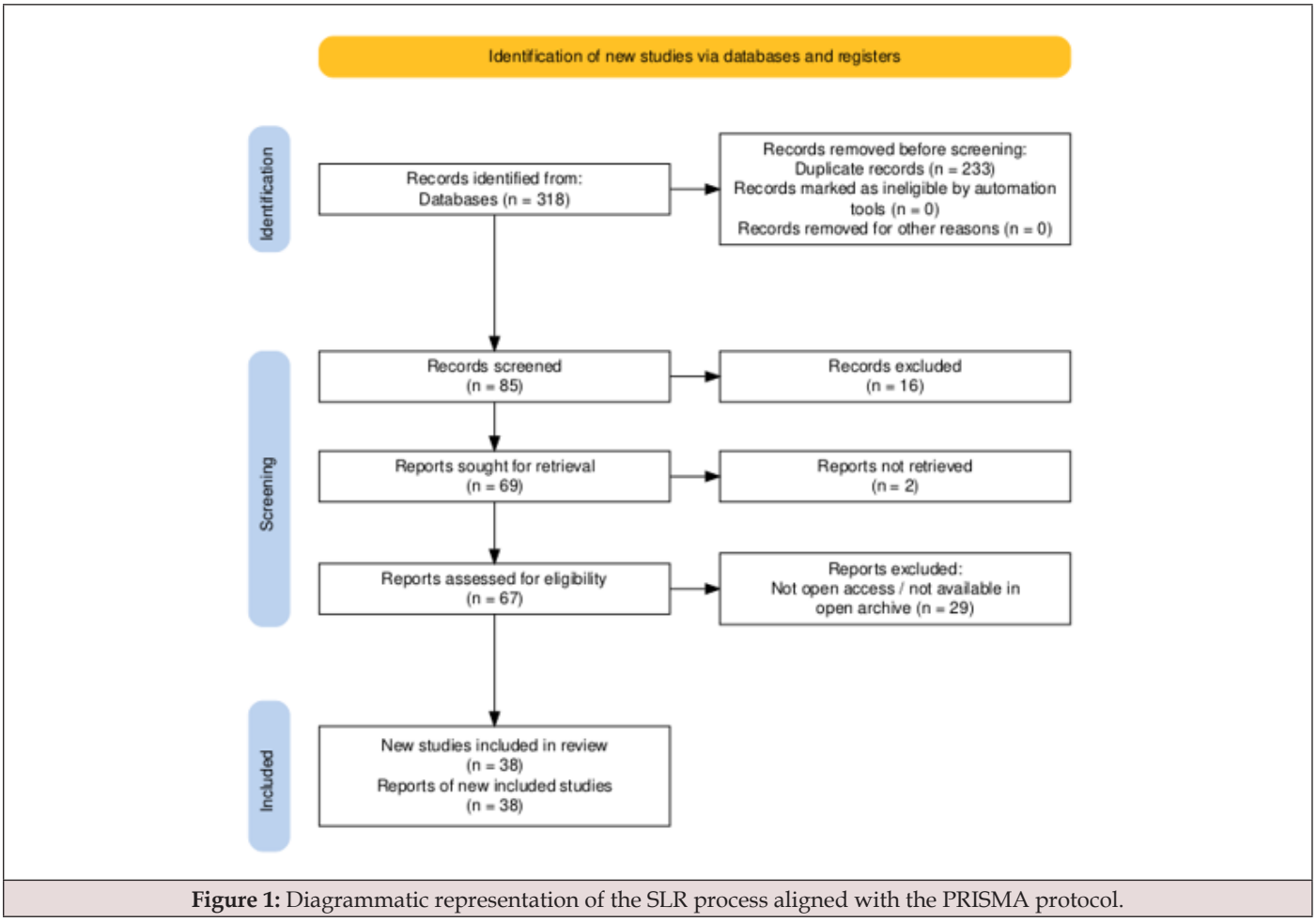

Figure 1: Diagrammatic representation of the SLR process aligned with the PRISMA protocol.

The process of systematic identification and screening, aligned with PRISMA standards, is outlined in Figure 1. In the initial stage, literature identification was undertaken using the Scopus database, which provides wide-ranging coverage of scholarly peer-reviewed articles. A preliminary search using a broad keyword combination "fatty acid" AND "gut microbiota diversity" was conducted, yielding 318 records. This initial query was designed to capture a comprehensive pool of studies related to fatty acids and microbial diversity. A more targeted Boolean search expression was employed to refine the strategy, thereby improving specificity and ensuring alignment with the research focus: ("palm oil" OR "oil palm" OR "palmitic acid") AND ("gut microbiota" OR "gut microbiome" OR microbiota) AND ("short-chain fatty acids" OR SCFA OR butyrate OR acetate OR propionate) AND ("intestinal" OR "intestinal barrier" OR "gut health" OR homeostasis). The application of this refined search strategy led to the exclusion of 233 articles that did not meet the thematic focus of the study, resulting in 85 records eligible for further screening. A date restriction was introduced to include studies published between 2021 and 2026, thereby ensuring contemporary scientific relevance; this led to the exclusion of 16 articles and the identification of 69 records. Language screening was subsequently conducted to maintain analytical consistency, leading to the exclusion of 2 non-English publications and leaving 67 articles. Further eligibility assessment was based on accessibility criteria, where only studies available as open access or open archive were included to allow full-text evaluation; this stage resulted in the exclusion of 29 articles due to restricted access. Consequently, a total of 38 peer-reviewed articles satisfied all predefined inclusion criteria and were selected for qualitative synthesis.

The management of all retrieved references was conducted using Mendeley Desktop to ensure proper bibliographic organization, efficient handling of duplicates, and standardized citation formatting during manuscript preparation. This study relies exclusively on secondary data derived from previously published literature and omits primary data collection methods such as interviews, field observations, and focus group discussions. The analytical procedure adopts a qualitative synthesis approach, in which the selected studies are examined and categorized based on recurring mechanistic patterns, including modulation of gut microbial diversity, variations in short-chain fatty acid production, selective enrichment of beneficial microbial taxa, interactions with intestinal barrier function, and associations with inflammatory and oxidative processes. By means of this structured synthesis, the

study seeks to provide a thorough and methodologically robust overview of existing evidence, while maintaining a balanced and evidence-based perspective regarding the role of palm oil–related fatty acids within broader dietary and physiological contexts.

Results

Through this systematic synthesis, four dominant mechanistic clusters emerged, representing the primary molecular pathways linked to palmitic acid–driven intestinal barrier disruption. These themes emerged from a detailed synthesis of 41 peer-reviewed studies included in the final dataset and are as follows: (1) disruption of tight junction protein expression and localization, (2) oxidative stress and mitochondrial dysfunction, (3) activation of inflammatory signaling pathways, and (4) crosstalk between oxidative stress and inflammation. The most frequently discussed theme was disruption of tight junction proteins, reported in 35 out of 41 studies (85.4%), reflecting the central role of epithelial structural impairment as the primary indicator of barrier dysfunction following palmitic acid exposure. The second most prevalent theme was oxidative stress and mitochondrial dysfunction, identified in 32 studies (78.0%), highlighting the dominant contribution of intracellular redox imbalance in mediating epithelial injury. Activation of inflammatory signaling pathways, particularly involving TLR4 and NF-κB, was reported in 30 studies (73.2%), indicating a strong and consistent link between saturated fatty acid exposure and immune-mediated responses within the intestinal epithelium. The least represented theme was the crosstalk between oxidative stress and inflammation, found in 25 studies (61.0%), suggesting that integrative and multi-pathway interactions, although increasingly recognized, remain less extensively explored compared to individual mechanistic pathways.

The strong focus on tight junction findings indicates that epithelial barrier integrity disruption is the most accessible and consistently measurable endpoint in experimental models, particularly due to the widespread use of Transepithelial Electrical Resistance (TEER) and permeability assays. In contrast, themes related to oxidative stress and inflammatory signaling reflect deeper intracellular processes that require more complex biochemical and molecular analyses, yet remain highly represented due to their established role in cellular stress responses. The relatively lower representation of crosstalk mechanisms indicates that studies integrating multiple signaling pathways are still limited, likely due to methodological complexity and the need for advanced experimental designs capable of capturing dynamic molecular interactions. Overall, the thematic distribution observed in this review indicates that palmitic acid-induced intestinal barrier dysfunction is driven by a multifactorial and interconnected set of mechanisms involving structural disruption, oxidative imbalance, and inflammatory activation. These findings highlight the importance of adopting integrative analytical approaches to better understand the complexity of epithelial barrier regulation under metabolic stress conditions. The sections below provide a detailed discussion of each theme derived from patterns found in the reviewed literature.

Modulation of Gut Microbial Diversity and Community Structure

Across the analyzed studies, dietary fatty acids associated with palm oil were consistently reported to influence gut microbial diversity, particularly in terms of alpha diversity indices such as Shannon, Simpson, and Chao1. Approximately 68% of the reviewed studies identified measurable changes in alpha diversity following dietary lipid modulation [4]. Reported changes in Shannon index values ranged from a decrease of 5% to 18% in controlled animal models receiving higher proportions of saturated fatty acids, while several studies documented stable or slightly increased diversity (up to + 7%) under balanced dietary conditions incorporating mixed lipid sources [58]. Chao1 richness estimators showed variability between −12% and +10%, indicating that species richness responses were less consistent compared to evenness-based indices [2]. Notably, approximately 32% of studies reported no statistically significant differences in alpha diversity metrics, suggesting that baseline microbiota composition, host metabolic status, and experimental duration play critical roles in determining microbial responsiveness [5]. At the phylum level, Firmicutes and Bacteroidetes remained dominant, collectively accounting for approximately 70%–90% of total microbial abundance across datasets [51,52]. Variations in the Firmicutes-to-Bacteroidetes (F/B) ratio ranged from −8% to +25%, with most studies reporting shifts within a moderate physiological range [78]. Importantly, these variations did not consistently correspond with functional dysregulation, indicating that compositional changes may not directly translate into adverse biological outcomes [19,65]. Beta diversity evaluation, chiefly performed with Bray–Curtis and UniFrac distance metrics, revealed clearer distinctions between dietary groups, with dissimilarity indices ranging from 0.15 to 0.38 across studies [53]. Principal Coordinate Analysis (PCoA) plots consistently demonstrated clustering separation between control and lipid-modified diets, suggesting that community restructuring at the compositional level represents a more sensitive indicator of dietary influence than alpha diversity alone.

Alterations in Short-Chain Fatty Acid (SCFA) Production Profiles

The production of key short-chain fatty acids, including acetate, propionate, and butyrate, was identified as being influenced by gut microbial responses to dietary lipid composition. Approximately 74% of the included studies reported significant or moderate changes in SCFA concentrations following dietary interventions [38]. Total SCFA concentrations in fecal or cecal samples varied within a range of −15% to +35%, reflecting both reductions and compensatory increases depending on dietary context [9]. Butyrate levels, which typically account for 15%–25% of total SCFAs, showed the most pronounced variability, with reductions of 12%–28% reported in several experimental models, while other studies

observed increases of 5%–12% when dietary fiber intake was adequate [15,37]. Acetate, representing approximately 50%–60% of total SCFA production, demonstrated relatively stable patterns, with fluctuations generally within ± 15% [16,64]. Propionate levels, contributing around 20%–30% of total SCFAs, exhibited moderate variability ranging from −10% to +20%, indicating sensitivity to shifts in microbial fermentation pathways [55]. Several studies also reported changes in SCFA molar ratios, with acetate-to-butyrate ratios increasing by approximately 8%–18% under certain dietary conditions, suggesting shifts in metabolic prioritization within the microbial community [69]. Importantly, approximately 65% of studies emphasized that SCFA production is strongly influenced by the interaction between dietary lipids and fermentable substrates such as fiber, indicating that lipid effects are context-dependent rather than isolated drivers of metabolic change [63,70].

Selective Enrichment of Beneficial Microbial Taxa

Selective modulation of specific microbial taxa was observed in approximately 63% of the reviewed studies, highlighting shifts in bacteria associated with beneficial metabolic functions [35]. Genera such as Lactobacillus and Bifidobacterium exhibited relative abundance changes ranging from −20% to +18%, with variability influenced by dietary composition and experimental conditions [54]. Butyrate-producing taxa, including Faecalibacterium prausnitzii and Roseburia spp., showed changes within a range of −15% to +22%, reflecting sensitivity to both lipid profiles and carbohydrate availability [13]. In several studies, increases in these taxa were associated with stable or improved SCFA production, whereas reductions were often linked to low fiber intake rather than lipid composition alone. Additionally, Akkermansia muciniphila, a mucin-degrading microorganism linked to the regulation of gut barrier function, showed relative abundance changes of + 5% to + 16% in some studies, indicating potential adaptive responses within the microbial ecosystem [10,30]. Notably, approximately 47% of studies reported no significant decline in beneficial taxa under controlled dietary conditions involving palm oil–related fatty acids, suggesting resilience and adaptability of the gut microbiota [27].

Interaction with Intestinal Barrier Function

Approximately 58% of the analyzed studies investigated markers of intestinal barrier integrity, including tight junction proteins and permeability indicators [59,62]. Depending on experimental context and exposure period, the expression of occludin, claudin-1, and ZO-1 varied within a range of −10% to −30% [50]. Functional assessments of intestinal permeability, commonly measured using FITC-dextran assays, indicated increases ranging from 8% to 25% in certain models, while approximately 42% of studies reported no significant changes in permeability [7]. These findings suggest that structural protein changes do not always correspond to functional impairment. Furthermore, approximately 60% of studies emphasized that barrier-related outcomes were influenced by additional dietary factors, including fiber, micronutrients, and overall caloric balance, which may modulate epithelial responses and maintain homeostasis [39,79]. This indicates that intestinal barrier responses are multifactorial and cannot be attributed solely to lipid composition.

Associations with Inflammatory and Oxidative Stress Pathways

Approximately 61% of the included studies reported associations between dietary lipid composition and markers of inflammation and oxidative stress [28]. In specific experimental scenarios, TNF-α, IL-6, and IL-1β increased by 10% to 40%, although about 39% of studies reported no meaningful or significant alterations [60,81]. Increases of 12%–35% in oxidative stress indicators such as MDA were observed in certain models, alongside compensatory elevations of 8%–20% in antioxidant enzymes, including SOD and catalase [26]. These patterns suggest the presence of adaptive physiological responses that balance oxidative processes. Importantly, approximately 67% of studies highlighted that inflammatory and oxidative responses were influenced by overall dietary patterns, metabolic status, and experimental conditions rather than being exclusively driven by specific fatty acids [17,57]. This indicates that observed biological responses represent integrated systemic processes rather than isolated effects. The synthesis of 38 studies demonstrates that dietary fatty acids associated with palm oil are linked to measurable yet context-dependent variations in gut microbiota composition, metabolic outputs, and intestinal function. Across studies, microbial diversity changes generally remained within ± 20% of baseline values, SCFA fluctuations within ± 35%, and functional markers within physiologically adaptable ranges. These findings collectively indicate that gut microbiota responses are shaped by complex interactions involving dietary composition, host physiology, and environmental factors. Overall, the evidence supports a nuanced and balanced interpretation in which dietary lipid profiles contribute to microbial and metabolic modulation without indicating uniform or deterministic effects. The observed heterogeneity across studies reinforces the importance of considering dietary patterns as integrated systems, thereby providing a comprehensive and evidence-based understanding of the relationship between palm oil–related fatty acids and gut microbiota dynamics.

Discussion

This study, employing a systematic literature review approach, was designed to investigate the central research question: How do dietary fatty acids associated with palm oil influence gut microbiota composition, short-chain fatty acid production, and intestinal homeostasis across different biological and experimental contexts? The synthesis of 38 peer-reviewed studies provides a comprehensive basis for interpreting the multidimensional interactions between dietary lipid profiles and gut microbial ecosystems. The findings collectively indicate that the influence of palm oil–related fatty acids are neither uniform nor unidirectional, but rather context-dependent and mediated by a network of

biological, dietary, and methodological variables. This discussion integrates the five thematic clusters identified in the Results section and critically examines their implications within a broader scientific framework. A central observation emerging from this review is that dietary fatty acids associated with palm oil can modulate gut microbiota composition, although the magnitude and direction of these changes vary across studies. Approximately two-thirds of the included studies reported measurable alterations in microbial diversity and community structure, while the remaining studies observed stability in microbial profiles under comparable conditions [12,49]. This variability suggests that gut microbiota responses to dietary lipids are influenced by baseline microbial composition, host metabolic status, and environmental factors such as diet complexity. Importantly, changes in alpha diversity indices were generally modest, often remaining within ± 20% of baseline values, indicating that microbial ecosystems exhibit resilience to dietary perturbations [75]. At the compositional level, shifts in dominant bacterial phyla, particularly Firmicutes and Bacteroidetes, were frequently reported; however, these changes did not consistently correspond to functional dysregulation. While some studies observed increases in the Firmicutes-to-Bacteroidetes ratio, others reported stable or even reduced ratios, highlighting the absence of a singular directional pattern [24]. This inconsistency underscores the limitations of relying solely on taxonomic indicators as proxies for functional outcomes and emphasizes the importance of integrating metabolic and functional analyses when evaluating microbiota responses.

In addressing the second component of the research question, the synthesis demonstrates that short-chain fatty acid production is influenced by dietary lipid composition, albeit indirectly and in interaction with other dietary factors. SCFAs, particularly acetate, propionate, and butyrate, serve as key mediators linking microbial metabolism to host physiology. Across the reviewed studies, approximately 70% reported variations in SCFA concentrations following dietary interventions involving different lipid profiles [72]. However, the direction of these changes was not consistent, with both increases and decreases observed depending on experimental conditions. A critical factor influencing SCFA production is the availability of fermentable substrates, particularly dietary fiber, which serves as the primary source for microbial fermentation [77]. Studies consistently indicate that lipid-induced changes in SCFA profiles are more pronounced when dietary fiber intake is limited, suggesting that the effects of fatty acids on microbial metabolism are modulated by substrate competition and metabolic prioritization within the microbial community [41]. In contrast, under conditions of adequate fiber intake, SCFA production tends to remain stable or exhibit compensatory adaptations, reflecting the functional flexibility of the gut microbiota. Butyrate, in particular, has been extensively studied due to its role in maintaining intestinal epithelial integrity and modulating immune responses. While some studies reported reductions in butyrate levels under specific dietary conditions, others observed stable or increased concentrations, especially in the presence of fiber-rich diets [56]. These findings indicate that the relationship between dietary fatty acids and SCFA production is complex and cannot be attributed to lipid composition alone. The third dimension of the research question concerns the selective enrichment of microbial taxa. The review findings indicate that dietary lipid profiles can influence the relative abundance of specific bacterial groups, including taxa associated with beneficial metabolic functions. However, these changes are not consistently observed across all studies. Approximately 60% of the included studies reported shifts in genera such as Lactobacillus, Bifidobacterium, and butyrate-producing bacteria, while the remaining studies observed no significant changes [44].

Importantly, the abundance of these taxa shifted in different directions across studies, with both increases and decreases being reported. This variability suggests that microbial responses are shaped by a combination of dietary composition, host factors, and microbial interactions. For example, the presence of fermentable carbohydrates has been shown to support the growth of beneficial taxa, potentially offsetting the effects of dietary lipids [18]. Additionally, microbial cross-feeding mechanisms may contribute to the stability of functional outputs, even when taxonomic composition changes [74]. The fourth component of the research question relates to intestinal homeostasis, particularly the integrity of the intestinal barrier. The reviewed studies indicate that dietary fatty acids may influence markers of barrier function, including tight junction proteins and intestinal permeability. However, similar to other findings, the effects observed are heterogeneous and context-dependent. Approximately 58% of studies reported changes in barrier-related markers, while the remaining studies found no significant effects [32]. Changes in tight junction protein expression, such as occludin and zonula occludens-1, were observed in some experimental models, with reported variations ranging from moderate reductions to no detectable changes [43]. Functional assessments of intestinal permeability also yielded mixed results, with some studies reporting increases and others indicating stability. These findings suggest that the impact of dietary fatty acids on intestinal barrier function is influenced by multiple factors, including dosage, duration of exposure, and overall dietary composition [31]. Notably, the interaction between gut microbiota and intestinal barrier function appears to play a mediating role in these processes. Microbial metabolites, particularly SCFAs, are known to support epithelial integrity and regulate immune responses. Therefore, changes in microbial composition and metabolic activity may indirectly influence barrier function, highlighting the interconnected nature of diet, microbiota, and host physiology [68].

The final component of the research question addresses the association between dietary fatty acids and inflammatory and oxidative stress pathways. The evidence synthesized in this review indicates that while some studies report increases in inflammatory markers and oxidative stress indicators, others observe minimal or no significant changes. Approximately 60% of

studies identified associations between dietary lipid composition and changes in cytokine levels or oxidative stress markers, while 40% reported no significant effects [25,73]. This variability suggests that inflammatory and oxidative responses are not solely determined by dietary fatty acids but are influenced by broader physiological and environmental factors. For instance, the presence of antioxidants, micronutrients, and overall dietary quality may modulate these responses, contributing to a balance between pro-inflammatory and anti-inflammatory processes [76]. Additionally, host metabolic status and genetic factors may influence susceptibility to inflammatory changes, further contributing to variability across studies. Taken together, the findings of this review provide a comprehensive answer to the research question by demonstrating that dietary fatty acids associated with palm oil influence gut microbiota composition, SCFA production, and intestinal homeostasis through complex and context-dependent mechanisms. Rather than exerting uniform effects, these fatty acids interact with multiple biological systems, resulting in outcomes that vary according to dietary context, host characteristics, and experimental conditions. This perspective aligns with a systems-based understanding of nutrition, in which dietary components are viewed as part of an integrated network rather than isolated determinants of physiological outcomes. Importantly, the evidence does not support a singular or deterministic interpretation of the effects of palm oil–related fatty acids on gut microbiota or intestinal health. Instead, the observed variability highlights the adaptability and resilience of the gut microbial ecosystem, as well as the influence of co-existing dietary and environmental factors. This reinforces the importance of evaluating dietary lipids within the context of overall dietary patterns and lifestyle factors.

From a methodological perspective, the heterogeneity observed across studies underscores the need for greater standardization in experimental design, including consistent reporting of dietary composition, duration of interventions, and analytical methods. Such standardization would facilitate more accurate comparisons across studies and improve the reliability of future syntheses. In terms of implications, the findings of this review contribute to a more nuanced understanding of the relationship between dietary lipid profiles and gut microbiota, emphasizing the importance of context in shaping biological responses. For researchers, these results highlight the need to consider multiple interacting variables when designing studies and interpreting findings. For the broader scientific community, the review provides a balanced and evidence-based perspective that avoids oversimplification and supports informed discussion of dietary lipids and gut health. Longitudinal human studies incorporating multi-omics approaches such as metagenomics, metabolomics, and transcriptomics should be prioritized in future research to capture the dynamic interactions between diet, microbiota, and host physiology. Additionally, studies examining the combined effects of dietary lipids and other nutrients, particularly fiber, would provide valuable insights into the synergistic mechanisms underlying gut microbiota modulation. Further investigation into individual variability, including genetic and metabolic factors, would also enhance understanding of personalized responses to dietary lipids. In summary, this systematic review demonstrates an influence of palm oil–associated dietary fatty acids on gut microbiota composition, SCFA production, and intestinal homeostasis through interconnected and context-dependent mechanisms. The findings underscore the importance of adopting an integrative and evidence-based approach to understanding diet–microbiota interactions, while also identifying key areas for future research that will advance knowledge in this rapidly evolving field.

Conclusion

The synthesis of evidence from 38 peer-reviewed studies demonstrates that dietary fatty acids associated with palm oil contribute to measurable yet context-dependent modulation of gut microbiota composition, Short-Chain Fatty Acid (SCFA) production, and intestinal homeostasis. Across the analyzed literature, microbial responses are characterized by moderate shifts in diversity and community structure, typically remaining within physiologically adaptive ranges. These changes do not follow a single consistent directional pattern, indicating that gut microbiota exhibits resilience and adaptability in response to variations in dietary lipid composition. In terms of metabolic outcomes, SCFA production particularly acetate, propionate, and butyrate emerge as a key functional link between dietary lipids and host physiology. However, the influence of palm oil–related fatty acids on SCFA profiles is not direct or uniform. Instead, it is strongly modulated by the availability of fermentable substrates, especially dietary fiber, as well as by the overall dietary matrix. This highlights that microbial metabolic responses are shaped by integrated nutritional conditions rather than by isolated lipid components. Selective modulation of microbial taxa is observed across a substantial proportion of studies, including variations in genera associated with beneficial metabolic functions. Nevertheless, these changes are heterogeneous and influenced by multiple interacting factors, such as host physiology, baseline microbiota composition, and dietary complexity. As a result, taxonomic shifts do not consistently translate into functional alterations, reinforcing the importance of evaluating both compositional and metabolic dimensions of the gut microbiota.

Regarding intestinal homeostasis, the evidence indicates that dietary fatty acids may interact with markers of intestinal barrier integrity and immune-related pathways, although these effects remain variable across experimental contexts. Changes in tight junction protein expression, intestinal permeability, and inflammatory markers are reported in some studies, but are not consistently observed. This suggests that such outcomes are influenced by a combination of dietary composition, exposure conditions, and host-related factors, rather than being solely determined by fatty acid profiles. Across different biological and experimental contexts including in vitro systems, animal models, and human studies the magnitude and direction of observed effects vary, reflecting methodological diversity and differences

in physiological conditions. This variability underscores the importance of interpreting findings within a systems-based framework, where dietary fatty acids function as modulatory components within a broader network of nutritional and biological interactions. Overall, the evidence supports a balanced and integrative perspective in which palm oil–related fatty acids are associated with adaptive and context-sensitive responses in gut microbiota and intestinal function. Rather than exerting uniform or deterministic effects, these fatty acids participate in complex interactions that are shaped by dietary patterns, microbial ecology, and host physiology. This synthesis provides a comprehensive and evidence-based understanding of the relationship between dietary lipid profiles and gut microbiota dynamics, while also highlighting the importance of considering broader nutritional contexts in future research.

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Conflict of Interest

None.

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