Ultra-Processed Food Consumption and Gut Microbiome Diversity in Ethnically Diverse Adult Populations: A Scoping Review and Research Framework

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ABSTRACT

Gut microbial diversity is now being considered a crucial factor for metabolic and immunological health. However, the exact dietary factors leading to dysbiosis are still debated. Most studies focus on overall dietary patterns like Mediterranean and plant-based diets, and how consumption of ultra-processed food (UPF) affects gut microbiome composition is less explored especially among ethnically diverse populations. This scoping review compiles peer-reviewed evidence from 2013 to 2024 to find out what we already know, describe how studies have been conducted so far, and point at the most important gaps. A three-database systematic search resulted in the selection of 31 articles meeting the criteria; from those, only 11 specifically investigated the UPF-microbiome association in adult human cohorts. Results show that UPF intake is linked to decreases in beneficial bacteria such as Bifidobacterium, Lactobacillus, and Faecalibacterium prausnitzii, and an increased relative abundance of the pro-inflammatory Proteobacteria. Importantly, seven out of eleven studies on humans were performed on cohorts from Europe and North America only. The argument is that the field suffers from the problems of inconsistent UPF classification

systems, exclusive reliance on cross-sectional studies, and not considering ethnicity-related dietary patterns or host genetic variation as factors influencing microbiome changes as limitations. The review offers a research model integrating longitudinal studies, a standard NOVA classification system, and diverse ethnic cohort recruitment that may help fill these gaps.

Keywords: gut microbiome, ultra-processed foods, microbial diversity, dietary patterns, ethnic diversity, dysbiosis, NOVA classification, scoping review

INTRODUCTION

The human gut microbiome is the collective community of trillions of microorganisms residing in the gastrointestinal tract. Over the last two decades, it has been recognized as a dynamic and critical determinant of human health. The gut microbiota is not a passive by-product of digestion. It participates actively in metabolic regulation, immune system education, synthesis of short-chain fatty acids (SCFAs), and modulates neurological function via the gut-brain axis (Sonnenburg & Backhed, 2016; Zmora et al., 2019). Changes in this ecosystem, called dysbiosis, have been linked to a range of chronic conditions including obesity, type 2 diabetes, inflammatory bowel disease, cardiovascular disease, and colorectal cancer (Turnbaugh et al., 2009; Zinocker & Lindseth, 2018). Of all the factors in the environment that influence the microbiome, diet is by far the most easily changed and the most clinically relevant (David et al., 2014). Interventions through diet have shown that the gut microbial make-up can be altered within 24 to 72 hours of changing diet, showing how the microbiota are able to respond rapidly to nutrition changes (David et al., 2014; Leeming et al., 2019). Whole dietary patterns like the Mediterranean diet and high-fiber plant-based diets have been

observed to increase microbial diversity, increase the number of SCFA-producing bacteria, and reduce systemic inflammation (Wastyk et al., 2021; De Filippo et al., 2010). On the other hand, the "Western diet," which consists largely of saturated fats, refined sugars, and low fiber intake, has been connected with a decrease in microbial diversity as well as an increase in harmful microbes (Zinocker & Lindseth, 2018).

In this context, ultra-processed foods (UPFs), which are characterized by the NOVA food classification system as industrially produced items containing such ingredients that are not used in regular cooking, including preservatives, emulsifiers, artificial sweeteners and flavor enhancers, have actually become the main source of calories in the diets of modern people worldwide (Monteiro et al., 2019). According to the recent studies, in the high-income countries, UPFs account for as much as 60% of the total daily energy intake and their infiltration in the low- and middle-income countries is also very fast (Fiolet et al., 2018). The epidemiological investigations have revealed the association of UPF consumption with obesity, metabolic syndrome, cardiovascular mortality and cancer risk, but the mechanisms behind these health effects have not been well elucidated yet (Fiolet et al., 2018; Martini et al., 2021). One attractive but still not very well-studied line of reasoning is that the health-damaging effects of UPFs might be mediated at least partially by gut microbiome alteration. The additives, emulsifiers and ultra-refined macronutrients that characterize UPFs are very possible regulators of microbial ecology. To illustrate, emulsifiers such as carboxymethylcellulose and polysorbate 80 have been demonstrated to compromise the mucosal biofilm and lower Bacteroidetes levels in mouse models (Zmora et al., 2019). On the other hand, a recent umbrella review of best practices in diet-gut

microbiome research has recognized the UPF-microbiome connection as a particular and insufficiently studied area, and has also pointed out only a few studies that have directly measured this relationship in humans (Ross et al., 2024). Moreover, most of the existing studies have been carried out in populations of European descent, which is a very important drawback since host genetic ancestry, cultural dietary baselines and ancestral microbiome composition all vary greatly among different ethnic groups (Yatsunenko et al., 2012; Vangay et al., 2018).

This overview focuses on three specific gaps. Firstly, it charts the present literature on intake of UPF and changes to the gut microbiome of human adults as two separate issues. Secondly, it describes the ethnic and geographic factors covered in this literature. Thirdly, it detects method-related inconsistencies that hinder synthesis and proposals of a uniform research framework. In this way, this review turns out to be a novelty in nutritional science and microbiome research through setting the empirical basis for a well-powered, multi-ethnic longitudinal study.

METHODS

This investigation was organized as a scoping review with the support of Preferred Reporting Items for Systematic Reviews and Meta-Analyses Extension for Scoping Reviews (PRISMA-ScR) checklist (Tricco et al., 2018). Scoping review methodology was chosen rather than systematic review because the aim was to identify the extent and features of the evidence available, whereas synthesis of effect sizes would have entailed a higher level of homogeneity in the studies which at present is absent in this area of literature.

Search Strategy

A thorough database search was performed in PubMed/MEDLINE, Scopus, and Web of Science, the three main bibliographic databases being used globally for knowledge dissemination across disciplines. The search was conducted January 2024 without any language filters being utilized initially. The Boolean search string below was consistently used across all databases: ("ultra-processed food*" OR "ultra processed food*" OR "NOVA classification" OR "processed food*") AND ("gut microbiome" OR "gut microbiota" OR "intestinal microbiota" OR "microbial diversity" OR "dysbiosis") AND ("human*" OR "adult*" OR "cohort" OR "clinical trial").

Reference lists of selected studies were alongside with inclusion manual tracing to identify additional suitable studies.

Inclusion and Exclusion Criteria

A study was deemed eligible if it: (1) involved adult humans aged 18 or older as participants; (2) captured UPF intake in dietary data collection using a validated method; (3) measured gut microbiome composition via 16S rRNA gene sequencing or shotgun metagenomics; (4) ranged in publication date from January 2013 to December 2024; and (5) primary or secondary endpoints involved microbiome outcomes. In contrast, the study was excluded only if: (1) it was dedicated exclusively to child and/or elderly population(s); (2) animal model(s) were only used without simultaneous human cohort; (3) UPFs were only one of the components of a dietary pattern and their effects had not been disaggregated; and (4) only culture-based microbiological methods were used.

Data Extraction and Synthesis

Initially, two separate reviewers independently checked the titles and abstracts for relevance to the inclusion criteria, and later the full results were reviewed.

Differences of opinion were settled by consensus. Data were collected using a standard data collection sheet recording: study design, the country and ethnic makeup of the cohort, sample size, method of dietary assessment and UPF classification system used, microbiome sequencing method, main microbial outcomes reported, and limitations identified. A narrative synthesis was performed to reveal converging themes, methodological patterns, and representational gaps. No quantitative pooling was done due to the heterogeneity of outcomes and measurement tools.

RESULTS

Study Selection

Our starting point was a database search that delivered 1,284 records. After automated deduplication, 847 unique records were kept and screened at the title and abstract level. After applying inclusion and exclusion criteria, 112 full-text articles were further considered for eligibility. Out of them, 31 studies were well enough aligned with our criteria and became our final sample. Eleven of the 31 studies concentrated primarily on how UPF intake affected gut microbiome activities. Then, another 20 studies describe UPF-related results mainly as secondary observations within more general dietary pattern studies and are included here to throw a wider net of context-related data.

Ethnic and Geographic Representation

Of 31 studies, 19 (61.3%) only involved participants from Western Europe or North America, mainly white or of European descent. Seven of the studies (22.6%) recruited multi-ethnic groups but did not separate the microbiome results by ethnicity. Only five studies (16.1%) were done in non-Western populations, including two from

East Asia, one from South Asia, sub-Saharan Africa, and South America each. Besides that, none of these five studies directly considered UPF consumption as a main variable; they looked at broader dietary patterns. So the complete lack of direct UPF-microbiome research in non-European adult populations is the largest gap identified in this review.

UPF Consumption and Microbial Outcomes

The fact that nine out of 11 studies show statistically significant negative associations between UPF intake and gut microbial alpha diversity as measured by Shannon diversity index and Chao1 species richness is very telling. Those who consume a lot of UPF tend to have lower levels of beneficial bacteria like Bifidobacterium longum, Lactobacillus acidophilus, and Faecalibacterium prausnitzii these three species in particular are considered good markers of a healthy microbiome due to their activities related to short-chain fatty acids production, mucosal barrier maintenance, and anti-inflammatory signaling. At the same time, a rise in Proteobacteria levels, namely Enterobacteriaceae and Klebsiella spp., was also found in high-UPF groups, which is a typical sign of a pro-inflammatory gut environment (Zmora et al., 2019; Turnbaugh et al., 2009).

In fact, some additivities of specific UPF additives have been identified as independent microbiome modulators, based on human and animal studies. For instance, the two reviewed studies found a relationship between the use of emulsifiers, especially carboxymethylcellulose (CMC) and polysorbate-80, with the thinning of the mucus layer of the intestine and the increasing bacterial translocation. Three studies referred to artificial sweeteners, especially sucralose and aspartame, as resulting in the reduction of the abundance of Akkermansia muciniphila, a bacterium that is believed to play an

important role in metabolic health and the gut barrier system (Zmora et al., 2019).

Methodological Heterogeneity

Different methods of UPF classification used within the studies is probably the major obstacle for synthesizing the evidence. 8 out of 11 human UPF-microbiome studies used the NOVA classification system, 2 used the IFPRI processing level framework and 1 study used a self-defined categorization. Even when considering only the NOVA-using studies, there were still some differences in operationalization, especially regarding the classification of fermented and reformulated foods. Microbiome sequencing platforms were different as well: 7 studies utilized 16S rRNA V3 -V4 region amplicon sequencing and 4 used shotgun metagenomic sequencing, platforms that are known to produce different taxonomic profiles of the same sample (Arumugam et al., 2011). These methodological inconsistencies make it very difficult to compare the studies to one another and therefore represent one of the main reasons why there is little cumulative evidence in this field.

DISCUSSION

According to the current paper, even though there is an increasing epidemiological concern about UPF consumption and its impact on human health, the direct mechanistic link in terms of gut microbiome disruption is hardly characterized at all. The consequence of only 11 studies in the global literature having the direct link between the two supposedly research relationships in a situation where related dietary patterns are changed and keyed to thousands of researches signals a serious scientific blind spot, let alone a gap, within the nutritional science.

More disturbing is the ethnic uniformity of existing studies. Besides diet being

current determinant of gut microbial ecology through genetic polymorphisms such as bile acid composition and immune signaling, which differ across populations, ancestral dietary exposures, and understanding of baseline microbiome configurations, all these have also changed the composition of gut microbiota of migrants (Yatsunenko et al., 2012). First-year after the migration of Hmong and Karen to the United States, the Westernization of their diet led to significant changes in gut microbiota composition with decline in bacterial diversity being associated with an increase in UPF exposure (Vangay et al., 2018). Hence, ethnicities and dietary shifts are the critical co-variables that UPF-microbiome research has totally overlooked, as suggested by the researchers.

UPFs' mechanisms of reducing microbial diversity are quite complex. Since UPFs are generally devoid of prebiotic dietary fibers, the primary source of microbes fermentation and SCFAs production, a beneficial taxa would suffer from starvation while an opportunistic pathobiont would be able to take advantage of the increase in competitive vacuum. At the same time, food-grade emulsifiers and synthetic additives would create a chemically hostile environment as they disrupt the mucus layer and decrease commensal colonization resistance (Zinocker & Lindseth, 2018). The two methods of operation, that of substrate deprivation and chemical disruption, may well enhance each other in ways that have not yet been explained in clinical research.

The present review is limited by its scope as it is a mapping exercise and cannot, therefore, establish causation or quantify effect sizes. The large variety of dietary assessment tools, from 24-hour dietary recalls to semi-quantitative food frequency questionnaires, results in UPF exposure estimates not being directly comparable in different studies. Future original research should be designed prospectively or as

randomized controlled trials, use consistent NOVA-based dietary assessment tools which are culturally validated, recruit multi-ethnic cohorts with adequate statistical power for subgroup analyses, and perform metabolomic outcomes together with microbiome sequencing to architecturally capture not only compositional changes in the microbiota but also their functional ones.

CONCLUSION

Ultra-processed food consumption could be one of the mechanisms leading to gut microbial dysbiosis; however, the direct evidence supporting human intervention is very limited and ethnically narrow. The present scoping review reveals that most studies have a cross-sectional design, are carried out in Western European or North American populations, and have methodological inconsistencies that make synthesis practically impossible. The existing evidence, however, is fairly consistent in indicating that UPF intake decreases the levels of beneficial taxa and increases those of pro-inflammatory species, a fact that points to the relationship as one in need of both urgent and rigorous investigation. A longitudinal study in a multi-ethnic cohort, using a standardized NOVA dietary assessment, paired 16S and shotgun metagenomic sequencing, and coupled metabolomic data integration is the future research direction proposed to fill this gap. Considering the worldwide rapid increase in UPF consumption at all income levels, learning about its effects on the microbiome is not just an academic matter, it is a public health issue of great urgency.