Journal of Education, Health and Sport. eISSN 2391-8306.

Journal Home Page
https://apcz.umk.pl/JEHS/index

KAMIŃSKA, Kamila, BĘDKOWSKA-KUŚMIEREK, Matylda, ZŁOTNIK, Anna, KRZYSZTOFIK, Kinga, KLAMKA, Antoni, KAWALEC, Paulina, BRONIKOWSKI, Kamil, RYSZKOWSKI, Maksymilian, FORNAL, Krystian, and BĘDKOWSKA-KUŚMIEREK, Natalia. The Association Between Sugar-Sweetened Beverage (SSB) Consumption and Gut Microbiota Composition and Related Metabolites in Adults: A Systematic Review. Journal of Education, Health and Sport. 2026;90:70498. eISSN 2391-8306. https://doi.org/10.12775/JEHS.2026.90.70498

The journal has had 40 points in Minister of Science and Higher Education of Poland parametric evaluation. Annex to the announcement of the Minister of Education and Science of 05.01.2024 No. 32318. Has a Journal's Unique Identifier: 201159. Scientific disciplines assigned: Physical culture sciences (Field of medical and health sciences); Health Sciences (Field of medical and health sciences).
Punkty Ministerialne 40 punktów. Załącznik do komunikatu Ministra Nauki i Szkolnictwa Wyższego z dnia 05.01.2024 Lp. 32318. Posiada Unikatowy Identyfikator Czasopisma: 201159. Przypisane dyscypliny naukowe: Nauki o kulturze fizycznej (Dziedzina nauk medycznych i nauk o zdrowiu); Nauki o zdrowiu (Dziedzina nauk medycznych i nauk o zdrowiu).
Received: 01.04.2026. Revised: 12.04.2026. Accepted: 23.04.2026. Published: 23.04.2026.

The Association Between Sugar-Sweetened Beverage (SSB) Consumption and Gut Microbiota Composition and Related Metabolites in Adults: A Systematic Review

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ABSTRACT

Background. Sugar-Sweetened Beverages (SSB) are a major source of dietary sugars worldwide. Emerging evidence suggests that dietary factors, including sugar intake, may influence the composition of the gut microbiota, which plays a crucial role in human physiology. However, the relationships between habitual SSB intake, gut microbiota composition, and related metabolites in adults remain insufficiently studied.

Aim. This systematic review aimed to synthesize available evidence on the associations between SSB consumption, gut microbiota composition, and related metabolite profiles in adults, while identifying methodological differences and gaps in literature.

Material and methods. A systematic search identified observational studies investigating SSB intake and gut microbiota or metabolite outcomes in healthy adult populations.

Results. Higher SSB intake was consistently associated with alterations in gut microbial composition, including shifts in the Firmicutes: Bacteroidetes ratio. Changes included reductions in short-chain fatty acid producing species including Eubacterium eligens, Ruminococcus callidus, and several Clostridium species. Metabolomic analyses revealed changes in branched-chain amino acids, aromatic amino acids, glycerophospholipids and bile acids with distinct patterns observed for specific SSB types. Overall, 56 serum metabolites were significantly related to SSB intake and implicated in diabetes risk. SSB was also linked to higher visceral adiposity index, total and LDL-cholesterol. Added sugar intake was positively associated with the genus Lachnobacterium.

Notably, studies employed diverse methods for microbiota and metabolite assessment, highlighting heterogeneity in the evidence base.

Conclusions. Habitual SSB consumption may influence gut microbial composition and related metabolites in adults, contributing to metabolic dysregulation. The limited number of studies, methodological differences and observational nature of available evidence, highlight the need for interventional studies and the necessity of standardized methods.

Keywords: sugar-sweetened beverages, gut microbiota, metabolites, short-chain fatty acids, metabolic health, adults, systematic review

1.1. Introduction

Humans, for most of their evolutionary history, functioned in environments that exposed them to microorganisms present in soil, water, air, plants, and animals. Consequently, from the moment of birth, the epithelial surfaces of the human body were gradually colonized by diverse microorganisms [17].

Microorganisms are the result of more than three billion years of the evolution of life on Earth and existed long before the emergence of multicellular organisms. With the development of more complex organisms, a long-term coevolution occurred between microorganisms and their hosts, referred to as metaorganisms [5,6]. As a result of this process, mutually beneficial symbiotic relationships developed across all epithelial barriers [7].

The human gut microbiota constitutes a complex ecosystem of microorganisms inhabiting the gastrointestinal tract and plays an important role in maintaining host’s homeostasis. This term refers to the entire host-associated microbial community together with its genetic material. This ecosystem covers representatives of multiple kingdoms of organisms, including bacteria, archaea, prokaryotic and eukaryotic viruses, fungi, protozoa, and other microorganisms colonizing the gastrointestinal tract [7]. It is estimated that the number of bacterial cells in the human body is comparable to the number of human cells, and their total mass is approximately 0.2 kg [10]. Among gut microorganisms, five major bacterial phyla are distinguished: Firmicutes, Bacteroidetes, Actinobacteria, Proteobacteria, and Verrucomicrobia [8,9]. The largest proportion of the gut microbiota consists of bacteria belonging to the phyla Firmicutes and Bacteroidetes, which dominate in the healthy human intestine [11]. At the same time, the genus Bacteroides is considered one of the most abundant, but also highly variable between individuals [11].

In recent years, a growing number of studies have indicated that gut microbiota participates in many key biological processes of the host. Gut microorganisms are involved, among others, in the regulation of metabolic processes, modulation of immune responses, and maintenance of proper gastrointestinal function, which translates into the overall health status of humans [9]. Disturbances in microbial balance, referred to as dysbiosis, may lead to the development of numerous metabolic and inflammatory diseases [3].

Many factors influence the composition, abundance, and diversity of microorganisms inhabiting the gastrointestinal tract. Among the most important are host genetic factors, environmental conditions, level of physical activity, lifestyle hygiene, and exposure to xenobiotics [13]. However, one of the most important roles is played by nutrition, including dietary composition, eating patterns, and long-term dietary habits [12]. This has been repeatedly demonstrated in various studies [8,14,15,16].

Dietary components constitute not only a source of energy and nutrients for the host organism but also are substrates for gut microorganisms [8]. Undigested food residues reaching the colon undergo bacterial fermentation, resulting in the production of numerous bioactive metabolites such as short-chain fatty acids (SCFA), secondary bile acids, and amino acid metabolites [17]. Gut microorganisms also participate in the synthesis of certain vitamins, including B vitamins and vitamin K [8,9]. Metabolites produced by the gut microbiota play an important role in communication between microorganisms and the human body. SCFA play a particularly important biological role, as in addition to influencing the proliferation and functioning of intestinal epithelial cells, they also affect the immune system and numerous metabolic pathways of the host [2,17].

Long term dietary patterns appear to be crucial in shaping both the composition and functionality of the gut microbiota and, consequently, host metabolism. A diet considered beneficial for health, characterized by an appropriate energy value, high intake of fruits and vegetables, high dietary fiber content, the presence of unsaturated fatty acids (MUFA and PUFA), and a greater proportion of plant protein, promotes increased diversity and activity of gut microorganisms. Previous studies have shown that the composition of the gut microbiota differs between lean and obese individuals, as well as in individuals with metabolic disorders [9].

Individual dietary components may influence the structure of the gut microbiota in different ways. A diet rich in animal protein, saturated fats, simple sugars, and salt may promote the proliferation of potentially pathogenic bacteria at the expense of microorganisms considered beneficial to health, which may lead to disturbances in intestinal barrier function. On the other hand, the consumption of complex polysaccharides and plant protein may be associated with an increase in the number of beneficial bacteria, stimulating SCFA production [14].

Different dietary patterns, especially diets characterized by high intake of simple sugars, may lead to significant changes both in the composition of the gut microbiota and in the profiles of metabolites produced by gut microorganisms and circulating in the host organism [23]. Despite the growing number of studies analyzing the relationships between diet and gut microbiota, the mechanisms linking SSB consumption with changes in microbiota structure and metabolite production remain insufficiently investigated.

SSB currently constitutes one of the main dietary components contributing to excessive intake of simple sugars worldwide. This category includes all non-alcoholic beverages containing so-called free sugars, including carbonated and non-carbonated soft drinks, fruit drinks, nectars, energy drinks, isotonic beverages, flavored waters, ready-to-drink teas and coffees, as well as sweetened milk beverages or plant-based milk alternatives. According to data presented in the Global Report of the World Health Organization (WHO) on SSB consumption, in many countries these products represent one of the most common sources of sugar in the daily diet despite providing little nutritional value [18]. In many high-income countries, the consumption of Sugar-Sweetened Beverages approaches or has already exceeded the recommended limit set at less than 10% of total daily energy intake from added or free sugars [20]. Global data indicate that the consumption of these beverages has been increasing in recent years. Estimates based on market data indicate that between 2013 and 2024 global consumption of non-alcoholic beverages (excluding water) increased by approximately 14%. At the same time, in many countries an increase in the economic availability of SSB has been observed. Over the past three decades their purchase has become relatively cheaper in relation to income, particularly in low- and middle-income countries. This means that these products are now more accessible to a larger proportion of the population than in the past [18]. Regular consumption of SSB is associated with numerous adverse health consequences. Results of numerous studies indicate a relationship between frequent SSB consumption and an increased risk of overweight and obesity, as well as the development of type 2 diabetes, cardiovascular diseases, dental caries, and non-alcoholic fatty liver disease [19,20,21]. Moreover, it has been suggested that high SSB intake may be associated with the occurrence of mood disorders, including depression, as well as an increased risk of inflammatory bowel diseases [19,21]. Excessive intake of sugar in liquid form may also contribute to the development of metabolic disorders and potentially affect bone mineral density [18]. In the case of some other diseases, such as stroke or selected cancers, available research findings remain inconclusive [19]. At the same time, there is convincing evidence that replacing SSB with healthier alternatives may help reduce the risk of chronic diseases, particularly in adult and older populations, and may potentially extend both life expectancy and healthy life years [22]. Therefore, reducing SSB consumption has become one of the important targets of public health actions. These strategies include both nutritional education and policy level interventions, such as the introduction of taxes on SSB or regulations regarding the marketing of these products [18].

Despite the growing number of studies on the impact of Sugar-Sweetened Beverages on metabolic health, the mechanisms linking their consumption with changes in gut microbiota composition and metabolite production remain an area of ongoing interest. Understanding these relationships may provide new insights into the biological mechanisms through which diet influences health and may help develop more effective strategies for the prevention of metabolic diseases. Understanding these relationships is particularly important in the adult population, in which SSB consumption is widespread and microbiota changes may significantly influence the development of metabolic diseases. The aim of this systematic review is to collect and evaluate the available evidence regarding the impact of SSB consumption on gut microbiota composition and related metabolites in adults. Additionally, it identifies and compares the methods used in studies to assess microbiota in the context of SSB and highlights research gaps and future research directions in order to better understand the mechanisms linking diet, gut microbiota, and metabolic health.

1.2.1. Research Objective.

The objective of this systematic review is to systematically assess and synthesize the existing evidence on the relationship between Sugar-Sweetened Beverage consumption and alterations in gut microbiota composition and diversity, as well as associated microbial metabolites, in adult populations.

1.2.2. Research Problems.

This systematic review aims to investigate whether the consumption of Sugar-Sweetened Beverages is associated with factors linked to chronic conditions such as obesity, diabetes, and systemic inflammation. In addition, it seeks to address the following questions:

- what is the association between SSB consumption and gut microbiota composition;
- what is the association between Sugar-Sweetened Beverage consumption and related microbial metabolites in adults;
- which bacterial taxa are most strongly associated with high SSB intake.

2. Research materials and methods

2.1. Procedure.

We searched in PubMed, Embase, MEDLINE ultimate and Scopus databases from their inception to February 24th, 2026. The search key phrases were Sugar-Sweetened Beverages (SSB) and Gut Microbiota.

2.2. Inclusion And Exclusion Criteria.

Studies were included if they met following criteria:

1. The study population involved adults over 18 years old;
2. Exposure involved SSB;
3. It contains data about microbiota composition or related metabolites;
4. The study design was an original study as cohort, case-control, or cross-sectional study;
5. It was available in the English language.

Studies were excluded if they met the following criteria:

1. The research consisted of individuals with specific health problem;
2. It was performed on animals;
3. The research involved studies only on Artificially-Sweetened Beverages (ASB);
4. The data extracted did not distinguish SSB as a separate part of the human diet.

2.3.1. Study Selection And Data Extraction.

Three reviewers independently screened the titles and abstracts of identified articles, followed by a full-text assessment of studies considered potentially eligible. Data from the included texts were extracted independently by the other three authors. Any disagreements at any stage of study selection or data extraction were resolved through consultation with a separate reviewer.

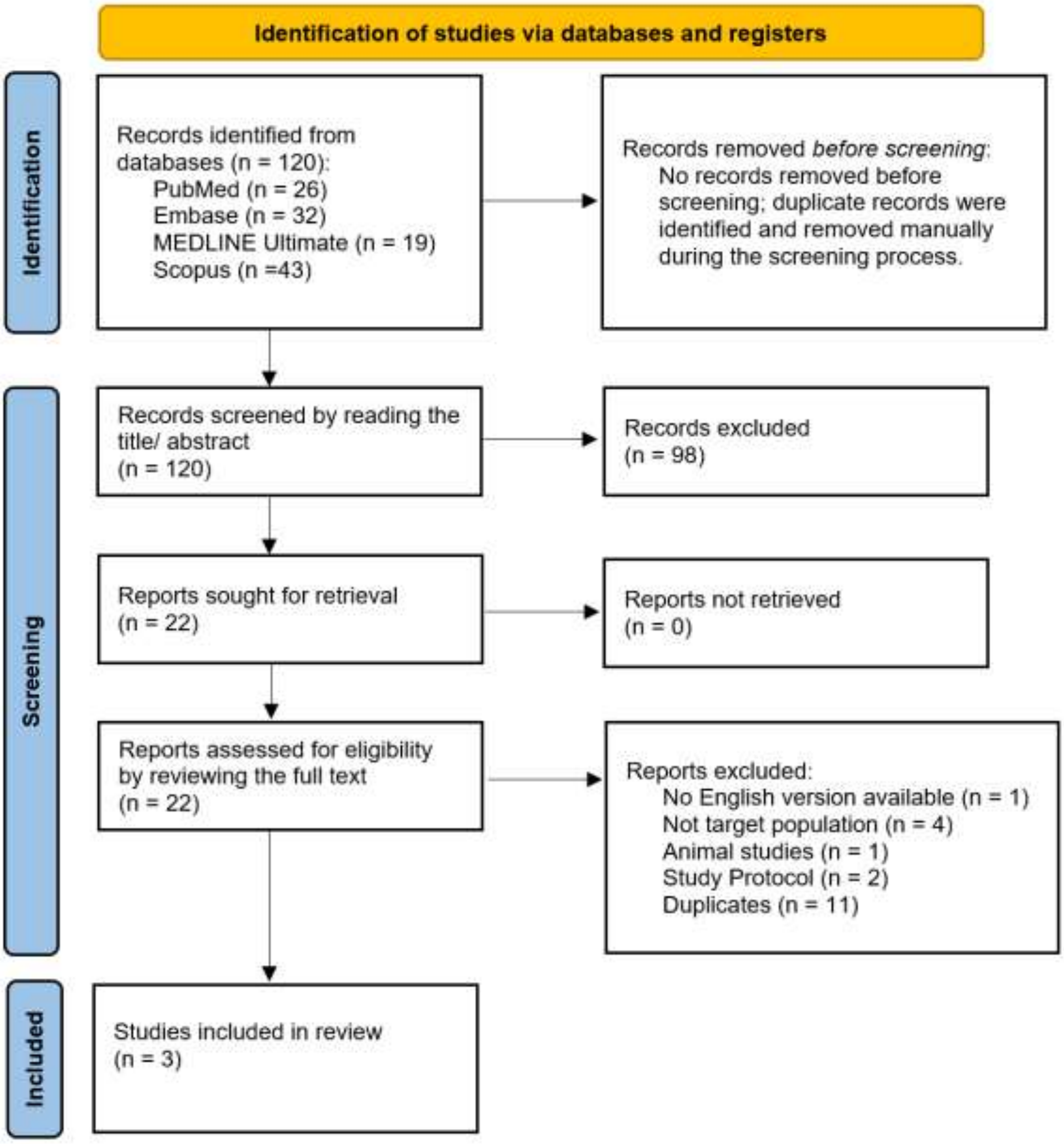

Fig. 1 PRISMA flow diagram of study selection

3.1. Search Results.

The search equaled 26 records in PubMed, 32 records in Embase, and 19 records in MEDLINE Ultimate. After applying predefined exclusion criteria and removing duplicate records, three articles remained eligible for further analysis and were included in the systematic review.

3.2. Quality Assessment.

The methodological quality of the included studies was independently evaluated by two reviewers using the Newcastle-Ottawa Scale (NOS). Any disagreements between the reviewers were resolved through discussion with a third investigator. The NOS enclose three domains: selection, comparability, and exposure. The cohort study was evaluated using the standard pertinent NOS cohort version (Table 1), while cross-sectional studies were estimated using an adapted cross-sectional NOS (Table 2).

3.3. Quality Assessment Results.

The quality of the works showed that they were of high quality. The cohort study was awarded 9 out of 9 stars (Table 1), indicating high methodological quality. One of the cross-sectional studies received 7 out of 8 stars therefore was also classified as high quality (Table 2). The second cross-sectional study achieved 6 out of 8 stars (Table 2), corresponding to moderate methodological quality.

Table 1 NOS: Cohort version

Study	Selection				Comparability	Outcome			Sum
	Representativeness of the exposed cohort	Selection of the non-exposed cohort	Ascertainment of exposure	Demonstration that outcome was not present at start	Control for confounders	Assessment of outcome	Follow-up long enough	Adequacy of follow-up	
Yanbo Zhang, 2025	*	*	*	*	**	*	*	*	9/9

Table 2 NOS: Cross-Sectional Studies

Study	Selection					Outcome			Sum
	Representativeness of the sample	Sample size justification	Non-respondents	Ascertainment of exposure	Comparability of subjects	Assessment of outcome	Statistical test	Control for confounders	
Stina Ramne, 2020	*	*	0	*	**	*	*	*	7/8
Tao Yan, 2022	0	*	0	*	*	*	*	*	6/8

3.4. Study Characteristics.

Three studies were included in this systematic review, comprising one cohort study and two cross-sectional studies, with a total of 10 257 participants. The studies were conducted in the USA [1], China [2], and Sweden [3]. Sample sizes ranged from 86 to 2,970 participants, and the age of participants was above 18 years old.

SSB intake was assessed using either 24-hour dietary recalls (Zhang et al., 2025), food frequency questionnaires (Yan et al., 2022), or web-based 4-day food records combined with short FFQs (Ramne et al., 2020). Gut microbiota composition and related metabolites were measured using shotgun metagenomic sequencing, 16S rRNA sequencing, or untargeted LC-MS metabolomics.

The studies varied in methodological approach, sample size, and assessment methods, reflecting some heterogeneity, however given the limited number of studies available in this area, three were included in this review.

Table 3 Characteristics of Included Studies

Author, year	Country	Study Design	Sample Size SSB intake	Age Mean or Range	SSB Assessment	Gut Microbiota Identification Method
Yanbo Zhang, 2025	USA	Cohort	n^A = 6115 n^B = 2970	n^A: 48,3 ± 13,2 n^B: 51,0 ± 11,0	Two 24-hour dietary recalls via NDSR ^{C} v2011	Shotgun sequencing; serum metabolites
Tao Yan, 2022	China	Cross-Sectional	n = 86	male: 23 ± 4 female: 22 ± 3	FFQ ^{D} adapted from China Kadoorie Biobank	Untargeted LC-MS metabolomics to analyze plasma samples
Stina Ramne, 2020	Sweden	Cross-Sectional	n = 1086	18 - 70 years old	Web-based 4 day food records and short FFQ ^{D}	16S rRNA sequencing

^{A} subset included participants with both dietary data and metabolite data at baseline; ^{B} subset included participants with both dietary data and gut microbiota data; ^{C} NDSR Nutrition Data System for Research ; ^{D} FFQ food frequency questionnaire

5. Results In Microbiota Composition And Related Metabolites.

5.1. Yanbo Zhang et al. (2025).

The study reported that higher SSB intake was associated with changes in nine gut bacterial species, without significant associations with alpha- or beta-diversity. Most SSB related bacteria were linked to fructose and glucose obtained from SSB, whereas no bacteria were associated with sugars from non-SSB sources. Concordance between bacteria related to total sugar intake and those specific to sugars acquired from SSB was low.

The identified taxa belonged primarily to the phyla Proteobacteria and Firmicutes. Within the phylum Proteobacteria, Dakarella massiliensis was inversely associated with SSB intake.

Among phylum Firmicutes, Clostridium bolteae was positively associated with SSB intake. Anaerostipes caccae was also positively associated and correlated with circulating metabolites; however, this association was less consistent and did not exhibit a significant dose response trend across increasing SSB intake groups. Several short-chain fatty acid (SCFA) producing bacteria, including Clostridium sp. KNHs214, Clostridium sp. M62/1, Ruminococcus callidus, Bacteroides pectinophilus, and Lachnospiraceae bacterium TF01-11 were inversely associated with SSB intake. Notably, Eubacterium eligens, another SCFA producing species, was inversely associated with SSB consumption and showed inverse correlations with 2-hour blood glucose, fasting insulin, insulin resistance (HOMA-IR), beta-cell function (HOMA-B), and triglyceride levels. However, this association appeared to be partly influenced by broader dietary patterns, overall diet quality, and fruit intake.

The nine SSB associated bacteria were correlated with glycerophospholipids as well as aromatic (AAA) and branched-chain amino acid (BCAA) metabolites. Overall, 173 serum metabolites were associated with the gut microbiota score (GMS) derived from these taxa, of which 56 were also significantly related to SSB intake and implicated in diabetes risk. These associations remained significant after excluding participants with major chronic diseases, were independent of BMI and overall diet quality, and were confirmed in validation analyses using 100 repeated random sample splits. Furthermore, SSB intake and the GMS were positively associated with glycerophospholipids (including seven individual metabolites), BCAA derivatives (four metabolites), and 19 additional metabolites, whereas inverse associations were observed for phenylsulfates and AAA derivatives.

5.2. Tao Yan et al. (2022).

In a study conducted in China among young adults, the analysis focused solely on blood metabolites influenced by gut microbiota, without examining the specific bacterial species that might have contributed to these changes. Plasma samples were analyzed using untargeted LC-MS metabolomics, identifying 3,084 metabolite features, of which 143 were classified as gut microbiota host cometabolites, based on literature and validated assays. Seventy-nine were independently associated with both SSB intake and metabolic health outcomes.

Different SSB categories demonstrated distinct metabolite association patterns. Carbonated beverages and fruit juice were positively associated with branched-chain amino (BCAA) acids (leucine and isoleucine), glutamic acid, phenylglycine, tyrosine, aconitic acid, and methylmalonic acid. These beverages were additionally linked to higher visceral adiposity index (VAI), total cholesterol (TC), and LDL cholesterol. Energy drinks and coffee were positively associated with tryptophan and its microbial-derived metabolites, including indole, indole-3-lactic acid, indole acrylic acid, and ketobutyric acid, while showing inverse associations with nor-deoxycholic acid. Notably, inverse associations with adiposity measures were observed for coffee intake but not for energy drinks. Bubble tea consumption was positively associated with several bile acids (including lithocholic acid, chenodeoxycholic acid, and glycocholic acid), triglycerides, LDL cholesterol, hydrocinnamic acid, pipecolic acid, and docosapentaenoic acid.

When considering overall SSB intake, significant associations were observed across multiple biochemical classes, including carboxylic acids (e.g., glutamine, leucine, phenylglycine), fatty acyls (e.g., linolenic acid, 2-hydroxycaproic acid, myristic acid), organooxygen compounds (e.g., ribose, ribonic acid, N-acetyl-D-glucosamine), and benzene derivatives (e.g., hydroxyphenylpyruvic acid, vanillic acid, phenylacetic acid). Pathway enrichment analysis identified BCAA catabolism and aminoacyl-tRNA biosynthesis as significantly overrepresented after correction for multiple testing, with additional nominal enrichment in phenylalanine, tyrosine, tryptophan, arginine, and coenzyme A biosynthesis pathways.

5.3. Stina Ramne et al. (2020).

In the Malmö cohort, high SSB consumption was predominantly reported by men and was associated with higher total energy intake and a greater percentage of energy derived from carbohydrates, alongside lower fat, protein, and fiber intake. No significant association with BMI was observed. In contrast, high ASB consumption was more common among women and was associated with higher BMI and lower fiber intake, but not with total energy or macronutrient distribution. Lower educational attainment was associated with high SSB intake but not with ASB intake.

Regarding gut microbiota composition, high SSB consumption was significantly positively associated with the Firmicutes: Bacteroidetes ratio. Added sugar intake was positively associated with the genus Streptococcus and inversely associated with Oxalobacter, Paraprevotella, Lachnobacterium, Odoribacter, and Succiniclasticum. After further adjustment for fiber intake and BMI, only the inverse association with Lachnobacterium remained significant following FDR correction.

SSB intake was positively associated with Dialister, Lactobacillus, [Eubacterium], Anaerotruncus, and an unclassified genus within the Peptostreptococcaceae family, while inverse associations were observed for Lachnobacterium and Roseburia. After multivariable adjustment, Lachnobacterium, Dialister, and Lactobacillus remained nominally associated, although only Lachnobacterium remained significant after correction for multiple testing.

In contrast, ASB intake was positively associated with Prevotella, Sutterella, [Eubacterium], and an unclassified genus within the RF16 family, and inversely associated with Lachnospira and two unclassified genera within the Christensenellaceae family and SHA98. After full adjustment, several associations remained nominally significant; however, none persisted after correction for multiple comparisons.

6. Discussion.

This systematic review synthesized evidence from three observational studies examining the associations between Sugar-Sweetened Beverage (SSB) consumption, gut microbiota composition, and related metabolites in adults. At the time of initiating this review, the available evidence on this topic was limited, moreover some of the identified studies were conducted in animal models. Across the three included studies, higher SSB intake was consistently associated with variations in specific gut bacterial species as well as changes in metabolite profiles. In particular, short-chain fatty acid (SCFA) producing bacteria were generally inversely associated with SSB consumption. A reduced abundance of SCFA-producing bacteria may impair intestinal barrier function, energy homeostasis, and immune responses, which is consistent with the observed alterations in metabolites associated with metabolic risk [17].

Metabolomic analyses identified consistent involvement of pathways related to branched-chain amino (BCAA) acid metabolism, glycerophospholipids, and aminoacyl-tRNA biosynthesis. Although associations vary depending on SSB subtype, analytical methods, population characteristics, the data implies that habitual SSB consumption may influence both gut microbial composition and circulating metabolites relevant to metabolic health, sequentially affecting health.

Across diverse populations, habitual SSB intake was linked to alterations in specific bacterial taxa. Some studies observed shifts in the Firmicutes: Bacteroidetes ratio, along with changes in circulating metabolite profiles, particularly involving BCAA, aromatic amino acids (AAA), and glycerophospholipids. These findings suggest that SSB consumption may contribute to metabolic dysregulation through microbiota mediated pathways. Several mechanisms may explain these associations. Inverse relationships were observed between SSB intake and SCFA producing bacteria, including Eubacterium eligens, Ruminococcus callidus, and Clostridium species such as KNHs214 and M62/1. This suggests that higher sugar intake may reduce the abundance of microbes involved in SCFA production, which may consequently impair gut barrier function, energy regulation, and anti-inflammatory processes. The observed metabolite patterns, including enrichment in BCAA catabolism and aminoacyl-tRNA biosynthesis pathways, further support a microbiota-mediated influence on amino acid metabolism. Disturbances in these pathways have previously been associated with insulin resistance, obesity, and an increased risk of type 2 diabetes.

Specific beverage types, such as bubble tea and carbonated drinks, demonstrated distinct metabolite signatures, highlighting heterogeneity in the interactions between different SSB and the gut microbiome. Moreover, the consumption of seemingly similar beverages may influence metabolite profiles differently. For example, beneficial associations with body fat control were observed for coffee intake but not for energy drink consumption. This could suggest interactions between specific beverage ingredients and the gut microbiome, although further research is needed to clarify these mechanisms.

The findings from Zhang et al. (2025) align with those reported by Yan et al. (2022), suggesting that SSB intake influences metabolites related to gut microbiota activity. After excluding individuals with major chronic diseases, these associations remained significant and were not fully explained by overall diet quality. Moreover, the results from Zhang et al. (2025) correspond partly with findings from Ramne et al. (2020). The Malmö cohort study identified a negative association between Lachnobacterium and SSB consumption, which was also observed in the U.S. population. Additionally, a shift toward a higher Firmicutes: Bacteroidetes ratio was reported. Together, these studies indicate both shared and population specific microbiota responses to SSB consumption. Some of these associations may be influenced by dietary patterns, genetic background, and lifestyle factors, although certain microbial changes appear to be specifically linked to SSB intake.

Higher SSB intake was associated with reduced abundance of several SCFA producing bacteria and shifts in the Firmicutes: Bacteroidetes ratio. It was also inversely associated with Dakarella massiliensis from the phylum Proteobacteria. Within the phylum Firmicutes, inverse associations were observed for species including Bacteroides pectinophilus, Clostridium sp. KNHs214, Clostridium sp. M62/1, Eubacterium eligens, Lachnospiraceae bacterium TF01-11, and Ruminococcus callidus, whereas positive associations were reported for Clostridium bolteae and Anaerostipes caccae. These microbial alterations were linked to changes in metabolite profiles, including triglycerides, LDL-cholesterol, several bile acids, and BCAA and AAA. This suggests that SSB consumption may influence metabolic pathways related to obesity, cardiometabolic traits, and bile acid metabolism involved in lipid regulation.

The findings could support the hypothesis that reducing SSB intake may positively influence gut microbial composition and metabolite profiles, potentially lowering obesity and cardiometabolic risk. Future research should include longitudinal and intervention studies with standardized dietary and microbiome assessments to clarify relationships and identify mechanistic pathways. Additionally, studies exploring individual SSB types, interactions with overall diet quality, and population specific responses will be essential to translate these findings into evidence based dietary recommendations.

7. Limitations.

Several limitations should be acknowledged when interpreting the findings of this systematic review. First, all included studies were observational, which prevented casual inference. This limits control over other dietary and lifestyle factors beyond SSB intake that may significantly influence the observed associations. Second, the differences in research methodology, microbial profiling approaches and in selected articles introduce variability and restrict direct comparability of results. In particular, Yan et al., 2022 focused only on metabolites without profiling gut bacterial species, which prevents direct linkage between microbial composition and metabolite changes compared with other studies. Third, heterogeneity across studies in terms of population characteristics and geographic regions may partially explain differences in microbiota composition and metabolite responses. Fourth, SSB intake was self-reported, which may be subject to recall bias, under- or overestimation, and overall measurement error. Despite these limitations, this review provides a coherent overview of the potential microbiota mediated effects of SSB consumption on metabolic health.

8. Conclusions.

This systematic review indicates that Sugar-Sweetened Beverage (SSB) consumption is associated with variations of gut microbiota composition and related metabolite profiles in adults. Several studies reported links between higher SSB intake and changes in specific bacterial taxa as well as metabolites related to microbiome involved in amino acid, lipid, and bile acid metabolism. These findings suggest that SSB consumption may influence metabolic health through microbiota related pathways. Evidence also indicates that gut microbiota responses may depend not only on the total amount of sugar consumed but also on its dietary source and nutritional context. Although these associations highlight a potential role of SSB intake in shaping gut microbial and metabolic profiles, most available evidence is observational.

Therefore, further longitudinal and interventional studies are needed to clarify the causal relationships and underlying mechanisms.

9. Disclosure

9.1. Supplementary Materials.

No supplementary materials are available.

9.2. Author Contributions.

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All authors have read and agreed to the published version of the manuscript.

9.3. Funding.

This research received no external funding.

9.4. Institutional Review Board Statement.

Not applicable.

9.5. Informed Consent Statement.

Not applicable.

9.6. Data Availability Statement.

The study did not report any data.

9.7. Conflicts of Interest.

The author declares no conflict of interest.

During the preparation of this work, the authors used ChatGPT for the purpose of language editing to improve clarity and readability. After using this tool, the authors reviewed and edited the content as needed and take full responsibility for the substantive content of the publication.

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