

SYSTEMATIC REVIEW

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Effects of dietary interventions on gut microbiota and related cardiometabolic changes in pediatric obesity: a systematic review and meta-analysis

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BACKGROUND: Gut microbiota imbalances may contribute to obesity, yet whether dietary interventions can modulate the microbiota and improve metabolic health in pediatrics has not been thoroughly reviewed. This systematic review and meta-analysis explores the impact of dietary interventions on the gut microbiota of children and adolescents with overweight or obesity, and its association with cardiometabolic improvements.

METHODS: A systematic search of clinical trials in Pubmed, Cochrane and EMBASE was conducted following PRISMA guidelines (PROSPERO n°CRD42024505494). Risk of bias was assessed with RoB2 and ROBINS, for randomized and non-randomized intervention studies.

RESULTS: Overall, 60 articles were assessed for full-text eligibility, 8 were included, and 4 provided alpha-diversity data for meta-analysis. A total of 200 participants were included (6–16 years). Six studies implemented calorie-restricted diets, one a low free-sugar diet, and one CHLD-1 diet. The meta-analysis revealed a significant increase in Chao1 (48.76 [95%CI 1.81; 95.70]; $I^2 = 86.8\%$, $p < 0.001$) following a balanced calorie-restricted dietary intervention. Although there was heterogeneity in taxa-level changes, several butyrate-producing genera (*Clostridium* XVIa, *Coprococcus*, *Roseburia*, *Faecalibacterium*, *Blautia*, *Butyricimonas*) increased following dietary intervention.

CONCLUSIONS: Balanced dietary interventions with calorie-restriction adequate for pediatric age could increase gut microbiota richness and butyrate-producing bacteria abundance. Future trials should clarify diet-driven gut microbiota changes in childhood obesity and related metabolic changes.

Pediatric Research; <https://doi.org/10.1038/s41390-026-05312-w>

IMPACT:

- Balanced calorie restriction diet may increase gut microbiota richness in childhood obesity
- Butyrate-producer expansion needs long-term dietary intervention
- Gaps in linking microbiota-metabolism interplay in pediatric obesity

INTRODUCTION

The prevalence of obesity and overweight in the pediatric population has increased dramatically in recent decades.¹ By 2025, 30% of children aged 5–19 years are expected to suffer from obesity.² The persistence of obesity from pediatric age to adulthood is of great concern, moreover, children with obesity are at increased risk of complications, including metabolic and cardiovascular diseases (CVD).³

Lifestyle factors such as diet and physical activity have been closely related to overweight and obesity and the development of its associated comorbidities. However, biological, behavioral and environmental factors also play an important role.⁴ One such

influential factor could be the gut microbiota, which is in turn associated with diet, physical activity and environmental factors.⁵

Gut microbiota is considered a central metabolic hub that promotes physiological homeostasis, metabolic and immune functions through a close symbiotic relationship with the host.⁶ Over the last few decades, investigations have been conducted to assess the interplay between diet, obesity and altered gut microbiota.^{7,8} Gut microbiota, acting as a bioreactor in the human body, can influence metabolic health by releasing several metabolites among which Short Chain Fatty Acids (SCFAs), including acetate, propionate, and butyrate, are the most representative.⁹ Several studies have investigated whether gut

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Received: 14 January 2026 Revised: 26 May 2026 Accepted: 20 June 2026

Published online: 08 September 2026

Table 1. PICOS inclusion criteria.

Parameter	
Population	Children or adolescents (2–18 years) with overweight or obesity, with or without cardiometabolic alterations or metabolic dysfunction-associated steatotic liver disease (MASLD) [previously known as NAFLD]
Intervention	Any dietary/nutritional intervention (promotion specific dietary patterns, caloric-restriction diet, tailored dietary recommendations or the intake of a specific food group in the diet)
Control	Usual care, no dietary intervention, or only advice to follow the habitual diet (both between and within group differences)
Outcomes	Modification of gut microbiota and the observed related-health effect. a. Diversity indexes (alpha and beta) b. Firmicutes/Bacteroidetes ratio c. Changes in taxa levels (phylum, class, order, family, genus and species) d. Association between observed gut microbiota changes and cardiometabolic health changes
Study design	Clinical trials with a randomized (RCT) or quasi-randomized design or single-arm intervention studies.

microbiota and SCFAs, could affect host energy homeostasis, adiposity, feeding behavior and satiety through different mechanisms.¹⁰ Most studies have been carried out in adults, but there is also emerging scientific evidence showing the difference in gut microbiota composition between healthy children and children with obesity.¹¹

Gut microbiota imbalances, known as dysbiosis,¹² may contribute to the development of obesity and its associated comorbidities.⁹ Dysbiosis in obesity is characterized by a lower microbial diversity, a higher *Firmicutes/Bacteroidetes* (F/B) ratio, and a decrease in specific bacteria such as *Akkermansia muciniphila* in both adults and children.^{13–15}

Research, mainly in adults, has shown that changes in dietary patterns could have an impact on the gut microbiota composition, contributing to the alleviation of metabolic alterations.^{16,17} For instance, the Mediterranean Diet (MD), rich in fiber, vitamins and antioxidants, increases the gut microbiota taxonomic diversity, in particular of beneficial genera such as *Bifidobacterium* or *Roseburia*, which have been associated with a reduction of CVD risk factors.^{17,18} In contrast, a Western dietary pattern, high in saturated fats, salt and sugar, reduces beneficial bacteria such as *Bifidobacterium* and *Lactobacillus*, negatively affecting cardiovascular health.^{19–21}

Haro et al.²² observed that adults with obesity following a low-fat and high-complex carbohydrate diet, presented an increase of SCFA-producer bacterial lineages such as *Faecalibacterium prausnitzii*, a well-known butyrate-producing bacterium with potential benefits on BMI and insulin sensitivity both in adults and children.^{23,24}

A previous systematic review and meta-analysis investigated to what extent dietary interventions targeting gut microbiota can modulate cardiometabolic diseases in adults.²⁵ This work found remarkable associations between diet and changes in gut microbiota, but concluded that the exact interplay between dietary interventions, gut microbiota composition, and their role in cardiometabolic outcomes remained unclear.²⁵

A thorough review of the evidence on diet-driven gut microbiota modulation in children and adolescents with obesity is needed to guide future research on personalized nutrition interventions.

Therefore, this systematic review and meta-analysis aimed to study the impact of dietary interventions on gut microbiota in children and adolescents with overweight or obesity and, to determine if these microbiota changes are directly associated with cardiometabolic health changes.

METHODS

Registration and protocol

The protocol for this systematic review was registered in PROSPERO (CRD42024505494) and was conducted in accordance with the guidelines of the Preferred Reporting Items for

Systematic Reviews and Meta-Analysis (PRISMA; see Supplementary Table S1.²⁶

Research question

What is the effect of dietary interventions on gut microbiota diversity and composition in children and adolescents with overweight or obesity, and how are these changes associated with cardiometabolic health changes?

Eligibility criteria

Studies were selected according to the PICOS criteria (based on the acronym Patients/ Population, Intervention, Comparison, Outcomes, Study design) and are described in Table 1. Briefly, only pediatric age groups aged 2–18 years with a diagnosis of overweight or obesity, with or without metabolic alterations or metabolic dysfunction-associated steatotic liver disease (MASLD) [previously known as NAFLD, non-alcoholic fatty liver disease] were included. Studies carried out in cohorts of healthy children or adolescents, children or adolescents with gastrointestinal disease or related symptoms and neurodevelopmental disorders were excluded from the present review. Interventions could include any dietary or nutritional intervention, such as promotion of specific dietary patterns, caloric-restriction diet, tailored dietary recommendations, or the intake of a specific food group in the participants' diet. On the contrary, interventions with supplements, including biotics (such as prebiotics, probiotics, postbiotics, symbiotics) as well as vitamins or minerals taken in the form of supplements (tablets, powders, softgels, liquids...) and not provided in a food matrix were excluded.

We included clinical trials with a randomized or quasi-randomized design or single-arm intervention studies.

The comparator was identified according to the type of study. For controlled trials assessing “between group differences”, the control was defined as usual care, no dietary intervention, or only advice to follow habitual diet. In the case of single-arm intervention studies, the reference for comparison were the subjects themselves before the intervention (baseline) or after a wash-out period with their habitual diet.

Studies had to report at least one of the following outcomes to be included: (a) diversity indexes, namely alpha-diversity (e.g., Shannon index, Chao1 index, Simpson index, ACE, Fisher) or β -diversity (e.g., Bray-Curtis and UniFrac distances), (b) changes in F/B ratio, (c) changes in relative abundance of lineages at various phylogenetic resolutions (i.e., phylum, class and order, family, genus and species), (d) association between observed gut microbiota changes and cardio-metabolic health.

Only records published in English were considered eligible.

Literature search

The literature search was performed on MEDLINE [accessed via PubMed], EMBASE and the Cochrane Central Register of Controlled Trials (CENTRAL), with no date restriction up until 1st

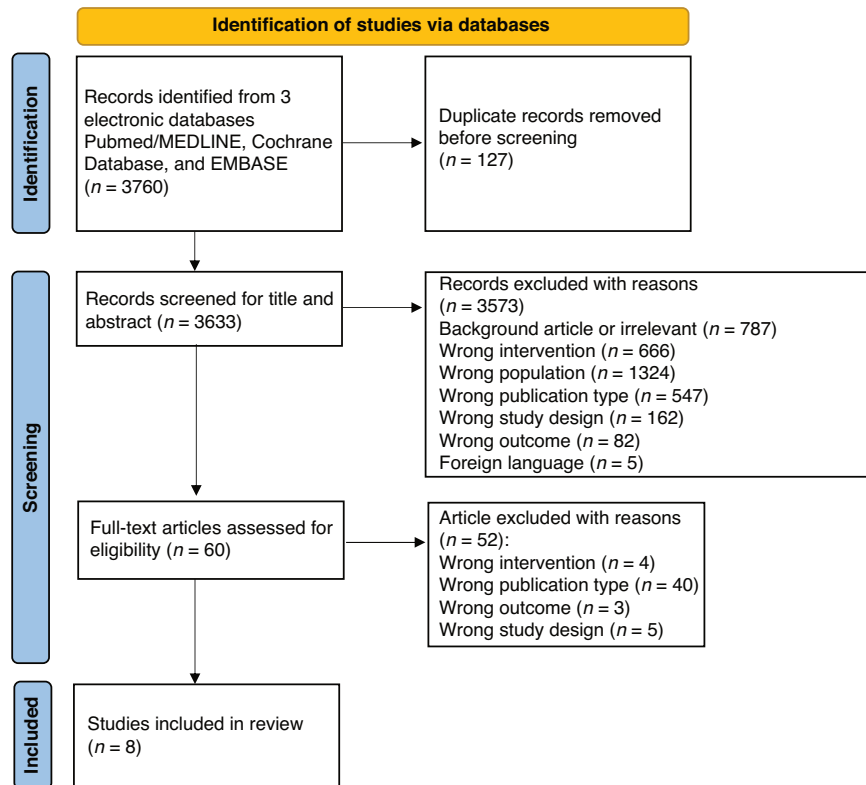


Fig. 1 Flow diagram of study selection.

September 2025. The complete search strategy terms are listed in Supplementary Table S2.

Study selection

Search results were merged into the web-based reference management software and de-duplicated before screening with the use of Rayyan software.²⁷

The remaining papers were examined independently by two pairs of authors in a double-blinded fashion. After removal of duplicate records, all articles were screened for title and abstract and excluded with reasons (background articles or irrelevant, wrong intervention, wrong population). Afterwards, full text selection was performed, and disagreement was resolved consensually in a group meeting. Reason for exclusion included wrong intervention, wrong publication type and wrong outcome. Exclusion reasons were recorded and are listed in Fig. 1.

Data extraction

Data extraction was performed in parallel by two independent authors in a double-blinded fashion. Disagreements were resolved by consensus-based discussion. Selected articles were fully analyzed to extract the following information in a data collection spreadsheet: author name, year, type of study (RCT, intervention trial), population, sample size, nutritional intervention, duration of intervention, intervention in control group (if any), Alpha-diversity Indexes, Beta-diversity, F/B ratio, phylum changes, class changes, order changes, family changes, genus changes, species changes, methods of gut microbiota evaluation, anthropometry, hematological parameters, MASLD/other metabolic, nutritional impacts and confounders.

Risk of bias assessment

Each selected article was assessed by one of the authors and then discussed in a meeting with all the authors involved in the quality assessment revision.

To assess the methodological validity of included articles, we used RoB2 for RCTs,²⁸ and ROBINS to examine intervention studies.²⁹ The following domains were assessed for RoB2: Randomization process, deviation from intended interventions, missing outcome data, measurement of the outcome, selection of the reported result and overall. The domains evaluated according to ROBINS, were biases: due to confounding, in selection of participants, in classification of interventions, due to deviations from intended interventions, due to missing data, in measurement of outcomes, in selection of the reported results and overall. For both RoB2 and ROBINS all the domains were classified in low, moderate or high risk of bias. The synthesis of the risk-of-bias assessment for each study was conducted by applying the Risk-of-bias VISualization (ROBVIS) tool.³⁰

Data synthesis

Considering the heterogeneity among dietary interventions and the complexity to assess the effect on gut microbiota diversity and composition after the intervention, the results obtained after data extraction were divided into four main sections for data synthesis:

- Gut microbiota diversity (alpha- and beta-diversity as main outcomes)
- F/B ratio
- Taxa level modifications
- Changes in health outcomes
- Associations between changes in gut microbiota and changes in health outcomes

Studies that allowed a quantitative analysis of the effects of the interventions were included in a meta-analysis as per PROSPERO protocol.

Non-published data were retrieved by contacting corresponding authors. Detailed descriptions of exclusion from meta-analysis are presented in Supplementary Table S3.

Table 2. Extraction table of the included articles (for more information see Supplementary Table 3).

Author, year	Country	Sample	Age (years)	Duration	Study design	Intervention	Population	Control	Microbiota analysis technique	Alpha-diversity assessment	F/B ratio	Taxa level assessed	Main correlation between changes in gut microbiota and changes in health outcomes
Huang et al. ³² 2020	China	n = 24	9–16	6 weeks	NRI	Hypocaloric dietary plan + a specific exercise program	Obesity	Baseline VS final	16S rRNA	Observed species, Chao, Ace, Shannon, Simpson	✓	Phylum, class, order, family, genus	Positive correlation between: - Glucose and <i>Eubacterium ruminantium</i> , <i>Paraprevotella</i> , - Triglycerides and Family XIII UCG-001 - LDL-C and Family XIII UCG-001, <i>Odoribacter</i> Negative correlation between: - Glucose and <i>Eubacterium ventriosum</i>
Ruiz et al. ³³ 2017	Spain	n = 13	13–16	1 year	NRI	Hypocaloric dietary plan + educational assessment on physical activity	Obesity	Baseline VS final	16S rRNA	Fisher, Chao, Shannon, evenness	✓	Phylum, family, genus	×
Cohen et al. ³⁴ 2023	USA	n = 40	11–16	8 weeks	RCT	Free sugar intake <3% of TEI + participant's usual physical activity	Overweight, obesity, NAFLD	Control: usual diet	16S rRNA, HILIC-MS	Shannon, Simpson, evenness	×	Phylum, class, order, family, genus, species	×
Morán-Ramos et al. ³⁵ 2022	Mexico	n = 6	11–14	6 weeks	NRI	Hypocaloric dietary plan + a specific exercise program	Obesity	Baseline VS final	16S rRNA	Chao, Shannon	×	Phylum, family, genus	Negative correlation between waist circumference and <i>Odoribacter</i> .
Santacruz et al. ³⁶ 2009	Spain	n = 36	13–15	10 weeks	NRI	Hypocaloric dietary plan + a specific exercise program	Obesity	Baseline VS final	16S rRNA-gene-targeted group specific primers	×	×	Genus, species	Positive correlation between weight and <i>Bifidobacterium/</i> <i>Clostridium</i> <i>coccoides</i> ratio, <i>Bifidobacterium/</i> <i>B.fragilis</i> ratio, <i>E.coli</i> . Negative correlation between: - Weight and <i>Lactobacillus</i> , <i>B. fragilis</i> group, <i>C.coccoides</i> ; - BMIz and <i>Lactobacillus</i> , <i>B. fragilis</i> group.

Table 2. continued

Author, year	Country	Sample	Age (years)	Duration	Study design	Intervention	Population	Control	Microbiota analysis technique	Alpha-diversity assessment	F/B ratio	Taxa level assessed	Main correlation between changes in gut microbiota and changes in health outcomes
Zhou et al. ³⁷ 2024	China	n = 30	6–12	12 weeks	NRI	Hypocaloric dietary plan	Obesity	Baseline VS final	16S rRNA, GC-MS for fecal SCFA quantification	Chao, Ace (no data available)	×	Phylum, Genus, SCFA	×
Aqeel et al. ³⁸ 2024	USA	n = 33	6–11	4 weeks	RCT	CHILD-1 diet (evidence-based adaptation of the DASH diet)	Obesity	Control: usual diet	16S rRNA	Chao, Shannon, Simpson	×	Genus, Species	×
Peng et al. ³⁹ 2024	China	n = 86	<15	6 weeks	NRI	Hypocaloric dietary plan + a specific exercise program	Obesity	Baseline VS final	16S rRNA	Observed species, Chao, Shannon, Simpson, Faith's Phylogenetic Diversity	×	Family, Genus, Species	×

GC-MS gas chromatography–mass spectrometry, NRI non-randomized intervention trial, RCT randomized controlled trials.

Statistical analysis

A meta-analysis was conducted to compare the means of two groups using the “metafor” package in RStudio (version 4.5.0).³¹ The mean difference (MD) model was used to synthesize the results of the studies included. The studies compared pre-intervention data with post-intervention data. The heterogeneity of the results was evaluated by I^2 . The results of the meta-analysis were presented using forest plots to visualize the point estimates and confidence intervals of each study, as well as the combined overall estimate.

RESULTS

The flowchart of the literature search and exclusion process is depicted in Fig. 1. Three electronic databases were used to identify records, resulting in a total of 3760 findings. After removing duplicate records, 3633 articles underwent screening based on title and abstract. Subsequently, irrelevant articles ($n = 3573$) were discarded based on different reasons. Following this, the remaining 60 articles underwent full-text eligibility assessment. Fifty-two articles were then excluded for the following reasons: wrong intervention (4), wrong publication type (40), wrong outcome ($n = 3$) and wrong study design ($n = 5$). Consequently, only 8 studies were deemed suitable for inclusion in the review.

Study characteristics

This systematic review included eight studies.^{32–39} Two of them were randomized controlled trials (RCT) of participants diagnosed with obesity, or obesity with MASLD.^{34,38} The remaining six studies were non-randomized clinical trials focusing on simple pediatric obesity.^{32,33,35–37,39} Key characteristics of the included studies are summarized in Table 2, and detailed information is reported in Supplementary Table S4. The publication dates ranged from 2009 to 2024. A total of 200 participants were analyzed, aged between 6 and 16 years. Criteria for categorizing obesity in participants varied across studies. Three applied Chinese BMI national reference growth charts with a cut-off point of 95% to diagnose obesity.^{32,37,39} Another study defined obesity status as BMI z-score >1.64 or body fat percentage $>32\%$.³⁵ Additionally, in two studies childhood overweight and obesity were defined as BMI >95 th percentile for age and sex or according to the International Obesity Task Force cutoffs for BMI.^{33,36} One of them did not report the references used to classify the children in overweight or obesity.³⁴ NAFLD diagnosis criteria included liver biopsy or hepatic fat $>10\%$ based on magnetic resonance imaging-proton density fat fraction (MRI-PDFF), along with ALT >45 U/L.³⁴

Among the included studies, the majority (6/8) implemented a calorie-restricting dietary plan^{32,33,35–37,39}; one provided to participants a low free-sugar version of their habitual diet,³⁴ another prescribed CHILD-1 diet (an evidence-based adaptation of the DASH diet) without calorie-restriction.³⁸ All intervention programs had short-term follow up (4–12 weeks),^{32,34–39} apart from one study with a longer follow up (1 year).³³ In the intervention realized by Huang et al.⁴⁰ participants received a nutritionally complete diet based on their age, and meeting their basal metabolic rate calculated using the Mifflin equation. In three articles individual dietary plans were composed as follows: 50–60% carbohydrates, 20–25% protein, and 20–30% fat.^{32,37,39} In the study of Ruiz et al.,³³ participants received a nutritional intervention aimed at caloric restriction and lifestyle education (at the end of the study, there was an average reduction of 25% of the total daily dietary intake kcal compared to baseline). In another study participants were provided with a hypocaloric dietary plan consisting of 60% energy from carbohydrates, 20–25% from fats, and 15–20% from proteins.³⁵ A separate study implemented an energy-restricted diet with a reduction ranging

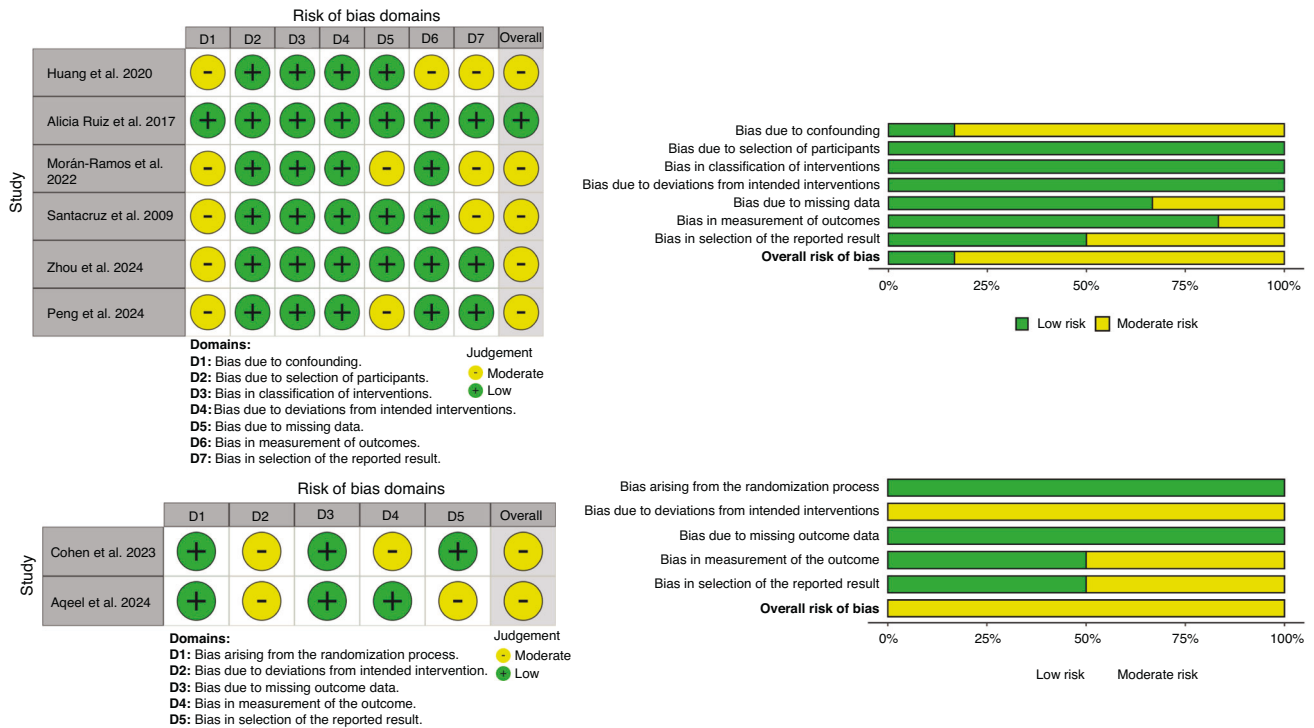


Fig. 2 Risk of bias assessment of randomized controlled trials (RoB2) and non-randomized clinical trials (ROBINS-I/ROBVIS) included in the systematic review. Traffic light (left) and summary plot (right) presenting the risk of bias within the RCT (RoB2, above) and non-randomized clinical trials (ROBVIS, below).

from 10 to 40% of the energy requirements.³⁶ Finally, one study focused on providing participants with a low free-sugar version of their usual diet, with the aim of limiting free-sugar intake to less than 3% of total energy intake.³⁴ Lastly, one study provided CHIL-1 diet, an evidence-based adaptation of DASH diet, with dietary counseling and no calorie restriction.³⁸

The majority of articles (6/8) suggested different approaches to increasing physical activity, including the recommendation to achieve at least 150 min/week of physical activity or to combine endurance with strength training. In four short-term calorie restriction (STCR) studies, children and adolescents were instructed to follow a physical exercise program.^{32,35,36,39} The study with a long-term calorie restriction (LTCR) follow up provided an educational assessment on physical activity,³³ and only in the study of Cohen et al.³⁴ (which followed a low free sugar diet) children were advised not to make major changes in their physical activity routines. Two articles did not report on physical activity intervention.^{37,38}

Microbiota analysis was conducted using the 16S rRNA gene sequencing technique in all studies,^{32–35,37–39} apart from one in which targeted quantitative real-time PCR for specific bacterial genera or species was applied.³⁶ One study performed the analysis of metabolomics in plasma employing HILIC-MS (Hydrophilic Interaction Liquid Chromatography-Mass Spectrometry),³⁴ and one the quantification of fecal SCFA levels by means of gas chromatography-mass spectrometry (GC-MS).³⁷ The overall risk of bias assessment of the articles included is presented in Fig. 2. On average the overall risk of bias was graded as moderate, with only one article graded as low risk of bias.

Meta-analyses: effect of dietary interventions on gut microbiota diversity

We evaluated the gut microbiota diversity based on four main indexes, Shannon, Simpson, ACE and Chao1. Data from one of the articles was excluded because it was a pilot study with a reduced

number of participants, which could introduce bias into the results.³⁵ Three articles reported quantitative information regarding the Shannon index, Simpson and Chao1 index.^{32,33,39} Additional data on the gut microbiota diversity index were requested for one of the studies that had missing data.³⁸

Finally, three meta-analyses were conducted assessing the effect of balanced and calorie-restricted dietary interventions on Chao1, Shannon and Simpson indices, pooling data from four studies that allowed the quantitative analyses effects.^{32,33,38,39} Fig. 3 shows the mean difference (MD) with 95% confidence intervals (CIs) for the different diversity indices. All of the four studies included in the analysis reported an increase in Chao1. Regarding the Shannon index, all studies reported an increase, except Aqeel et al.³⁸ who observed a decrease. Simpson index was reduced in all of the articles except from Peng et al.³⁹

The meta-analysis revealed significant increases in the richness index Chao1 (mean: 48.76 [95%CI 1.81; 95.70]; $I^2 = 86.8\%$, $p < 0.001$) after a balanced calorie-restriction dietary intervention. On the contrary, the Shannon and Simpson index, both, estimators of species richness and evenness, did not show a significant change (mean: 0.11 [95%CI -0.28; 0.50]; $I^2 = 84.6\%$, $p < 0.001$ and mean: -0.00 [95%CI -0.04; 0.04]; $I^2 = 83.2\%$, $p < 0.001$). The articles included in the meta-analysis yielded a heterogeneous risk of bias, from low to moderate risk of bias.

Cohen et al. showed a significant increase in sample richness after a low free-sugar diet ($p = 0.0188$).³⁴ No article reported correlation between changes in alpha-diversity and changes in cardiometabolic outcomes.

Firmicutes/Bacteroidetes Ratio

Two of the five reviewed articles reported information about the F/B ratio.^{32,33} Both of them observed a reduction in the ratio after a balanced diet and calorie-restricted intervention. Specifically, Huang et al.³² reported a significant decrease (mean pre-intervention 1.11 ± 0.205 ; mean post-intervention 0.737 ± 0.09 ;

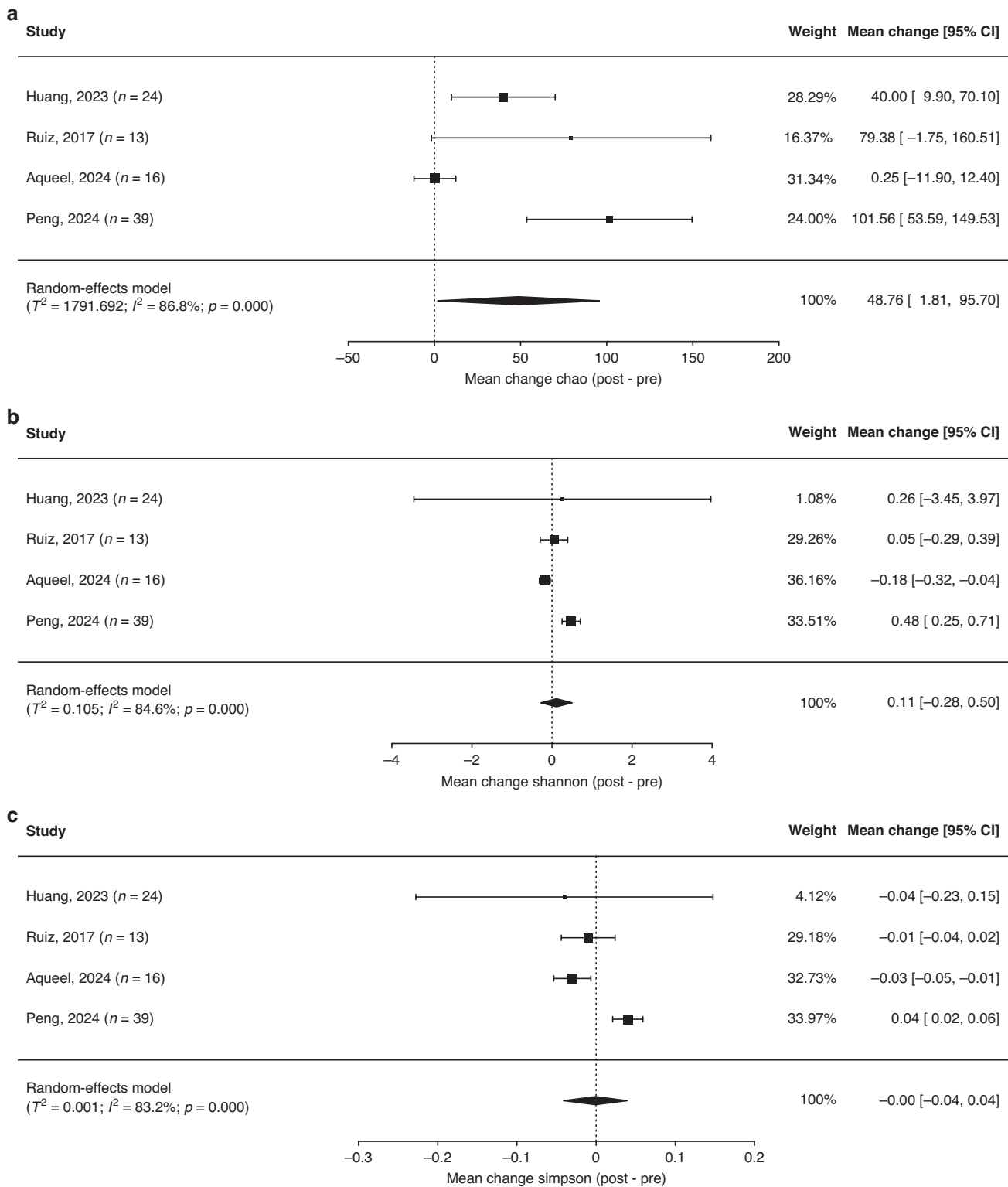


Fig. 3 Effect of dietary interventions on gut microbiota alpha-diversity in children and adolescents with overweight or obesity. **a** Meta-analysis of changes in Chao1 index; **b** Meta-analysis of changes in Shannon index; **c** Meta-analysis of changes in Simpson index. Forest plots show mean differences with 95% confidence intervals comparing post-intervention and pre-intervention values.

$p = 0.011$), while Ruiz et al.³³ also reported a reduction although the difference was not statistically significant ($p = 0.062$). None of the articles reported associations between F/B ratio and the cardiometabolic health outcomes

Taxa level modifications

Changes at taxonomic level of gut microbiota are presented in Supplementary Table S5.

At the phylum level, two articles reported an increase of *Bacteroidetes* (synonym *Bacteroidota* according to Oren A.⁴¹)

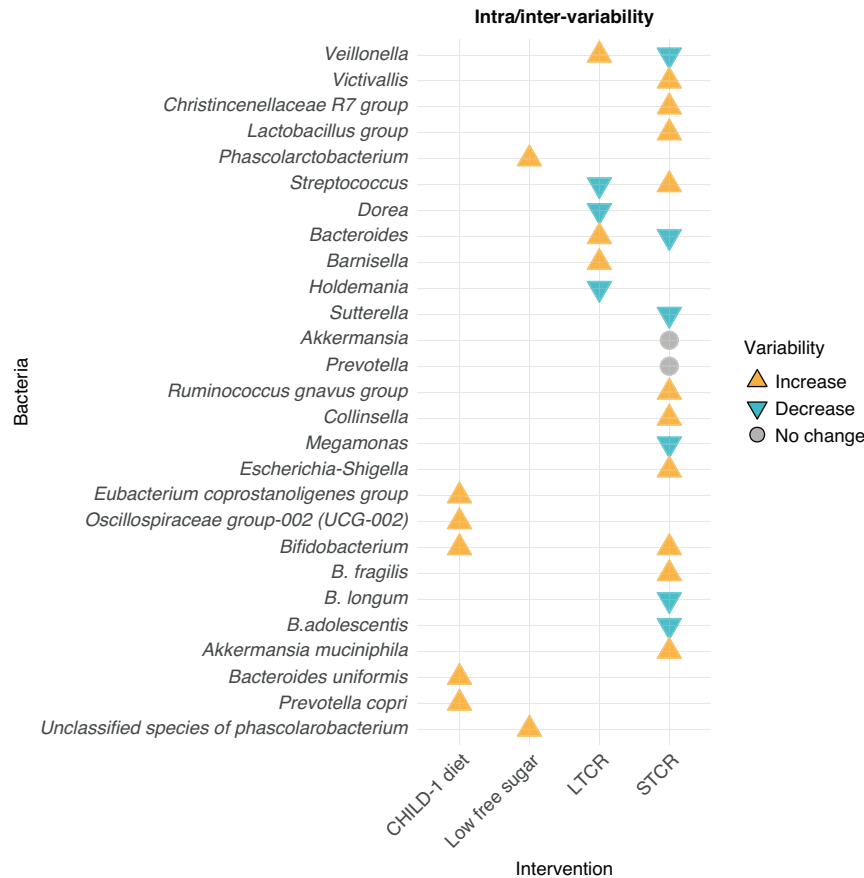


Fig. 4 Inter and intra-study variability in gut microbiota taxa at the genus and species levels following dietary interventions in children and adolescents with obesity. Taxa reported to increase or decrease after dietary interventions are displayed according to intervention type. LTCR, long-term calorie restriction (>12 weeks); STCR, short-term calorie restriction (≤12 weeks).

following both STCR³² and LTCR³³ and an article reported a decrease after a STCR.³⁷ After a STCR, one article showed a reduction of *Firmicutes* (synonym *Bacillota*),³² while another one reported no differences.³⁷ While Ruiz et al.³³ reported a decrease in *Actinobacteria* (syn *Actinomycetota*) and *Proteobacteria* (syn *Pseudomonadota*) following LTCR, Zhou et al.³⁷ reported an increase in *Actinobacteria* and no changes in *Proteobacteria* after a STCR. In contrast no significant differences were observed in *Verrucomicrobia* (syn *Verrucomicrobiota*) after both, LTCR³³ and STCR³⁷ interventions. Only one article showed significant changes at the class and order levels.³² Huang et al.³² reported that, after a STCR combined with exercise, the class *Bacilli* and the order *Lactobacillales* significantly decreased, while the class *Lentisphaera* and order *Victivallales* significantly increased.

Four articles reported family-level changes after dietary interventions.^{32–34,39} STCR combined with exercises resulted in a significant decrease of *Streptococcaceae*, and an increase of *Christensenellaceae* and *Victivallaceae* reported by Huang et al.³² Peng et al.,³⁹ after a STCR reported an increase of *Enterobacteriaceae* and *Rikenellaceae*, and a decrease of *Alcaligenaceae*. LTCR combined with educational assessment significantly reduced *Coriobacteriaceae*, *Costridales incertae sedis XIII*, *Eubacteriaceae*,³³ while *Veillonellaceae* increased significantly after both LTCR³³ and a low free sugar diet intervention ($p = 0.035$) (Supplementary table S5).³⁴

Figure 4 summarizes intra and inter-variability at the genus and species levels according to dietary intervention allocated. There are four genera that overlap in two studies: *Veillonella* ($p = 0.04$) and *Bacteroides* ($p = 0.04$), which increased after a LTCR,³³ and

decreased after a STCR ($p < 0.05$).^{32,37} On the contrary *Streptococcus* decreased ($p = 0.01$) after a LTCR,³³ and increased after a STCR ($p < 0.05$).^{32,37} Lastly, *Bifidobacterium* showed an increase after both STCR ($p < 0.05$),³⁷ and the CHILD-1 diet.³⁸

Focusing on butyrate-producing bacteria (Fig. 5), at the genus level, STCR increased the relative abundance of *Butyricimonas* ($p < 0.05$),³² and *Blautia* ($p < 0.05$).³⁷ Moreover, a LTCR increased *Clostridium* *XVIa* ($p = 0.005$), *Coprococcus* ($p = 0.005$), *Roseburia* ($p = 0.02$), *Faecalibacterium* ($p = 0.01$).³³ One article found an increase of *F. prausnitzii* following the CHILD-1 diet.³⁸

However, there is a reduction on other butyrate-producing bacteria such *Eubacterium* spp. ($p = 0.03$) and *Clostridium* *coccoides* ($p = 0.028$) after a LTCR³³ and a STCR,³⁶ respectively.

Lastly, at species level, the low free-sugar diet resulted in a significant reduction of butyrate-producing *Ruminococcus* *bromii*.³⁴ Lastly, Moran-Ramos et al. reported that the gut microbiota composition remained unchanged after a STCR diet and physical activity recommendations.³⁵

Changes in health outcomes

Regarding the anthropometric parameters, all the included studies reported improvements after the intervention period, except from one implementing dietary quality intervention without calorie-restriction.³⁸ Among the studies that implemented STCR, four of them found a significant reduction in weight and BMI,^{32,36,37,39} one reported a significant reduction in waist circumference,³⁵ and one also showed a reduction in body fat and the waist-to-hip ratio.³² The LTCR follow up study showed a significant reduction on BMI,³³ moreover children who follow a low free sugar diet had



Fig. 5 Inter- an intra-study variability in butyrate-producing bacteria at the genus and species levels according to dietary interventions in children and adolescents with obesity. Taxa reported to increase or decrease after dietary interventions are displayed according to intervention type. LTCR- long-term calorie restriction (> 12 weeks); STCR, short-term calorie restriction (≤ 12 weeks).

a higher reduction on weight, BMI, BMI z-score, waist circumference and systolic blood pressure compared to the control group.³⁴

The hematological parameters were reported in three studies.^{32,34,35} Huang et al. observed a reduction in fasting blood glucose, serum triglycerides and LDL-cholesterol and an improvement in some cardiorespiratory markers,³² while the other STCR study that analyzed the biochemical parameters found no differences before and after the intervention period.³⁵ Children on a low free-sugar diet showed significantly lower levels of glucose and total and LDL-cholesterol compared to the control group that followed their usual diet.³⁴

Associations between changes in gut microbiota and changes in health outcomes

Three studies with a STCR reported an association between changes in anthropometric or biochemical parameters and changes in the gut microbiota after the intervention (Table 3).^{32,35,36} The LTCR intervention study did not report any significant association.³³

Huang et al.³² reported that changes in triglycerides, serum total cholesterol and LDL-cholesterol were positively associated with changes in the relative abundance of Family XIII UCG-001. The change in total cholesterol was also positively associated with the change of *Ruminococcus torques* group, *Alloprevotella* and *Eubacterium coprostanoligenes* group but was inversely associated with the change in *Bacteroides*. A negative association was found between HDL-cholesterol and *Ruminococcaceae* UCG-003. The change in glucose levels was positively associated with *Eubacterium ruminatum* and *Paraprevotella* but negatively with

Eubacterium ventriosum. Changes in LDL-cholesterol were positively correlated with *Odoribacter*, while changes in waist circumference were negatively correlated with *Odoribacter*.³⁵ Santa Cruz et al.³⁶ observed that weight loss was negatively associated with the ratio of *Bifidobacterium*/*C. coccoides* and the ratio of *Bifidobacterium*/*B. fragilis*.

DISCUSSION

To the best of our knowledge, this is the first systematic review investigating the impact of dietary interventions, without any supplementation, on the gut microbiota of children and adolescents with obesity. Gut microbiota composition has been increasingly investigated over the past years for its direct relation with metabolic health. Surprisingly, the modulation of gut microbiota through dietary intervention alone appears insufficiently explored in childhood obesity, as only a limited number of studies were retrieved in our systematic search.

One of the most relevant difficulties in synthesizing the effect of dietary interventions on gut microbiota and cardiometabolic health outcomes is the high number of potential variations and microbiota composition modifiers. There is a huge amount of possible taxonomical combinations and inter-individual variations for the gut microbiota at the different taxonomic levels, some of which strictly dependent on the geographical area of provenience of the cohort under study.⁴² Although the studies involved pediatric groups with obesity undergoing similar interventions, microbiota changes reported varied across taxonomic levels. However, since most articles reported alpha-diversity, a

Table 3. Summary of changes in gut microbiota associated with changes in health-related outcomes.

Bacterial taxa	Health outcome	Observed change	Reference
<i>Odoribacter</i>	Waist circumference	↓	Moran Ramos et al. ³⁵
	LDL-cholesterol	↑	Huang et al. ³²
<i>Bifidobacterium/C. coccoides</i> ratio	Waist circumference	↑	Santa Cruz et al. ³⁶
<i>Bifidobacterium/B. fragilis</i> ratio	Waist circumference	↑	Santa Cruz et al. ³⁶
<i>Lactobacillus</i>	Weight	↓	Santa Cruz et al. ³⁶
	BMIZ	↓	Santa Cruz et al. ³⁶
<i>B. fragilis</i> group	Weight	↓	Santa Cruz et al. ³⁶
	BMIZ	↓	Santa Cruz et al. ³⁶
<i>E. coli</i>	Weight	↑	Santa Cruz et al. ³⁶
<i>C. coccoides</i>	Weight	↓	Santa Cruz et al. ³⁶
<i>Eubacterium ruminantium</i>	Glucose	↑	Huang et al. ³²
<i>Eubacterium ventriosum</i>	Glucose	↓	Huang et al. ³²
<i>Paraprevotella</i>	Glucose	↑	Huang et al. ³²
Family XIII UCG-001	Triglycerides	↑	Huang et al. ³²
	LDL-cholesterol	↑	Huang et al. ³²

All the biochemical and anthropometric parameters included were significantly different between baseline and after the intervention. Direct associations were represented with ↑, and negatives with ↓.

recognized marker of health,^{11,43} the effectiveness of the interventions was more easily synthesized.

Dietary interventions and gut microbiota diversity

In the present review we showed that dietary interventions for pediatric obesity significantly increased gut microbiota richness compared to baseline levels. The observed increase in the Chao-1 richness estimator may reflect enhanced bacterial diversity following the dietary intervention, presumably due to the expansion of low-abundance bacterial lineages that strongly influence richness metrics, particularly Chao-1.⁴⁴ The dietary interventions that most effectively improved the gut microbiota profile, by increasing richness and beneficial bacteria, consisted of recommendations aiming at achieving balanced diets with a mild calorie-restriction suitable for the pediatric age. These calorie-restricted diets could modulate the gut microbiota profile for several reasons: the energy restriction itself, but also the increase of fiber-rich, low-energy density foods (such as vegetables) and the parallel reduction of high-energy density foods.⁴⁵

Conversely, studies conducted in adults showed a loss of microbiota diversity after a dietary restriction,⁴⁶ or reported minimal and inconsistent effects of food-based weight loss interventions on alpha-diversity and relative bacterial abundance at the phylum and genus level.⁴⁷ This could be the result of a highly hypocaloric dietary plan, which is not in line with the balanced dietary treatment endorsed in pediatric age groups.

Dietary interventions and Firmicutes-to-Bacteroides ratio

One key hallmark of the gut microbiota in individuals with obesity is the increase in F/B ratio, a reproducible and easy measure reflecting the expansion of *Firmicutes* over *Bacteroidetes* in individuals with obesity. The opposite, i.e., a significant reduction of the F/B ratio, was reported in two studies in adolescents with obesity undergoing dietary interventions, compared to baseline values.^{32,33}

Although the F/B ratio has been reported as a hallmark of obesity and thus *Firmicutes* could be detrimental to health, both *Firmicutes* and *Bacteroidetes* include many different species with known health benefits and/or others with undesirable health effects. Nowadays, this assumption is controversial.⁴⁸ It has been reported that most of the butyrate-producing bacteria, associated with beneficial health effects, belong to the *Firmicutes* phylum.

Thus, interpreting changes and extracting conclusions about F/B holds difficulties and discrepancies.

Dietary interventions and changes in butyrate-producing bacteria

Based on the taxonomic shifts observed, we hypothesize that STCR primarily alters community ecology by increasing richness and overall α -diversity, as previously outlined. In contrast, the expansion of butyrate-producing taxa appears to require prolonged intervention, such as LTRC.

Butyrate is the SCFA considered to be a major contributor to several physiological functions and is associated with protective effects against obesity-related cardiometabolic alterations.²⁴ *Roseburia*, together with other genera such as *Faecalibacterium*, are recognized as a butyrate-producing bacteria.^{49,50} In particular, we observed an expansion of *Faecalibacterium*, with *F. prausnitzii* being one of the most relevant species, and of *Roseburia* following LTRC. This enrichment may be driven by the higher dietary fiber intake typically associated with the nutritional interventions described. Not surprisingly, *Roseburia* spp., *Ruminococcus* spp., and *Eubacterium* spp. are polysaccharide-fermenting bacteria strongly influenced by fiber-rich diets. According to Caputo et al., their abundance may nonetheless be modulated by the pre-existing microbiota and by resilience mechanisms promoting a return to an obesity-associated microbial phenotype.⁵¹ These factors could potentially explain the observed reduction in certain butyrate-producing bacteria, such as *Eubacterium* and *Clostridium coccoides*, following dietary intervention.^{33,36}

Butyrate abundance has been reported to be reduced in different pathologies, including type 2 diabetes, colorectal cancer, and inflammatory bowel diseases. Its role in promoting gut health is increasingly recognized, to the point that it has been suggested to consider its monitoring as a biomarker to assist in the diagnosis and prognosis of gut-related disorders.⁴⁹ Thus, interventions aimed at increasing butyrate-producing bacteria and enhancing butyrate absorption could be an important focus for tailored treatments for children with obesity.

Changes in gut microbiota and cardiometabolic parameters

Despite the few studies available for the pediatric cohort, in our review we studied the association between changes in gut microbiota and the association with metabolic parameters. Mainly,

interventions were associated with changes in butyrate-producing bacteria, which in turn exhibited certain improvements in cardiometabolic markers. *Eubacterium ruminantium* and *Paraprevotella* were positively associated with changes in fasting glucose levels.³² Moreover, the increase of *Odoribacter*, had been associated with a reduction in waist circumference after a STCR intervention,³⁵ but with an increase in LDL-c levels.³² In line with these results, it has been reported that butyrate-producing bacteria, such as *Faecalibacterium* or *Eubacterium hallii*, are mainly related to beneficial effects on insulin homeostasis.⁵² The beneficial effects of butyrate may be mediated by an increase in the richness of the gut microbiota composition. Alternatively, it has been suggested that butyrate can influence body weight, energy intake, and insulin sensitivity through the stimulation of gut-derived hormones such as GLP-1.⁵³ Although most evidence points in the same direction, some articles have reported controversial results, and this is not fully elucidated yet.⁵² The results are inconsistent and do not clearly indicate whether changes in health outcomes are attributable to gut microbiota modulation, dietary treatments or multicomponent interventions. Future studies should include mediation analyses to unravel the mechanisms underlying these associations. If the observed changes in gut microbiota diversity prove to be resilient, it is reasonable to hypothesize that corresponding improvements in cardiometabolic parameters may occur. However, the current evidence remains insufficient to answer this question.

Limitations and strengths

One of the main limitations of the present review is the limited number of articles retrieved. Overall, the included studies were graded with moderate risk of bias. Among the identified biases, it is worth citing the often small sample sizes of patients enrolled in study cohorts, the different countries of origin and the lack of controls (which we overcome by selecting pre-post clinical intervention) as well as the absence of information on dietary adherence. Nevertheless, no serious or critical risk of bias were identified for included articles. A further limitation of this systematic review is the methodological and clinical heterogeneity across included studies (e.g., intervention type, study design, duration, and presence of co-interventions such as physical activity).

It is important to highlight that the activity and composition of the microbiota are affected by many modifier factors other than the diet and the geographical provenience (often interconnected), such as genetic background, the consumption of drugs such as antibiotics or the practice of physical activity. There was no adjustment for confounding variables such as physical activity in the included articles, so the observed result could be a synergistic effect of different exposures.

One of the relevant strengths of this review is that it includes the first meta-analysis carried out to assess changes in the alpha-diversity index in children and adolescents with overweight or obesity under dietary intervention. Additionally, the well-defined protocol enabled the identification and synthesis of interventions of similar nature, yielding consistent results. Although the dietary interventions differed, they all implemented conservative and balanced dietary interventions, making them reasonably comparable for quantitative synthesis.

The majority of publications retrieved from the search focused exclusively on probiotics, vitamins, and mineral supplementation, highlighting a substantial gap in studies on diet-driven gut microbiota changes in pediatric populations. Studying diet remains challenging due to its multifactorial nature, difficulties in standardizing dietary exposures and adherence. Future research should prioritize studies that evaluate the effects of diet itself, with pre- and post-intervention measurements, and consider long-term observed changes (6–12 months). Lastly, documenting dietary intake before and after the intervention is crucial to better

understand microbiota modulation, considering physical activity and fiber intake as important confounding factors.

Future perspectives Future research may be directed towards identifying microbial strains that can be defined as early indicators of both dysbiosis and effectiveness of nutritional interventions. More RCTs are needed to clarify and understand the relationships between dietary interventions, gut microbiota changes and associated health outcomes in children and adolescents with overweight or obesity. Clinical and methodological homogeneity across studies is also needed to allow a more reliable evaluation of the effectiveness of dietary interventions and to interpret findings on gut microbiota more accurately.

In addition, metabolomics could help understand a missing link between gut microbiota functionality, corroborating changes observed in cardiometabolic health. In this context, the study from Cohen et al. provided a rationale of utility of “omics” application to examine systemic biological adaptations alongside gut microbiota changes associated with dietary intervention in adolescents with obesity.³⁴

To conclude, dietary interventions seeking healthy and balanced energy reductions in children and adolescents with obesity have been associated with increased gut microbiota richness. Although, the heterogeneity among the bacterial communities appraised in the included articles made synthesis across studies challenging, there was a tendency to increase in the abundance of butyrate-producing bacteria after balanced dietary interventions with a calorie-restriction adequate for pediatric age.

DATA AVAILABILITY

The original data presented in this systematic review is included in the main manuscript and supplementary material. Further requirements can be directed to the corresponding authors.

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ACKNOWLEDGEMENTS

We acknowledge authors Morán-Ramos et al.³⁵ and Peng et al.³⁹ for sharing the original study data, which contributed to these meta-analyses.

AUTHOR CONTRIBUTIONS

All authors meet full criteria for authorship, their respective roles in the submitted work are listed as follows: Giulia Fiore—project administration, methodology, investigation, writing—original draft preparation. Mireia Alcázar—investigation, formal analysis, writing—original draft preparation. Judit Muñoz-Hernando—investigation, writing—original draft preparation. Irene Hernández-Pérez—investigation, writing—original draft preparation. Emma Peruchó—investigation, writing—original draft preparation. Simona Panelli—writing—review and editing, methodology. Natalia Ferré—writing—review and editing. Joaquín Escribano—conceptualization, writing—review and editing, supervision. Elvira Verduci—conceptualization, methodology, supervision. Veronica Luque—conceptualization, methodology, funding acquisition, supervision.

FUNDINGS

G.F. is the holder of a Ministerial Fellowship within the Nutritional sciences PhD programme at the University of Milan. M.A. is the holder of a Predoctoral Training Program grant from Instituto de Salud Carlos III—Health Strategic Action, Code: FI19/00257. I.H. is the holder of a Predoctoral Training Program grant Joan Oró (FI) from AGAUR, Code: 2023FI-101041. V.L. is the holder of a Serra Hunter Fellowship of the Generalitat de Catalunya. Open access funding provided by Università degli Studi di Milano within the CRUI-CARE Agreement.

COMPETING INTERESTS

The authors declare no competing interests.

ADDITIONAL INFORMATION

Supplementary information The online version contains supplementary material available at <https://doi.org/10.1038/s41390-026-05312-w>.

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