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A systematic review of gut microbiota profile in obesity

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ABSTRACT: Obesity is the accumulation of too much fat, which can result in problems like metabolic syndrome. The importance of the gut microbiota in obesity has been recognised for the past ten years, although it is still unclear how much it contributes to obesity and its associated comorbidities. The majority of research on the relationship between the microbiome and obesity has been based on correlations between the microbiota and obesity. The understanding of the gut microbiota's function has advanced recently, raising the possibility of new therapeutic strategies based on changing the microbiome. The unique lifestyle, dietary customs (high carbohydrate and fat intake, low fibre intake), and uncontrolled antibiotic use may all be contributing factors to the variance in gut microbiota. Next-generation sequencing is the primary research tool used to investigate the connections between the microbiota and obesity, type 2 diabetes, and other metabolic diseases. The baseline material used in these studies is made up of bacterial DNA isolates from patient faeces, which are then processed appropriately and subjected to metagenomic analyses. Reviews are essential to summarising the pertinent accomplishments due to the volume and diversity of material published. Articles were reviewed from studies based in America, Europe, and Asia. In many population groupings, we discovered particular microorganisms linked to metabolic diseases and obesity. We give a summary of the available data on the link between intestinal microbiota and obesity in this systematic review.

KEY WORDS: gut microbiomes, obesity, metabolic diseases

I. INTRODUCTION

The gut microbiota has attracted our attention in the last decade as an element that directly affects our health or illness status. It is defined as an assortment of bacteria that inhabit the gastrointestinal tract. These bacteria are symbiotic and play a significant role in physiological processes, for example, digestion, or they can intervene in metabolism. It is known that most of the human population's microbiota is composed of five phyla: Bacteroidetes, Firmicutes, Actinobacteria, Proteobacteria, and Verrucomicrobia, with Bacteroidetes and Firmicutes accounting for around 90% of the total bacterial species. [1, 2]

Numerous pathological diseases, including obesity, cardiovascular illness, inflammatory bowel disease (IBD), and autism, have been causally linked to the gut microbiome. The sequencing of specific sections of 16S or 18S ribosomal genes permits the identification of organisms and their relative abundance in pure DNA. [3]

New information about the phylum Cytophaga-Flavobacterium-Bacteroides, which has recently been discovered to be prevalent in the intestines of mice, rats, and humans, has been gained through the analysis of 16S rRNA. [4] Recent developments in sequencing technologies have led to the broader use of metagenomic analysis for understanding complex ecosystems such as the human gut. [5] However, metagenomic sequencing of the gut microbiome has some limitations. The intestinal epithelium is composed of three functional barriers: a physical barrier, an innate immunological barrier, and an adaptive immune barrier. [6] The interaction between commensal gut flora and the intestinal barrier is complicated and happens at each of these interfaces, and faecal metagenomics does not thus measure ecological changes at all levels.

Abnormal or excessive fat accumulation that poses a risk to health is what is meant by the terms "overweight" and "obesity." A body mass index (BMI) over 25 is considered overweight, and over 30 is obese. [7] About 13% of the world's adult population (11% of men and 15% of women) were obese in 2016. 39% of adults aged 18 years and

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over were overweight in 2016, and 13% were obese.[8] Numerous illnesses, such as hypertension, coronary artery disease, stroke, diabetes mellitus, gallstones, cancer, non-alcoholic fatty liver disease, obstructive sleep apnea, osteoarthritis of the knee, and aberrant metabolic processes, are more common in obese persons.

One of the astounding discoveries over the past ten years is the link between gut bacteria and obesity and their causal role in it. Recent research has revealed that the composition of the bacterial variety appears to differ between lean and obese people, with an increase in Firmicutes and a decrease in Bacteroidetes. [9] In this comprehensive review, we give a summary of the most recent data supporting the link between intestinal microbiota and obesity.

II. MATERIALS AND METHODS

We analysed human observational studies or clinical trials that assessed the gut flora of people with obesity. BMI is the result of dividing the body's actual weight in kilograms by the body's height in square meters. BMI = Weight / (Height) [2]

Table 1 . WHO classification of obesity[10]

BMI	Nutritional status
Below 18.5	Underweight
18.5–24.9	Normal weight
25.0–29.9	Overweight
30.0–34.9	Obesity class I
35.0–39.9	Obesity class II
Above 40	Obesity class III

Search strategy

This systematic review was performed in accordance with the PRISMA 2009 guidelines (Figure 1). [11] We selected the MeSH terms "obesity" and "microbiota" with the following filters: language: English; publication date: 5 years from April 20, 2023. The search was performed in MEDLINE, accessed by PubMed. Based on the title and abstract, each one was screened. The reference lists of the chosen papers were checked for additional potential articles. We chose observational studies and human clinical trials after reading the title and abstract.

Study selection

The following criteria were met by studies to be included: 1) Case-control studies comparing the gut microbiota of people with and without obesity 2) Shotgun metagenomic sequencing or next-generation sequencing (16sr RNA amplicon) were used to evaluate the intestinal microbiota, and 3) body mass index was used to characterise obesity. 4) Research on people who have metabolic issues There were studies in every age range.

Case reports, reviews, meta-analyses, reanalyses of public datasets, conference abstracts, studies without data for specific bacterial groups, studies not written in English, and studies without a case-control design were all disqualified from consideration.

III. RESULTS

As per a literature search, the general characteristics of the studies are as follows: From the 220 articles retrieved from the search, 40 articles were selected based on the title and abstract to be read in depth. Finally, 15 studies were included and are described in Table 2. 12 studies were performed on adults, and 3 were done on children. 25 were omitted from the study, including reviews we reviewed but did not include unless they were systematic. Most of the studies were performed in Asia (46%), America (27%), and Asia (27%). Most of the journals were published during 2019–2020.

Table 2. General characteristics of the studies

First Author,Year	Country	Ethnicity	Age	Sample size (control)	Sample size (case)	Sample	Sequencing method
Alejandra Chavez-carbajal,[12] 2019	Mexico	Hispanic / Latino	19-45	25	17	Stool	16s RNA gene sequencing (v4)
Yanrong LV,[13] 2019	China	Asian	>18yrs	10	9	Stool	16s next generation sequencing (NGS)

Brandily A Peters,[14] 2018	USA	Caucasian	>62yrs	211	142	Stool	16s RNA gene sequencing (v4)
Robert C Kaplan, [15] 2019	USA	Hispanic	18-74	294	293	Stool	16s RNA gene sequencing (v4)
Esther Nistal,[16] 2019	Spain	Spaniards	20-60	20	36	Stool	RNA gene Sequencing
Ayesha Monga Kravetz, [17] 2020	Italy	Italian	12-25	29	44	Stool	RNA gene sequencing
Aftab Ahmad,[18] 2019	Pakistan	Asian	25-55	20	40	Stool	16s RNA gene sequencing
Yeojun Yun,[19] 2019	Korea	Asian	>40	192	76	Stool and Blood	16s RNA gene sequencing
Fateme Ettehad Marvasti, [20] 2019	Iran	Asian	20-60	50	50	Stool	16s RNA gene sequencing (v3 – v4 region)
Agnieszka Sroka – Oleksiak, [21] 2020	Poland	Polish	20-70	27	39	Biopsy from descending part of duodenum	16s RNA gene sequencing (v3 – v4 region)
Carmela Nardelli, [22] 2020	Italy	Italian	20-80	16	19	Duodenal biopsy	16s RNA gene sequencing
Xiaowei Chen,[23] 2020	China	Asian	6-11	23	28	Stool	16s RNA gene sequencing
Luigui Gallardo Becerra, [24] 2020	China	Asian	6-11	23	28	Stool	16s RNA gene sequencing
Xiaolin Gao,[25] 2018	China	Asian	6-9	38	39	Stool	16s RNA gene sequencing
Zhiying song,[26] 2022	China	Asian	25-35	15	7	Stool	16s RNA gene sequencing

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PRISMA 2009 Flow Diagram

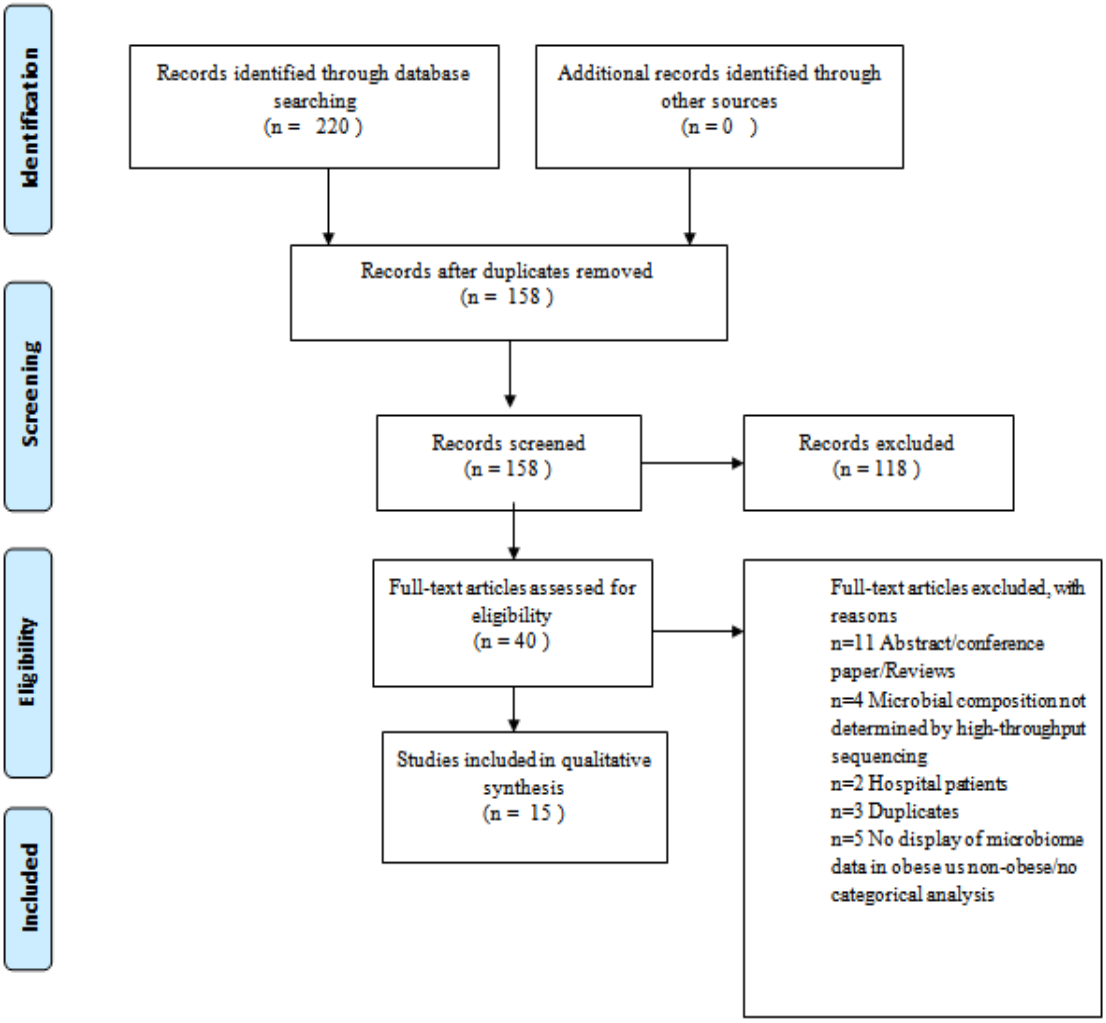

Fig 1. Study selection flowchart

The gut microbiota was measured at baseline in each study, and any changes in microbial composition were evaluated as outcomes. We have concentrated on the analysis of microbial diversity among BMI. Numerous studies examined the differences in gut microbial profiles between lean and obese patients in order to identify those that were connected to obesity. We located 15 intriguing studies that contrast the microbiome of people with various BMIs.

In the first study, it was observed that there were significant changes in the gut microbiomes. [12] In obese women, Firmicutes was the most abundant bacterial phylum. In significant abundance, bacteria belonging to the Ruminococcaceae, Lachnospiraceae, and Erysipelotrichaceae families were found. In the second study, the predominant phyla were Bacteroidetes and Firmicutes. [13] There are no variations in the F:B abundance ratio. As BMI increased, the diversity of the gut microbiota decreased. In the third investigation, it was discovered that there was a decreased abundance of the class Clostridia and an increased abundance of Bacilli and their families Lactobacillaceae and Streptococcaceae. 14 In the fourth trial, there was a correlation between a rising BMI and a rise in the Prevotella to Bacteroidetes ratio. [15] The fifth study was done among obese patients with non alcoholic fatty liver disease and the results revealed abundance of Blautia, Alkaliphilus, Flavobacterium and reduced Akkermansia. [16]

The sixth study was done on obese youth with non-alcoholic fatty liver disease. The study showed an abundance of Firmicutes and a lower abundance of Bacteroidetes, Prevotella, Gemmiger, and Oscillospira. [17] The ratio of Firmicutes to Bacteroidetes was also higher. In the seventh study done among obese individuals with Type 2 Diabetes Mellitus, Firmicutes were dominant along

with Clostridia.decreased abundance of Verrucomicrobia, Bacteroidetes, Proteobacteria, and Elusimicrobia. The eighth study, which included obese people with non-alcoholic fatty liver disease, showed a decrease in gut microbiomes including Fastidiosiphila and Faecalibacterium. [19] They also showed a decrease in Weisella and its family, Leuconostococeae. The ninth study done with obese individuals showed the Firmicutes to Bacteroidetes ratio to be significantly increased, along with Faecalibacterium prausnitzii. [20] Decreased abundance of Akkermansia and Bifidobacterium.

The tenth study done with obese Type 2 diabetes mellitus patients reported a lower number of genus Bifidobacterium. [21] The eleventh study revealed a decrease in Firmicutes and a significant increase in Proteobacteria. [22] In the last two studies, specimens were collected by duodenal biopsy. [21, 22]

The twelfth study showed that there was no difference in F/B ratio. There was abundance of genus level Faecalibacterium, Phascolarctobacterium, Lachnospira, Megamonas and Hemophilus.3 The thirteenth study revealed an increase in Coriobacteraceae, Collinsella, and Erysipelotrichaceae and a decrease in Parabacteroides distasonis. [24] The fourteenth study showed significant abundance in Bacteroidetes.[25] The above three studies were performed among obese children. The last study was done in obese women with gestational diabetes mellitus and had significantly higher Bacteroidetes namely Faecalibacterium, Verrucomicrobia and Akkermansia. [26]

IV. DISCUSSION

This review aims to summarise the data gathered over the last five years on the relationship between gut microbiota and obesity. Whether or not obesity is linked to greater or lesser microbiome diversity and if the F/B ratio rises with obesity is one of the key debating issues. The strength of this study is that we applied a robust method of grouping various types of disease-microbiome associations into "lean, metabolically healthy states" or "obese, metabolically diseased states." Despite the fact that various metabolic disorders may affect the gut microbiota in different ways, the inter-study variation often supersedes the intra-study variation between disease and control groups. [27]

Overall, the inconsistent nature of the outcomes across research is the most startling finding. This most likely has to do with the limitations of the studies that were used in this review. Additionally, it depends on the adult microbiota's remarkable distinctiveness and stability as it evolves through time. In systematic reviews, heterogeneity between studies is sometimes a problem. The microbiota was evaluated using a variety of different techniques, which makes it challenging to compare results across studies and probably accounts for the variations in outcomes.

V. CONCLUSION

In this review, papers examining the relationship between obesity and gastrointestinal tract microbial diversity in obese people were carefully evaluated. These findings served as a roadmap for the future creation of live biotherapeutics made from certain bacteria that may be useful in the treatment of metabolic diseases and obesity. Obesity is linked to various gut microbiota profiles, but studies don't always come up with consistent findings. This is likely because there are a number of variables that can affect the results, including the various methodologies and expanding knowledge of data management. To make judgements regarding the role that microbial diversity plays in obesity, more studies and the development of this shotgun sequencing data management system are required.
To further understand their involvement in the treatment of obesity and metabolic illnesses, more in vitro and in vivo studies are required.

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