DOI: https://doi.org/10.36955/RIULCB.2024v11n2.018

Original Article

Association Between Human Gut Microbiota and Obesity According to Body Mass Index

Asociación entre la microbiota intestinal humana y la obesidad según el índice de masa corporal

Alejandra V. Valdivia[1] Solange Z. Sánchez[2] Diana Flores-León[3]

dianaflores.df454@gmail.com

1.- Universidad Le Cordon Bleu. Lima, Peru.
2.- EsSalud. Lima, Peru.
3.- Instituto Nacional de Salud. Lima, Peru.

Received: 15/03/2024 Review: 10/04/2024 Accepted: 22/06/2024 Published: 30/06/2024

ABSTRACT

Research on gut microbiota as a tool to address obesity is a promising field. The influence of gut microbiota on the endocrine system and host metabolism is crucial to understanding how it can affect body weight. For this review, relevant keywords such as “gut microbiota and obesity,” “gut microbiota and BMI,” and “gut microbiota composition” were used in the search for articles. A total of 50 articles in English and Spanish were identified, of which 15 were selected for meeting the established inclusion criteria. Comparative studies analyzing gut microbiota in groups of individuals from different regions of the world, classified according to their BMI, are particularly valuable. The 16S rRNA sequencing technology, based on the analysis of fecal samples, has consistently demonstrated a significant association between gut microbiota composition and BMI. Although specific bacteria that directly contribute to obesity have not yet been identified, certain predominant bacterial types have been observed in populations with this condition. It is important to highlight that the types of bacteria associated with obesity may vary between studies, although predominant patterns can be identified in each BMI classification, particularly between lean and obese individuals. In the Peruvian context, the lack of studies on the association between gut microbiota composition and obesity represents a significant opportunity. Future research in Peru could provide fundamental data for developing effective prevention and treatment strategies for obesity in the local population.

Keywords: Gut microbiota, obesity, BMI.

RESUMEN

La investigación en la microbiota intestinal como una herramienta para abordar la obesidad es un campo prometedor. La influencia de la microbiota en el sistema endocrino y el metabolismo del huésped es crucial para entender cómo esta puede afectar el peso corporal. Para esta revisión, se emplearon palabras clave relevantes como “microbiota intestinal y obesidad", "microbiota intestinal e IMC" y "composición de microbiota intestinal" en la búsqueda de artículos. Se identificaron 50 artículos en inglés y español, de los cuales se seleccionaron 15 que cumplían con los criterios de inclusión establecidos. Los estudios comparativos que analizan la microbiota intestinal en grupos de individuos de diferentes regiones del mundo, según su clasificación de IMC, son especialmente valiosos. La tecnología de secuenciación del ARNr 16S, basada en el análisis de muestras fecales, ha demostrado consistentemente una asociación significativa entre la composición de la microbiota intestinal y el IMC. Aunque aún no se han identificado bacterias específicas que contribuyan directamente a la obesidad, se han observado ciertos tipos predominantes en poblaciones con esta condición. Es importante destacar que los tipos de bacterias asociadas con la obesidad pueden variar entre estudios, aunque se pueden identificar patrones predominantes en cada clasificación de IMC, particularmente entre individuos delgados y obesos. En el contexto peruano, la carencia de estudios sobre la asociación entre la composición del microbioma intestinal y la obesidad representa una oportunidad significativa. Investigaciones futuras en Perú podrían proporcionar datos fundamentales para desarrollar estrategias efectivas de prevención y tratamiento de la obesidad en la población local.

Palabras clave: Microbiota intestinal, obesidad, IMC.

INTRODUCTION

According to the World Health Organization (WHO), obesity is a disease that has caused one of the most significant health crises in recent years (WHO 2020, WHO 2022) and has reached epidemic proportions, with an estimated 4 million annual deaths due to diseases associated with overweight and obesity, such as cardiovascular diseases, diabetes, cancer, neurological disorders, chronic respiratory diseases, and digestive disorders. According to the Organization for Economic Cooperation and Development (OECD, 2019), it is projected that in the next 30 years, obesity will result in a reduction of nearly 3 years in life expectancy.

Obesity is a multifactorial disease that manifests through physiological, psychological, and epigenetic changes, in addition to the effect of highly processed foods on health. Therefore, obesity and overweight cannot be simply attributed to a lack of willpower or individual effort, as multiple factors influence these conditions, making it essential to study all of them. However, this disease is reversible, and considering the increasing number of affected individuals worldwide, it is crucial to provide people suffering from obesity with all possible tools for treatment, including the potential role of gut microbiota (Tseng, 2018).

A potentially useful tool currently under study is the identification of microorganisms that are part of the gut microbiota and their effect on the host's endocrine system and metabolism, which could perpetuate or reverse obesity. The gut microbiota comprises all microorganisms and their genetic material that inhabit the human body, and the genes of the gut microbiome represent more than three million, being more than 100 times the number of human genes (Tseng, 2018). This underscores the complexity of studying gut microbiota.

According to recent research, more than 99% of the genes present in the gut microbiota are bacterial, which indicates a great diversity of bacterial species in each individual. Firmicutes and Bacteroidetes are the dominant bacterial phyla in the gut microbiota, representing approximately 90% of the total community (Quin, 2010).

Other phyla, such as Proteobacteria, Actinobacteria, and Verrucomicrobia, are less dominant. Advances in technologies such as next-generation sequencing have allowed for a better understanding of gut microbiome composition and its implications for health and disease (Pinart, 2021 and Rubio, 2020).

Conducting research on gut microbiota offers new opportunities to understand and address obesity from a holistic and multidisciplinary perspective, which may lead to more effective prevention and treatment strategies

MATERIALS AND METHODS

A search for articles was carried out in the PubMed and SCOPUS databases using terms related to gut microbiota and obesity, including “gut microbiota and obesity,” “gut microbiota and BMI,” “gut microbiota,” “obesity,” “gut microbiota composition,” “bacteria associated with obesity,” and “bacteria associated with leanness.” This search yielded a total of 50 articles in English and Spanish, of which 15 were selected for meeting the inclusion and selection criteria.

The search focused on research articles that examine the association between gut microbiota composition and body mass index (BMI). These studies were selected based on their relevance and quality, with the aim of providing a comprehensive understanding of how gut microbiota may influence an individual’s state of obesity or leanness.

Gut Microbiota by Geographic Region

Currently, research seeks to determine the types of bacteria that make up the gut microbiota that are associated with obesity and, conversely, the types of bacteria associated with leanness, to allow for future interventions in the gut microbiota in a way that favors a healthy weight in the host. The composition of the gut microbiota depends on many factors such as diet, physical activity, medication use, and the geographical area where a person lives, among others. It is important to consider how gut microbiota may differ depending on the host’s conditions. For example, groups of obese individuals without metabolic syndrome differ from groups of obese individuals with metabolic syndrome (Chávez-Carbajal *et al.*, 2019).

RESULTS AND DISCUSSION

Various comparative studies have examined the gut microbiota in groups of individuals from different parts of the world, classified according to their Body Mass Index (BMI). These studies, predominantly conducted through the analysis of fecal samples using 16S rRNA sequencing technology, have consistently found a significant association between gut microbiota composition and BMI (John and Mullin, 2016).

According to Valdés *et al.* (2018), gut microbiota play a crucial role in health by stimulating the immune system, protecting against pathogen invasion, and obtaining energy from nutrients. Changes in its composition can alter host homeostasis and negatively affect health.

Although the types of bacteria associated with obesity vary between different studies, it is possible to identify certain predominant bacteria in each BMI classification, particularly between lean and obese individuals. A summary of the selected studies, classified by the country of origin of the participants, is provided below:

United States of America

Chen *et al.* (2016) conducted a study with 647 participants from the Mayo Clinic Biobank and found that in obese individuals, there was an increase in the number of *Firmicutes*, *Fusobacteria*, and the genus *Eubacterium*, while a decrease in Bacteroidetes was observed. On the other hand, in the group of lean individuals, the *Christensenellaceae* family was predominant.

In the study by Kaplan *et al.* (2019), the gut microbiota of 1,674 Hispanics aged 18 to 74 years, residing in the United States, was compared. Unlike previous studies, an increase in the *Prevotella/Bacteroides* ratio was observed in participants with obesity, along with an increase in the bacterium *Acidaminococcus*. In contrast, in the same group, a decrease in *Oscillospira* and *Anaerotruncus* was recorded.

Finland

In the study by Org *et al.* (2017), 531 Finnish men participated. The results indicated that participants with a high BMI had a greater abundance of the *Tissierellaceae* family and the *Blautia* genus, as well as a decrease in the abundance of *Archaea* (*Methanobrevibacter*). In contrast, in lean participants, bacteria from the *Tenericutes* phylum and the *Christensenellaceae* family were predominant. Additionally, the results showed that there were no significant differences in the *Firmicutes/Bacteroidetes* ratio.

South Korea

Yun *et al.* (2017) analyzed the gut microbiome of 1,463 Korean subjects classified according to their BMI. The results showed that in obese individuals, bacteria from the *Veillonellaceae* family were predominant, while the abundance of *Akkermansia* decreased in this group. In contrast, in lean individuals, bacteria from the *Eggerthella* and *Adlercreutzia* genera, as well as the *Christensenellaceae* family, were predominant.

China

Gao *et al.* (2018) conducted a study with 551 Chinese participants classified according to their BMI. The results indicated that in obese and overweight individuals, *Fusobacterium*, *Bifidobacterium, Coprococcus, Dialister*, and *Actinobacteria* were predominant, while the abundance of *Phascolarctobacterium* decreased in this group. Additionally, an increase in *Bacteroidetes* was observed in obese individuals.

Lv *et al.* (2019) investigated the gut microbiota of 28 Chinese university students. The results showed that in obese and overweight individuals, the bacterium *Parasutterella* was predominant. In contrast, in lean individuals, bacteria from the *Porphyromonadaceae, Acidaminococcaceae, Rikenellaceae, Desulfovibrionaceae* families, and the genera *Blautia, Anaerotruncus,* *Parabacteroides*, and *Alistipes* were predominant. No significant difference was found in the *Firmicutes/Bacteroidetes* ratio.

Duan *et al.* (2021), in their publication "Characteristics of Gut Microbiota in People with Obesity," analyzed the gut microbiota of 42 people. The results showed that gut microbiota diversity decreased in obese individuals, with a significant reduction in the *Firmicutes/Bacteroidetes* ratio.

In the obese group, *Firmicutes* increased while *Bacteroidetes* decreased. Additionally, the *Prevotella, Megamonas, Fusobacterium*, and *Blautia* genera increased in obese individuals, while *Faecalibacterium, Lachnospiraceae Incertae sedis, Gemmiger*, and *Clostridium* significantly decreased.

South Africa

Oduaran *et al.* (2020), in their article "Gut Microbiome Profiling of a Rural and Urban South African Cohort Reveals Biomarkers of a Population in Lifestyle Transition," analyzed the gut microbiomes of 170 South African women (51 from Soweto and 119 from *Bushbuckridge*) classified into two groups: obese and lean.

In the obese group from *Bushbuckridge*, the predominant genera were P*revotella, Sutterella, Phascolarctobacterium, Ruminococcus, Clostridium, Alistipes, Acetanaerobacterium, Parabacteroides, Catenibacterium*, and *Akkermansia*. Meanwhile, in the obese group from Soweto, the predominant genera were *Prevotella, Clostridium, Haemophilus, Oscillibacter, Streptococcus, Escherichia, Shigella, Ruminococcus, Sporobacter, Oxalobacter, Intestinimonas*, and *Parabacteroides*. The bacterial composition in each obese group differed significantly according to geographic location.

Mexico

In the study by Chávez-Carbajal *et al.* (2019), "Gut Microbiota and Predicted Metabolic Pathways in a Sample of Mexican Women Affected by Obesity and Obesity Plus Metabolic Syndrome," the microbiota of 67 women was analyzed. The results showed that in obese women, the predominant phyla were *Firmicutes* and *Proteobacteria*.

The bacteria found in this group included *Faecalibacterium, Megamonas, Succinatimonas*, and the *Lachnospiraceae* family, while the *Bacteroidaceae* family decreased. In contrast, in lean participants, bacteria from the *Bacteroidetes* phylum, including *Bacteroides* and *Parabacteroides*, were predominant, as well as bacteria from the *Firmicutes* phylum, including the genera *Streptococcus, Staphylococcus, Turicibacter, Lactococcus*, and the *Erysipelotrichaceae* family.

Egypt

In the article by Salah *et al.* (2019), the gut microbiota of 60 participants was studied. The results showed a tendency for an increase in *Bacteroidetes* in obese participants and a significantly higher *Firmicutes/Bacteroidetes* ratio in these individuals. At the genus level, a greater abundance of *Faecalibacterium* and *Akkermansia* was observed in obese patients.

Japan

Andoh *et al.* (2016), in their article "Comparison of the Gut Microbial Community Between Obese and Lean

People Using 16S Gene Sequencing in a Japanese Population," studied the gut microbiota of 10 obese volunteers and 10 lean volunteers. The abundance of the *Bacteroidetes* phylum and the B/F ratio was not different between the obese and lean groups. The *Firmicutes* and *Fusobacteria* phyla were more abundant in obese individuals. Regarding bacterial genera, there was an increase in *Alistipes, Anaerococcus, Corpococcus, Fusobacterium*, and *Parvimonas* in the obese group. Meanwhile, the predominant bacteria in the lean group were B*acteroides, Desulfovibrio, Faecalibacterium, Lachnoanaerobaculum*, and *Olsenella filiformis*.

Italy

Borgo *et al.* (2018) analyzed the gut microbiota of 40 adults. In this study, it was found that in obese individuals, the predominant bacteria were *Veillonellaceae* and *Dialister*, while in lean individuals, the *Oscillospira* genus and the species *Faecalibacterium prausnitzii* and *Flavonifractor plautii* were more prevalent. In the obese group, there was a decrease in the *Oscillospira* genus.

Palmas *et al.* (2021) studied the gut microbiota of 92 volunteers, finding an increase in the *Prevotella/Bacteroides* ratio. The bacteria that increased in the obese group were *Firmicutes*, while *Bacteroidetes* decreased. The predominant bacteria in the obese group included *Lachnospiraceae, Gemellaceae, Paenibacillaceae, Streptococcaceae, Thermicanaceae, Gemella, Mitsuokella, Streptococcus, Acidaminococcus, Eubacterium, Ruminococcus, Megamonas, Thermicanus, Megasphaera*, and *Veillonella*. The bacteria present in the obese group, compared to the lean group, included *Flavobacteriaceae, Porphyromonadaceae, Sphingobacteriaceae, Flavobacterium, Rikenella, Pedobacter, Parabacteroides*, and *Bacteroides*.

In contrast, the bacteria that increased in the lean group were *Porphyromonadaceae, Sphingobacteriaceae*, and *Flavobacteriaceae* (including *Sphingobacterium* and *Flavobacterium*). The *Enterobacteriaceae* family, known for its endotoxic activity, was predominant in the obese group compared to the lean individuals.

Ukraine

Koliada *et al.* (2017) examined the gut microbiota of 61 individuals. The findings revealed that the *Firmicutes* proportion increased, while *Bacteroidetes* decreased as BMI increased in the study sample. Additionally, an increase in the *Firmicutes/Bacteroidetes* ratio was observed as BMI increased.

Thailand

Jinatham *et al.* (2018) studied the gut microbiota of 42 volunteers. In the group of lean individuals, the following bacteria were more abundant: *Bacteroidetes, Firmicutes, Staphylococcus*, and methanogens. In contrast, in the group of overweight individuals, *Christensenella minuta, Akkermansia muciniphila, Gammaproteobacteria*, and bacteria from the genus *Ruminococcus* predominated.

Iran

Ettehad *et al.* (2020) published a study on the gut microbiota of 100 Iranian subjects. The results showed a significant increase in the *Firmicutes/ Bacteroidetes* ratio in the obese group compared to lean individuals. In the obese group, Faecalibacterium prausnitzii was predominant, while *Akkermansia muciniphila* and *Bifidobacterium* significantly decreased.

Although specific bacteria that directly contribute to obesity are still unknown, it is possible to identify certain bacterial types that predominate in populations with this condition. The bacteria present in different human groups vary due to factors such as geographical location and lifestyle. However, in obese individuals, common bacteria observed include the *Firmicutes* phylum and the genera *Fusobacterium, Prevotella, Megamonas, Veillonella*, and *Ruminococcus*. On the other hand, in lean individuals, the *Christensenellaceae* genus is particularly notable.

CONCLUSION

Diet plays a crucial role in the fight against obesity and is closely related to gut microbiota composition. It has been observed that a balanced and appropriate diet can modulate the diversity of the gut microbiota, which in turn significantly impacts the maintenance of a healthy body weight.

The results of the review highlight that the consumption of processed foods exerts a significant influence on gut microbiota composition, in contrast to body mass index. This finding underscores the importance of diet quality in modulating gut microbiota and, consequently, in weight management.

It is essential to promote healthy eating habits and reduce the consumption of processed foods in the prevention and treatment of obesity. Additionally, new therapeutic strategies should be explored that focus on modulating gut microbiota through diet. On the other hand, although the types of bacteria associated with obesity may vary in different studies, it is possible to identify certain predominant bacteria in each BMI classification, especially between the group of lean individuals and the group of obese individuals. It is worth mentioning that in Peru, no studies have yet been conducted on the association between gut microbiota composition and obesity. Therefore, it is important to carry out research in various regions of the country to obtain information on gut microbiota in the Peruvian population and its relationship with obesity according to BMI classification, as well as its relationship with the diet consumed by specific groups. These studies will provide fundamental data to develop effective prevention and treatment strategies for obesity in the Peruvian population.

BIBLIOGRAPHIC REFERENCES

Andoh, A, Nishida, A, Takahashi, K, Inatomi, O, Imaeda, H, Bamba, S, Kito, K., Sugimoto, M., & Kobayashi, T. (2016). Comparison of the gut microbial community between obese and Lean Peoples using 16s gene sequencing in a Japanese population. Journal of Clinical Biochemistry and Nutrition. *59*(1): 65–70. https://doi.org/10.3164/jcbn.15-152

Basain, J., Valdés, C., Miyar, E., Linares, H., & Martínez, A. (2015). Alteraciones en el microbiota intestinal por la dieta y su repercusión en la génesis de la obesidad.

MEDISAN. *19*(12): 1536-1546. http://scielo.sld.cu/scielo.php?script=sci_ arttext&pi- d=S1029-30192015001200013&lng=es.

Borgo, F., Garbossa, S., Riva, A., Severgnini, M., Luigiano, C., Benetti, A., Pontriroli, A., Mo- race, G., & Borghi, E. (2018). Body mass index and sex affect diverse microbial niches within the gut. Frontiers in Microbiology. 9. https://doi.org/10.3389/fmicb.2018.00213

Chávez-Carbajal, A., Nirmalkar, K., Pérez-Lizaur, A., Hernández-Quiroz, F., Ramírez-del-Alto, S., García-Mena, J., & Hernández-Guerrero, C. (2019). Gut Microbiota and Predicted Metabolic Pathways in a Sample of Mexican Women Affected by Obesity and Obesity Plus Metabolic Syndrome. International Journal of Molecular Sciences. *20*(2):438. ht- tps://doi.org/10.3390/ijms20020438

Chen, J., Ryu, E., Hathcock, M., Ballman, K., Chia, N., Olson, J., & Nelson, H. (2016). Impact of demographics on human gut microbial diversity in a US Midwest population. PeerJ 4: e1514 https://doi.org/10.7717/peerj.1514

Ching-Hung, T., & Chun-Ying, W. (2019). The gut microbiome in obesity. Journal of the For- mosan Medical Association. *118*(1) S3-S9

Davis, J., Collier, F., Mohebbi, M., Stuart, A., Loughman, A., Pasco, J., & Jacka, F. (2020). Obesity, Akkermansia muciniphila, and Proton Pump inhibitors: Is there a link? Obesity Research and Clinical Practice. *14*(6):524–30. https://doi.org/10.1016/j.orcp.2020.10.006

Duan, M., Wang, Y., Zhang, Q., Zou, R., Guo, M., & Zheng, H. (2021). Characteristics of gut microbiota in people with obesity. PLOS ONE. *16*(8). https://doi.org/10.1371/journal. pone.0255446

Ettehad, F., Moshiri, A., Sadat, M., Riazi, S., Taati, M., Sadati, S., Ghaheri, A., Masoomi, M., Va- ziri, F., Fatet, A., Rohani, P., Tarashi, S., Masotti, A., Badi, S., & Siadat, S. (2020). The first report of differences in gut microbiota composition between obese and normal weight Iranian subjects. Iranian Biomedical Journal. *24*(3):148–54. https://doi.org/10.29252/ibj.24.3.148

Gao X, Zhang M, Xue J, Huang J, Zhuang R, Zhou X, Zhang, H., Fu, Q., & Hao, Y. (2018). Body mass index differences in the gut microbiota are gender specific. Frontiers in Microbiology. 9. https://doi.org/10.3389/fmicb.2018.01250 https://www.sciencedirect.com/ science/article/pii/S0929664618304376?via%3Dihub#bib9

Jinatham, V., Kullawong, N., Kespechara, K., Gentekaki, E., & Popluechai, S. (2018). Compa- rison of gut microbiota between lean and obese adult Thai individuals. Microbiology and Biotechnology Letters. *46*(3):277–87. https://doi.org/10.4014/mbl.1711.11003

John, G., & Mullin, G. (2016). The Gut Microbiome and Obesity. Current Oncology Reports. *18*(45). https://doi.org/10.1007/s11912-016-0528-7

Junjie, Q., Ruiqiang, L., Jeroen, R., Manimozhiyan, A., Kristoffer, S., Chaysavanh, M., Trine N., Nicolas, P., Levenez, F., Takuji Y., Mende, D., Junhua, L., Junming, X., Shao Chuan, L., Dongfang, L., Jianjun, C., Bo, W., Huiqing, L., Huisong, Z … Wang, J. (2010). A human gut microbial gene catalogue established by metagenomic sequencing. Nature. *464*(7285): 59–65. https://doi.org/10.1038/nature08821

Kaplan, R., Wang, Z., Usyk, M., Sotres-Alvarez, D., Daviglus, M., Schneiderman, N., Gregory, A., Talavera, M., Gellman, B., Jee-Young M., Vázquez-Baeza, Y., McDonald, D., Wi- lliams-Nguyen, J., Wu, M., North, K., Shaffer, J., Christopher, C., Qibin, S., Isasi, C. … Burk, R. (2019). Gut microbiome composition in the Hispanic Community Health Study/ study of Latinos is shaped by geographic relocation, environmental factors, and obesity. Genome Biology. *20*(1). https://doi.org/10.1186/s13059-019-1831-z

Koliada, A., Syzenko, G., Moseiko, V., Budovska, L., Puchkov, K., Perederiy, V., Gavalko, Y., Dorofeyev, A., Romanenko, M., Tkach, S., Sineok, L., Lushchak, O., & Vaiserman, A. (2017). Association between body mass index and *Firmicutes/ Bacteroidetes* Ratio in an adult Ukrainian population. BMC Microbiology. *17*(1). https://doi.org/10.1186/s12866- 017-1027-1

Lv, Y., Qin, X., Jia, H., Chen, S., Sun, W., & Wang, X. (2019). The association between gut microbiota composition and BMI in Chinese male college students, as analysed by next-generation sequencing. British Journal of Nutrition. *122*(9), 986–995. doi:10.1017/ S0007114519001909

Oduaran, O., Tamburini, F., Sahibdeen, V., Brewster, R., Gómez-Olivé, F., Kahn, K. A., Norris, S. M., Tollman, R., Twine, A. N., Wade, R. G., Wagner, Z., Lombard, A., & Hazelhurst, S. (2020). Gut microbiome profiling of a rural and urban South African cohort reveals biomarkers of a population in lifestyle transi- tion. BMC Microbiology. *20*(1). https://doi.org/10.1186/s12866-020-02017-w

Org, E., Blum, Y., Kasela, S., Mehrabian, M., Kuusisto, J., Kangas, A.J., Pasi, S., Zeneng, W., Ala-Korpela, S., Markku, L., & Aldons, J. (2017). Relationships between gut microbiota, plasma metabolites, and metabolic syndrome traits in the METSIM cohort. Genome Biology. *18*(1). https://doi.org/10.1186/s13059-017-1194-2

Organisation for Economic Co-operation and Development (OECD). (2019). The Heavy Burden of Obesity: The Economics of Prevention, OECD Health Policy Studies, OECD Publishing, https://doi.org/10.1787/67450d67

Organización Mundial de la Salud (OMS). (2020). Obesidad. https://www.who.int/es/health-to- pics/obesity#tab=tab_1

Organización Mundial de La Salud. (2022). A different scale: Global action to address obesity. https://www.who.int/news-room/events/detail/2022/05/24/default-calendar/a-diffe-rent-scale-global-action-to-address-obesity

Palmas, V., Pisanu, S., Madau, V., Casula, E., Deledda, A., Cusano, R., Uva, S., Vascellari, A., Loviselli, A., Manzin, A., & Velluzzi, F. (2021). Gut microbiota markers associated with obesity and overweight in Italian adults. Scientific Reports. *11*(1). https://doi.org/10.1038/ s41598-021-84928-w

Pinart, M., Dötsch, A., Schlicht, K., Laudes, M., Bouwman, J., Forslund, S.K., Pischon, T., & Nimptsch, K. (2022). Gut Microbiome Composition in Obese and Non-Obese Persons: A Systematic Review and Meta-Analysis. Nutrients. *14*(12). https://doi.org/10.3390/ nu14010012

Rubio, S., Pacheco-Orozco, R. A., Gómez, A. M., Perdomo, S., & García-Robles, R. (2020). Secuenciación de Nueva Generación (NGS) de adn: Presente y futuro en la práctica clínica. Universitas Médica.61(2). https:// doi.org/10.11144/Javeriana.umed61-2.sngs

Salah, M., Azab, M., Ramadan, A., & Hanora, A. (2019). New insights on obesity and diabetes from gut microbiome alterations in Egyptian adults. OMICS: A Journal of Integrative Biology. *23*(10):477–85. https://doi.org/10.1089/omi.2019.0063

Yun, Y., Kim, H., Kim, S. E., Heo, S. G., Chang, Y., Ryu, S., Shin, H., & Hyung-Lae, K. (2017). Comparative analysis of gut microbiota associated with body mass index in a large Korean cohort. BMC Microbiology. *17*(1). https://doi.org/10.1186/s12866-017-1052-0