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The Mediterranean Diet as a Potential Solution to the Gut Microbiome Dysbiosis in Psoriasis Patients

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Abstract

Background: Adherence to a Mediterranean Diet (MeD) has been associated with lower disease severity in patients with psoriasis. However, the mechanism behind how this diet may lead to disease modification remain understudied. Recent studies have revealed dysbiosis of the gut microbiome in patients with psoriasis suggestive of inflammation and altered immune regulation. Diet affects the gut microbiome and this review aims to evaluate whether correcting this dysbiosis may be one theoretical mechanism by which the MeD may be associated with lower psoriasis severity.

Methods: A literature search of the PubMed database was conducted for the terms 1) 'psoriasis' and 'microbiome' or 'microbiota,' and 2) 'Mediterranean diet' and 'microbiome' or 'microbiota' with manual screening for relevant articles. In total, we identified 9 relevant primary research studies investigating the gut microbiome in patients with psoriasis and 16 relevant primary research studies investigating changes in the microbiota for those consuming a MeD.

Results: Though varying in exact levels of certain bacteria, studies analyzing the microbiome in psoriasis revealed dysbiosis. Those analyzing the effect of the Mediterranean diet on the microbiome revealed beneficial changes, including alleviating some of the same alterations seen in the microbiome of those with psoriasis.

Conclusion: Microbiota change is a possible mechanism why the MeD has previously been associated with lower psoriasis severity.

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Ethical Statement
Ethical Approval and Consent
Our institution does not require ethics approval for reporting results of literature reviews. Informed consent for patient information to be published in this article was not obtained because no new patient information was obtained (i.e., information not in previously published studies) for purposes of this review. Guidelines for humane animal treatment did not apply to the present study because this study did not involve animals.

Keywords

psoriasis; microbiome; mediterranean diet; dysbiosis; psoriasis area and severity index; psoriasis; lifestyle modification; diet

Introduction

Psoriasis is a chronic inflammatory skin disorder, affecting 2%–4% of the Western population with incidence continuing to increase.[1,2] Psoriasis affects more than just skin, and is associated with co-morbidities such as cardiovascular disease, metabolic syndrome, and psoriatic arthritis[1]

While there have been exciting developments in medical treatments for psoriasis, the effects of lifestyle factors remains understudied. Lifestyle modification, especially dietary changes, is of interest to patients.[3] Studies show that most patients living with psoriasis have tried dietary changes in an attempt to control their disease.[4]

One diet of interest is the Mediterranean diet (MeD) due to its anti-inflammatory effects.[5] The MeD focuses on increased consumption of nutrient and anti-oxidant rich foods such as vegetables, olive oil, and legumes while limiting meat and dairy.[6] The diet has been widely studied with benefits such as improved cardiometabolic health and slowed cognitive decline.[5,6] In the few studies examining psoriasis and the MeD, results suggest the diet may be helpful in reducing psoriasis severity.[7] For instance, a cohort study of 3557 psoriasis patients found that dietary patterns more consistent with the MeD were associated with a lower psoriasis severity.[8] Given the MeD's many benefits, efforts have been made to determine by what physiologic mechanism the MeD causes its positive impact.[6] Its effect on the gut microbiome is one mechanism that has been explored.

The gut microbiome is a population of microbes in the gastrointestinal tract, which impact metabolism and immune functioning.[9] While the gut microbiome's existence has been known for many years, its association with disease and ability to be manipulated for better health outcomes is an exciting area of interest. The consumption of different foods alters the gut microbiome, with some microbiota associated with good health, and others associated with pro-inflammatory effects potentially leading to obesity and insulin resistance.[9]

When discussing the microbiome, one should be familiar with the concepts of alpha- and beta-diversity, microbial diversity, microbial richness, and bacterial taxonomy. Microbial richness can be described as the number of taxa while microbial diversity is the different types of taxa. Alpha-diversity encompasses abundance, while beta-diversity is the variability in the identity of taxa within that community.[10] The taxonomic classifications of bacteria are important as changes can occur at any of these levels (Figure 1).

In this review, we evaluate what is known about the gut microbiome in patients with psoriasis and in those who follow a MeD. We also propose that changes in gut microbiota induced by a MeD as a theoretical mechanism for why the diet is associated with lower disease severity.

Methods

A literature search of the PubMed database was conducted for the terms 1) 'psoriasis' and 'microbiome' or 'microbiota, ' and 2) 'Mediterranean diet' and 'microbiome' or 'microbiota' Our search was limited to English-language articles and those published prior to August 11th, 2023. For review, the authors manually identified relevant articles discussing the gut microbiome and psoriasis or the MeD specifically. Duplicate articles were excluded. In total, we identified 9 relevant primary research studies investigating the gut microbiome in patients with psoriasis and 16 relevant primary research studies investigating changes in the microbiota for those consuming a MeD as the study group.

On September 8th, 2023, our literature search was updated to include an article published August 31st, 2023.

Results

The Gut Microbiome in Patients With Psoriasis

One of the earlier studies to explore the microbiome in patients with psoriasis was conducted by Scher et al in 2015. They found that patients with psoriasis and PsA had lower relative abundance of multiple intestinal bacteria (reduced diversity) compared to healthy controls.[12] Their findings are summarized in Table 1. It is accepted in other fields that low diversity in the microbiota is correlated with disease and reduced ability to cope with bodily insults.[13] Additional studies (Table 1) revealed conflicting results surrounding diversity, with two studies confirming reduced diversity in psoriasis patients, five with no significant difference, and one finding increased diversity in their psoriasis cohort.[12–20]

As seen in the cladogram in Figure 1, taxonomic categorization of bacteria begins at the phylum and is followed by class.[11] At the phyla level, the human gut microbiome is composed primarily of the *Firmicutes* and *Bacteroidetes*. High levels of *Firmicutes* compared to *Bacteroidetes* (increased F/B ratio) has been correlated with greater BMI and higher levels of inflammatory markers.[21,22] In a 2018 Taiwanese study by Chen et al, researchers found an increased *Firmicutes* and decreased *Bacteroidetes* phyla in psoriasis patients when compared to age, gender, BMI, and geography matched controls, leading to an increased F/B ratio. Increased F/B ratios in psoriasis patients were found in three additional studies: a Caucasian cohort (n = 55) evaluated by Dei-Cas et al, Spanish psoriasis patients (n = 19) evaluated by Hidalgo-Cantabrana et al, and a cohort from Israel (n = 24) evaluated by Shapiro et al.[18] Short chain fatty acids (SCFAs) such as butyrate are produced by some bacteria and have been suggested to promote epithelial integrity and exert an anti-inflammatory effect.[23] A higher F/B ratio leads to altered SCFA production – including decreasing butyrate - potentially explaining the negative metabolic associations.[24] Interestingly, there was a reduction in the *Bacteroidetes* phylum found in the 2015 study by Scher et al[12]'s study in psoriasis patients vs those with psoriatic arthritis, presumably raising the F/B ratio, though this was not commented on specifically and this finding did not reach significance. The most recent study on the gut microbiome in psoriasis performed mendelian randomization on published large-scale genome wide association studies comparing greater than 10000 patients with psoriasis to healthy controls. They found that *Bacteroidetes* have a protective role in psoriasis (OR .81 [95% CI .67–.98]), further supporting the findings of low *Bacteroidetes* in psoriasis patients from previous studies.[25]

The next level of taxonomy is the genera level. In terms of significant findings for Scher at al., *Parabacteroides* genus was reduced compared to healthy controls which was replicated in one other study.[12,17] Tan et al sequenced the microbiome in a Chinese cohort (n = 14) finding several significant changes, including an increase in the *Bacteroides* genus and decrease in the *Akkermansia* genus including the *Akkermansia muciniphila* species. Higher *Bacteroides* is typically seen in animal-based diets, and though some species in the genus have beneficial properties, an overgrowth can degrade important intestinal mucus leading to intestinal inflammation and is associated with colonic cancer.[26] *Bacteroides* can also be thought of in the context of the *Prevotella/Bacteroides* (P/B) ratio, where a high ratio (lower *Bacteroides*) is associated with improved metabolic status.[27] Decreases in *Akkermansia muciniphila* are associated with chronic inflammatory states including obesity.[19] This decrease in the *Akkermansia* genus was replicated in a cohort of psoriasis patients (n = 32) in Taiwan and another cohort (n = 21) from Brazil.[13,15] However, other studies have challenged these findings with Codoner et al finding an increase in the *Akkermansia* genus and a decrease in the *Bacteroides* genus in their cohort of 52 psoriasis patients from Spain when compared to unmatched controls (n = 300) from the Human Microbiome Project. This decrease in *Bacteroides* was also seen in a separate cohort from Spain (n = 19) compared to age and geography matched controls.[17] These differences between studies may be due to the differences in severity of psoriasis, matching protocols used for controls, and geography of the study populations particularly considering both cohorts with a decrease in the *Bacteroides* genus were from Spain whereas 2/3 studies that found an *Akkermansia* genus decrease evaluated East Asian patients. Another consistency across both the studies out of Spain was increased *Blautia* genus in the psoriasis groups.[14,17] However, despite analyzing the microbiome of patients from the same country of Spain, Codoner et al and Hidalgo-Cantabrana et al did have some conflicting findings, with Codoner et al finding increased *Faecalibacterium* genus which was supported by an additional study, while Hidalgo et al found a decrease in psoriasis patients.[14,16,17] From the mendelian randomization study, the genus *Prevotella* was found to possibly have a protective impact (OR .87 [95% CI: .76–1.00] whereas *Eubacterium fissicatena* conferred an increase risk for psoriasis (OR 1.22 [95% CI: 1.10–1.35]).[25] The *Prevotella* genus was found to be decreased in a psoriasis cohort in a study that took place in Israel.[18] In the same family as *Prevotella*, the genus *Paraprevotella* was found to be decreased in two studies.[13,17]

Within genera, there are a few species of particular interest such as the discussed *Akkermansia muciniphila* species. Similarly, within the *Faecalibacterium* genus, one notable species is *Faecalibacterium prausnitzii*. Which is one of the main butyrate producers in the colon and its presence is reduced in inflammatory intestinal disorders.[28] In their study, Codoner et al found that although the *Faecalibacterium* genus was increased in their psoriasis cohort, *F prausnitzii* was actually reduced.[16] Hidalgo-Cantabrana et al did not report to the species level, though presumably *F prausnitzii* was reduced given the genus was reduced as a whole.[14] *Prevotella copri* is a member of the Prevotella genus, and two studies had conflicting significant results regarding levels in psoriasis patients.[13,18] This species is associated with high fiber, low fat diets and often linked with desirable health, although conflicting reports exist.[29]

The Gut Microbiome in Patients Consuming a Mediterranean Diet

Research on the effects of the Mediterranean diet on the gut microbiome can similarly be classified by taxonomic class. Of the studies that included results on diversity, 8 found no change, while 6 found increased diversity and/or richness (Table 2).[21,30–41] Studies that showed no change in microbiota were shorter duration (4–7 days) with less time for adherence, suggesting that to achieve a meaningful, anti-inflammatory change in one's microbiome, following the MeD for a longer timeframe leads to a greater likelihood of benefitting.[33,40] Others researched the effects on diversity more intricately, such as van Soest et al[21] who showed that increased alpha diversity was positively correlated with peanuts, seeds, nuts, and fresh fruit and negatively correlated with BMI. Some studies also chose to research the effects of the MeD on bacterial richness rather than diversity and found that richness was either increased or maintained.[30,42]

Starting at the phyla level, Haro et al[32] found that obese patients with metabolic syndrome were found to have decreased *Bacteroidetes* phylum at baseline which was increased following the MeD diet. Similarly, Van Soest et al,[21] Ismael et al, and Illesecas et al showed an increase in *Bacteroidetes* phylum following the MeD.[21,30,34] Van Soest specifically showed a positive relationship between plant-based carbohydrates and the *Bacteroidetes* phylum and an inverse relationship between protein and *fat*. Zhu et al evaluated the MeD vs a fast food (FF) diet. They found that although the phylum Firmicutes was increased following the MeD,[40] there was no significant change found in F/B ratio, which was consistent with one additional study.[9,19,36] Similar to previous studies associating a high F/B ratio with inflammation/obesity, Zhu et al found F/B ratio to be negatively correlated with HDL-C, emphasizing a possible negative metabolic impact.[21,40]

Genera was widely analyzed by the reviewed studies. Pagliali et al found a decrease in *Parabacteroides* following the MeD, while Zhu et al found an increase in this genus following a FF diet.[38,40] *Parabacteroides* has previously been associated with hypertension.[43] Ismael et al[30] quantified their results after varying time points, and found that after 4 weeks of MeD counseling, a higher ratio of *Prevotella* to *Bacteriodes* was detected. This P/B ratio has been examined in other studies such as Meslier et al[42] who found that the MeD may improve insulin sensitivity in patients with high baseline levels of the generally inflammatory *Bacteroides* genus and lower levels of *Prevotella* genus. The anti-inflammatory *Akkermansia* genus was increased by the MeD in two studies.[34,36]

Finally, at the most individualistic level there are species. Van Soest et al and Meslier et al found that animal product-rich foods resulted in a significant elevation in species associated with inflammation such as *R gnavus*, while plant-based food led to an increase in anti-inflammatory species such as *F prausnitzii*, emphasizing the importance of a vegetable centric diet, such as the MeD for gut health.[21,42] Tagliamonte also found a significant increase in *F prausnitzii*, in addition to *Akkermansia muciniphila* with the MeD which is decreased in T2DM, hypertension, obesity and IBD.[44] Vitale et al found similar results in their cohort of 29 overweight/obese individuals, with a significant increase in beneficial bacteria such as *Akkermansia muciniphila*, and a decrease in proinflammatory species. Specifically *Akkermansia muciniphila* is associated with increased production of butyrate, improving glucose metabolism and insulin sensitivity.[35] Results of Barber et al. study of 20 healthy similarly showed an increase in the butyrate-producing, colon protective species of *Akkermensia* genus.[41]

Discussion

Based on the dysbiosis found in psoriasis patients and the possible changes induced by the MeD on the gut microbiome, this may be one mechanism that the MeD may exert benefit for these patients. One way is by decreasing the F/B ratio by increasing *Bacteroidetes* as found in 4 studies and thus helping restore SCFA balance and promoting butyrate production.[21,30–33,45] This in turn could alleviate intestinal and systemic inflammation, having profound implications for psoriasis. Additional butyrate producers of the gut include species in the *Akkermansia* genus and *Faecalibacterium prausnitzii*, thus the MeD also promotes SCFA production through increasing these bacteria.[21,31,32,34–37,42,44] This is of particular interest as the *Akkermansia* genus was found to be low in several studies on psoriasis and *F prausnitzii* or the *Faacalibacterium* genus as a whole was found to be reduced in two studies[12,13,15,19] Overall, the MeD has been suggested to alter the microbiota in several ways to promote an immune-regulated and anti-inflammatory state that would presumably be beneficial to psoriasis.

Cardiovascular disease, metabolic syndrome, and obesity are co-morbidities associated with psoriasis and also can be improved by the MeD.[1] The study by Haro et al suggests the MeD-induced microbiota changes may be more pronounced in those with obesity and/or metabolic syndrome. The MeD diet reduces the risk of cardiovascular disease, type 2 diabetes, and neurodegenerative diseases.[5,46] In Rinott et al,[45] the researchers employed the Green MED score to determine adherence to a plant-based diet. They discovered that higher adherence to the Green MED diet, which reduces animal-based food consumption even further than the traditional MeD, resulted in a more significant shift in the microbiome, as well as a reduction in markers linked to cardiometabolic disease. This is another argument for encouraging this dietary pattern in patients with psoriasis. By adopting a MeD, one has the potential to not only improve their skin disease but alter their microbiome in a way that improves overall health and wellness. This is especially pertinent to psoriasis patients, given their higher propensity to develop cardiovascular and metabolic co-morbidities.[47] Many studies proved the MeD diet’s positive effects as it pertain to metabolic syndrome by evaluating markers such as insulin sensitivity and hypertension.[30,42,45]

The precise foods that impart beneficial effects within the MeD has also been studied.[5] The MeD diet has a similar total fat intake to western diets, however more of that fat comes from omega-3s such as in fish and monounsaturated fatty acids such as olive oil vs saturated fats.[5] There is evidence that this pattern of fat intake reduces LDL and triglycerides while raising beneficial HDL cholesterol, providing cardiovascular benefit.[5] Furthermore, high omega-3 intake impacts prostaglandin metabolism by suppressing pro-inflammatory pathways, such has cycloxygenase-2 (COX-2), one of the targets of non-steroidal anti-inflammatory medications.[48] It is also important to note the lower intake of dairy products and land meats in the MeD than the western diet when considering its metabolic advantages. Furthermore, the high fiber in the MeD has a direct impact on the gut microbiome, positively influencing colonic production of butyrate. High fiber intake decreases risk of insulin resistance, another benefit.[5]

Notably, Dei-cas et al developed a Psoriasis-Microbiota Index (PMI) that could discriminate between psoriasis patients and controls with high sensitivity and specificity. This study is the first to propose a PMI with the ability to discriminate between psoriasis patients and age-sex-and BMI matched controls and between samples from communities of different continents by performing a meta-analysis.[14] The successful development of a PMI suggests a signature dysbiosis of psoriasis patients Figure 2.

However, an important consideration is the ability to adhere to the MeD. Studies have indicated that significant changes in the microbiome only occur with a high level of adherence over extended periods of time. This suggests that to fully reap the benefits of microbial changes, one should follow a high-adherence pattern. In Meslier et al[42] the most significant changes in the microbiome were present during the high-adherence period, as defined by the MeD index. Pastor-Ibanez utilized a scoring system called MEDAS, with a score of 10 or higher being considered as high adherence. The study found significant results only in the high-adherence group, such as an increase in the presence of the fiber-degrading bacteria *Burkholderiales* and the anti-inflammatory bacteria *Bifidobacterium* and *Lactobacillus*.[39] Studies that showed no change in microbiota were shorter duration (4–7 days) with less time for the diet to be followed.[33,40] To achieve a meaningful, anti-inflammatory change in one's microbiome, the stricter one adheres to the MeD and for a longer timeframe the greater likelihood to reap benefits. A limitation of the studies evaluating the microbiome in those following a MeD was the study populations were not patients with psoriasis. Furthermore, it is feasible that an individual who adheres closely to a diet may also adhere more closely to their prescribed medications, which themselves will impact psoriasis severity and have even been suggested to affect the gut microbiome.[49]

Conclusion

The MeD has numerous health benefits including an association with lower psoriasis severity. A relationship between the gut microbiome and the MeD has been established. The changes induced by the MeD in the gut microbiome may possibly be beneficial for patients with psoriasis based on the dysbiosis patterns found in several studies, but this cannot be said with certainty as none of the MeD-microbiome studies were performed using psoriasis patients. Regardless, given the potential benefit for psoriasis and the overall state of health promoted by the MeD, there is little harm in recommending this diet to psoriasis patients who are interested in exploring if diet can impact their disease. Patients who do pursue a MeD should not stop their prescribed topical or systemic medicines.

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References

1. Parisi R, Symmons DPM, Griffiths CEM, Ashcroft DM. Global epidemiology of psoriasis: a systematic review of incid ence and prevalence. J Invest Dermatol. 2013;133(2):377–385. doi:10.1038/jid.2012.339. [PubMed: 23014338]
2. AlQassimi S, AlBrashdi S, Galadari H, Hashim MJ. Global burden of psoriasis – comparison of regional and global epidemiology, 1990 to 2017. Int J Dermatol. 2020;59(5):566–571. doi:10.1111/ijd.14864. [PubMed: 32250451]
3. Ingkapairoj K, Chularojanamontri L, Chaiyabutr C, Silpaarcha N, Wongpraparut C, Bunyaratavej S. Dietary habits and perceptions of psoriatic patients: Mediterranean versus Asian diets. J Dermatol Treat. 2022;33(4):2290–2296. doi:10.1080/09546634.2021.1959500.
4. Afifi L, Danesh MJ, Lee KM, et al. Dietary behaviors in psoriasis: patient-reported outcomes from a U.S. National survey. Dermatol Ther. 2017;7(2):227–242. doi:10.1007/s13555-017-0183-4.
5. Romagnolo DF, Selmin OI. Mediterranean diet and prevention of chronic diseases. Nutr Today. 2017;52(5):208. doi:10.1097/NT.0000000000000228. [PubMed: 29051674]
6. Mazza E, Ferro Y, Pujia R, et al. Mediterranean diet in healthy aging. J Nutr Health Aging. 2021;25(9):1076–1083. doi:10.1007/s12603-021-1675-6. [PubMed: 34725664]
7. Barrea L, Balato N, Di Somma C, et al. Nutrition and psoriasis: is there any association between the severity of the disease and adherence to the Mediterranean diet? J Transl Med. 2015;13:18. doi:10.1186/s12967-014-0372-1. [PubMed: 25622660]
8. Phan C, Touvier M, Kesse-Guyot E, et al. Association between mediterranean anti-inflammatory dietary profile and severity of psoriasis. JAMA Dermatol. 2018;154(9):1017–1024. doi:10.1001/jamadermatol.2018.2127. [PubMed: 30046840]
9. Armet AM, Deehan EC, O'Sullivan AF, et al. Rethinking healthy eating in light of the gut microbiome. Cell Host Microbe. 2022;30(6):764–785. doi:10.1016/j.chom.2022.04.016. [PubMed: 35679823]
10. Walters KE, Martiny JBH. Alpha-, beta-, and gamma-diversity of bacteria varies across habitats. PLoS One. 2020;15(9): e0233872. doi:10.1371/journal.pone.0233872. [PubMed: 32966309]
11. Ikee R, Sasaki N, Yasuda T, Fukazawa S. Chronic kidney disease, gut dysbiosis, and constipation: a burdensome triplet. Microorganisms. 2020;8(12):1862. doi:10.3390/microorganisms8121862. [PubMed: 33255763]
12. Scher JU, Ubeda C, Artacho A, et al. Decreased bacterial diversity characterizes the altered gut microbiota in patients with psoriatic arthritis, resembling dysbiosis in inflammatory bowel disease. Arthritis Rheumatol. 2015;67(1):128–139. doi:10.1002/art.38892. [PubMed: 25319745]
13. Schade L, Mesa D, Faria AR, et al. The gut microbiota profile in psoriasis: a Brazilian case-control study. Lett Appl Microbiol. 2022;74(4):498–504. doi:10.1111/lam.13630. [PubMed: 34897759]
14. Dei-Cas I, Giliberto F, Luce L, Dopazo H, Penas-Steinhardt A. Metagenomic analysis of gut microbiota in non-treated plaque psoriasis patients stratified by disease severity: development of a new Psoriasis-Microbiome Index. Sci Rep. 2020;10(1):12754. doi:10.1038/s41598-020-69537-3. [PubMed: 32728075]
15. Chen YJ, Ho HJ, Tseng CH, Lai ZL, Shieh JJ, Wu CY. Intestinal microbiota profiling and predicted metabolic dysregulation in psoriasis patients. Exp Dermatol. 2018;27(12):1336–1343. doi:10.1111/exd.13786. [PubMed: 30238519]
16. Codoñer FM, Ramírez-Bosca A, Climent E, et al. Gut microbial composition in patients with psoriasis. Sci Rep. 2018;8(1):3812. doi:10.1038/s41598-018-22125-y. [PubMed: 29491401]
17. Hidalgo-Cantabrana C, Gómez J, Delgado S, et al. Gut microbiota dysbiosis in a cohort of patients with psoriasis. Br J Dermatol. 2019;181(6):1287–1295. doi:10.1111/bjd.17931. [PubMed: 30920647]

18. Shapiro J, Cohen NA, Shalev V, Uzan A, Koren O, Maharshak N. Psoriatic patients have a distinct structural and functional fecal microbiota compared with controls. J Dermatol. 2019; 46(7):595–603. doi:10.1111/1346-8138.14933. [PubMed: 31141234]
19. Tan L, Zhao S, Zhu W, et al. The Akkermansia muciniphila is a gut microbiota signature in psoriasis. Exp Dermatol. 2018; 27(2):144–149. doi:10.1111/exd.13463. [PubMed: 29130553]
20. Chang HW, Yan D, Singh R, et al. Multiomic analysis of the gut microbiome in psoriasis reveals distinct host–microbe associations. JID Innov. 2022;2(3):100115. doi:10.1016/j.xjidi.2022.100115. [PubMed: 35757783]
21. van Soest APM, Hermes GDA, Berendsen AAM, et al. Associations between pro- and anti-inflammatory gastro-intestinal microbiota, diet, and cognitive functioning in Dutch healthy older adults: the NU-age study. Nutrients. 2020;12(11):3471. doi:10.3390/nu12113471. [PubMed: 33198235]
22. Verdam FJ, Fuentes S, De Jonge C, et al. Human intestinal microbiota composition is associated with local and systemic inflammation in obesity: obese Gut Microbiota and Inflammation. Obesity. 2013;21(12):E607–E615. doi:10.1002/oby.20466. [PubMed: 23526699]
23. Portincasa P, Bonfrate L, Vacca M, et al. Gut microbiota and Short chain fatty acids: implications in glucose homeostasis. Int J Math Stat. 2022;23(3):1105. doi:10.3390/ijms23031105.
24. Komaroff AL. The microbiome and risk for obesity and diabetes. JAMA. 2017;317(4):355. doi:10.1001/jama.2016.20099. [PubMed: 28006047]
25. Zang C, Liu J, Mao M, Zhu W, Chen W, Wei B. Causal associations between gut microbiota and psoriasis: a mendelian randomization study. Dermatol Ther. 2023;13(10). doi:10.1007/s13555-023-01007-w. Published online August 31.
26. Zafar H, Saier MH. Gut *Bacteroides* species in health and disease. Gut Microb. 2021;13(1):1848158. doi:10.1080/19490976.2020.1848158.
27. Precup G, Vodnar DC. Gut Prevotella as a possible biomarker of diet and its eubiotic versus dysbiotic roles: a comprehensive literature review. Br J Nutr. 2019;122(2):131–140. doi:10.1017/S0007114519000680. [PubMed: 30924428]
28. Lopez-Siles M, Duncan SH, Garcia-Gil LJ, Martinez-Medina M. Faecalibacterium prausnitzii: from microbiology to diagnostics and prognostics. ISME J. 2017;11(4):841–852. doi:10.1038/ismej.2016.176. [PubMed: 28045459]
29. Yeoh YK, Sun Y, Ip LYT, et al. Prevotella species in the human gut is primarily comprised of Prevotella copri, Prevotella stercorea and related lineages. Sci Rep. 2022;12(1):9055. doi:10.1038/s41598-022-12721-4. [PubMed: 35641510]
30. Ismael S, Silvestre MP, Vasques M, et al. A pilot study on the metabolic impact of mediterranean diet in type 2 diabetes: is gut microbiota the key? Nutrients. 2021;13(4):1228. doi:10.3390/nu13041228. [PubMed: 33917736]
31. Ghosh TS, Rampelli S, Jeffery IB, et al. Mediterranean diet intervention alters the gut microbiome in older people reducing frailty and improving health status: the NU-AGE 1-year dietary intervention across five European countries. Gut. 2020;69(7): 1218–1228. doi:10.1136/gutjnl-2019-319654. [PubMed: 32066625]
32. Haro C, García-Carpintero S, Rangel-Zúñiga OA, et al. Consumption of two healthy dietary patterns restored microbiota dysbiosis in obese patients with metabolic dysfunction. Mol Nutr Food Res. 2017;61(12):1700300. doi:10.1002/mnfr.201700300.
33. Forteza F, Bourdeau-Julien I, Nguyen GQ, et al. Influence of diet on acute endocannabinoidome mediator levels post exercise in active women, a crossover randomized study. Sci Rep. 2022;12:8568. doi:10.1038/s41598-022-10757-0. [PubMed: 35595747]
34. Illescas O, Rodríguez-Sosa M, Gariboldi M. Mediterranean diet to prevent the development of colon diseases: a meta-analysis of gut microbiota studies. Nutrients. 2021;13(7):2234. doi:10.3390/nu13072234. [PubMed: 34209683]
35. Vitale M, Giacco R, Laiola M, et al. Acute and chronic improvement in postprandial glucose metabolism by a diet resembling the traditional Mediterranean dietary pattern: can SCFAs play a role? Clin Nutr. 2021;40(2):428–437. doi:10.1016/j.clnu.2020.05.025. [PubMed: 32698959]

36. Calabrese FM, Disciglio V, Franco I, et al. A low glycemic index mediterranean diet combined with aerobic physical activity rearranges the gut microbiota signature in NAFLD patients. Nutrients. 2022;14(9):1773. doi:10.3390/nu14091773. [PubMed: 35565740]

37. Gómez-Pérez AM, Ruiz-Limón P, Salas-Salvadó J, et al. Gut microbiota in nonalcoholic fatty liver disease: a PREDIMED-Plus trial sub analysis. Gut Microb. 15(1). 2223339. doi:10.1080/19490976.2023.2223339.

38. Pagliai G, Russo E, Niccolai E, et al. Influence of a 3-month low-calorie Mediterranean diet compared to the vegetarian diet on human gut microbiota and SCFA: the CARDIVEG Study. Eur J Nutr. 2020;59(5):2011–2024. doi:10.1007/s00394-019-02050-0. [PubMed: 31292752]

39. Pastor-Ibáñez R, Blanco-Heredia J, Etcheverry F, et al. Adherence to a supplemented mediterranean diet drives changes in the gut microbiota of HIV-1-Infected individuals. Nutrients. 2021;13(4):1141. doi:10.3390/nu13041141. [PubMed: 33808476]

40. Zhu C, Sawrey-Kubicek L, Beals E, et al. Human gut microbiome composition and tryptophan metabolites were changed differently by fast food and Mediterranean diet in 4 days: a pilot study. Nutr Res. 2020;77:62–72. doi:10.1016/j.nutres.2020.03.005. [PubMed: 32330749]

41. Barber C, Mego M, Sabater C, et al. Differential effects of western and mediterranean-type diets on gut microbiota: a metagenomics and metabolomics approach. Nutrients. 2021; 13(8):2638. doi:10.3390/nu13082638. [PubMed: 34444797]

42. Meslier V, Laiola M, Roager HM, et al. Mediterranean diet intervention in overweight and obese subjects lowers plasma cholesterol and causes changes in the gut microbiome and metabolome independently of energy intake. Gut. 2020;69(7): 1258–1268. doi:10.1136/gutjnl-2019-320438. [PubMed: 32075887]

43. Yan Q, Gu Y, Li X, et al. Alterations of the gut microbiome in hypertension. Front Cell Infect Microbiol. 2017;7:381. doi:10.3389/fcimb.2017.00381. [PubMed: 28884091]

44. Tagliamonte S, Laiola M, Ferracane R, et al. Mediterranean diet consumption affects the endocannabinoid system in overweight and obese subjects: possible links with gut microbiome, insulin resistance and inflammation. Eur J Nutr. 2021;60(7):3703–3716. doi:10.1007/s00394-021-02538-8. [PubMed: 33763720]

45. Rinott E, Meir AY, Tsaban G, et al. The effects of the Green-Mediterranean diet on cardiometabolic health are linked to gut microbiome modifications: a randomized controlled trial. Genome Med. 2022;14:29. doi:10.1186/s13073-022-01015-z. [PubMed: 35264213]

46. Becerra-Tomás N, Blanco Mejía S, Viguiliouk E, et al. Mediterranean diet, cardiovascular disease and mortality in diabetes: a systematic review and meta-analysis of prospective cohort studies and randomized clinical trials. Crit Rev Food Sci Nutr. 2020;60(7):1207–1227. doi:10.1080/10408398.2019.1565281. [PubMed: 30676058]

47. Yamazaki F Psoriasis: comorbidities. J Dermatol. 2021;48(6): 732–740. doi:10.1111/1346-8138.15840. [PubMed: 33763899]

48. Jalili M, Hekmatdoost A. Dietary ω−3 fatty acids and their influence on inflammation via Toll-like receptor pathways. Nutrition. 2021;85:111070. doi:10.1016/j.nut.2020.111070. [PubMed: 33545546]

49. Olejniczak-Staruch I, Ciążyǹska M, Sobolewska-Sztychny D, Narbutt J, Skibiǹska M, Lesiak A. Alterations of the skin and gut microbiome in psoriasis and psoriatic arthritis. Int J Mol Sci. 2021;22(8):3998. doi:10.3390/ijms22083998. [PubMed: 33924414]

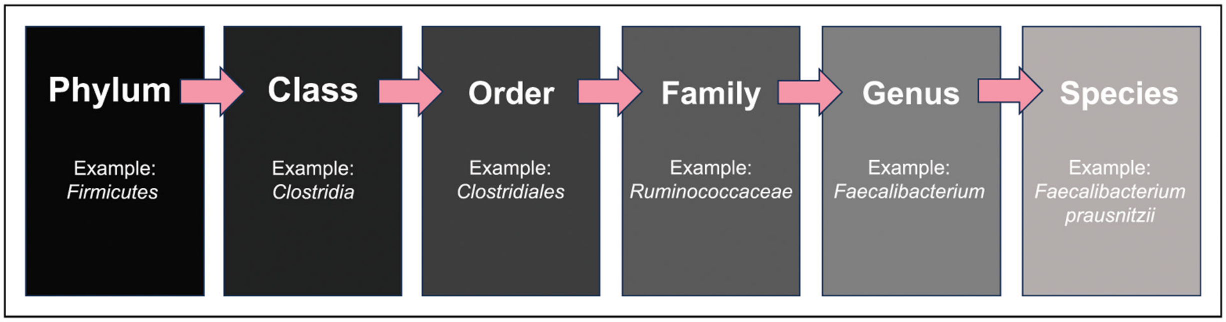

Figure 1.
An example of bacterial taxonomy in the gut.[11]

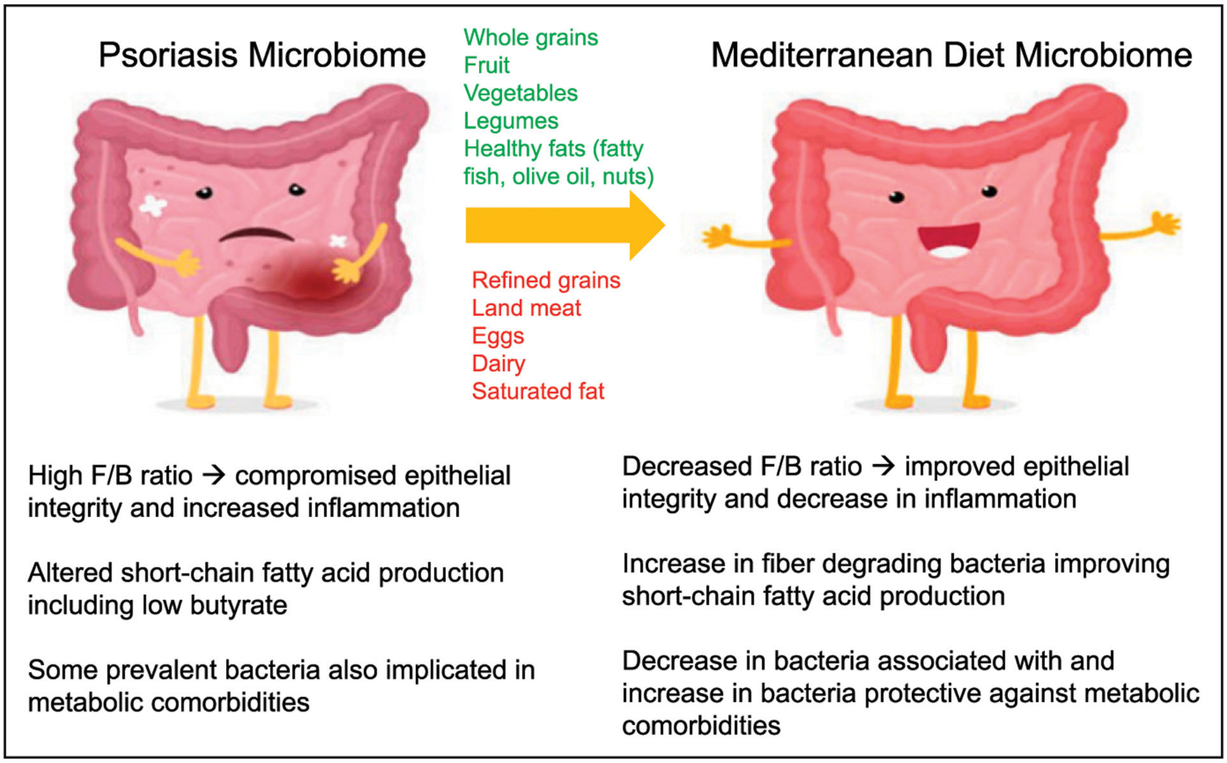

Figure 2.

The colon on the left represents the consequences of some of the proposed dysbiosis in psoriasis patients that the Mediterranean diet may alleviate. The colon on the right represents the relevant changes seen in the Mediterranean diet. The foods listed above the arrow are those eaten in large amounts in the Mediterranean diet, and those below the arrow are eaten sparingly.

Table 1.

Complete Differences Across Studies Evaluating the Gut Microbiome in Patients With Psoriasis Separated by Taxonomic Groupings. A "-" Indicates No Significant Findings in That Taxonomic Grouping for the Study, or the Study Did Not Perform Analysis Within That Grouping. F/B = Firmicutes/ Bacteroidetes Ratio. Pso = Psoriasis. PsA = Psoriatic Arthritis. HC = Healthy Control.

Authors	Cohort	Methods	Psoriasis Microbiome: Diversity	Psoriasis Microbiome: Phyla	Psoriasis Microbiome: Class/ Family	Psoriasis Microbiome: Genera	Psoriasis Microbiome: Species
Chang et al. 2022	United States Pso (n = 33) Age and gender matched controls (n=15)	shotgun metagenomic sequencing	Not significantly different	—	—	—	↑*Bacteroides coprocola* ↑*Bacteroides oleiciplenus* ↑*Bacteroides vulgatus* ↑*Clostridum hylemonae* ↑*Prevotella disiens* ↑*Parabacteroides goldsteinii* ↓*Bifidobacterium psseudocatenulatum* ↓*Bacteroides gallinarum*
Chen et al. 2018	Asian, Taiwan Pso (n = 32) Age, gender, BMI, and geography matched controls (n = 64)	16s rRNA sequencing (hypervaria-ble region V4–V4)	Not significantly different	↑*Firmicutes* and ↓*Bacteroidetes* → ↑ F/B ratio	—	—	↓*Akkermansia* spp.
Codoner et al. 2018	Spain PsO with PASI >6 (n = 52) Controls (n = 300) from Human Microbiome Project	16s rRNA sequencing (hypervariable region V3–V4)	↑ Diversity	—	—	↑*Faecalibact-erium* ↑*Ruminococ-cus* ↓*Bacteroides*	↑*Akkermansia* spp ↓*Faecalibacterium prausnitzii*
Dei-Cas et al. 2020	Caucasian, Argentina Pso (n=55; 28 mild disease; 27 mod-severe) Age, gender, BMI, geography matched controls (n = 27)	16s rRNA sequencing (hypervariable region V4) PMI validity: ROC Analysis; Meta-analysis *Hildago-Cantabrana* et *al*. dataset	Not significantly different	↑*Firmicutes* and ↓*Bacteroidetes* → ↑ F/B ratio	—	↑*Blautia* ↑*Faecalibacterium* ↓*Paraprevotella*	—
Hidalgo-Cantabrana et al. 2019	Spain Pso (n = 19) Age and geography matched controls (n = 20)	16s rRNA sequencing (hypervariable region V2–V3)	↓ Diversity	↑*Actinobacteria* ↑*Firmicutes* and ↓*Bacteroidetes* → ↑ F/B ratio ↓*Proteobacteria*	↑Ruminococcaceae family	Within *Ruminococcaceae* family: ↑*Ruminococcus* ↑*Subdoligraanulum* ↓*Faecalibactrium* Others: ↑*Bifidobactrium* ↑*Blautia* ↑*Collinsella* ↑*Slackia* ↓*Alistipes*	—

Authors	Cohort	Methods	Psoriasis Microbiome: Diversity	Psoriasis Microbiome: Phyla	Psoriasis Microbiome: Class/ Family	Psoriasis Microbiome: Genera	Psoriasis Microbiome: Species
						↓*Bacteroides* ↓ *Barnesiella* ↓*Parabacteroides* ↓*Paraprevotella*	
Schade et al. 2021	Brazil Pso (n = 21) Age, BMI, gender, smoking status, comorbidity matched controls (n = 24)	Massive 16S rRNA sequencing	↓ Diversity	—	—	↑*Dialister* ↑*Catenilbacterium* ↓*Blautia* ↓*Lachnospira* ↓*Ruminococcus*	↑ *Prevotella copri* ↓*Akkermansia* spp.
Scher et al. 2015	USA PsA (n = 16), Pso (n = 15), Age, sex, and ethnicity matched controls (n = 17) -	16s rRNA sequencing (hypervariable region V1–V2)	↓ Diversity v. HC	Pso v. PsA: → ↑ F/B ratio	—	Pso v. PsA: ↓*Coprobacillus* PsA v. HC ↓*Akkermansia* ↓*Ruminococcus,* ↓*Pseudobutyrivibrio* ↓*Parabacteroides* ↓ *Alistipes* ↓*Coprococcus*	
Shapiro et al. 2019	Israel Pso (n = 24) Age, gender, and comorbidity matched controls (n = 22)	16s rRNA sequencing (hypervariable region V4)	Not significantly different	↑*Actinobacteria* ↑*Firmicutes* and ↓*Bacteroidetes* → ↑ F/B ratio ↓*Proteobacteria*	—	↑*Blautia* ↑*Faecalibacterium* ↓*Prevotella*	↑*Collinsella aerofaciens* ↑*Dorea formicigeneran* ↑*Ruminococcus gnavus* ↓*Prevotella copri*
Tan et al. 2017	China Pso (n = 14) Gender matched controls (n = 14)	16s rRNA sequencing (hypervariable region V4)	↓ Diversity*	↓*Tenericutes* ↓*Verrucomicrobia*	—	↑*Bacteroides* ↑*Enterococcus* ↓*Akkermansia*	↑*Clostridium citroniae* ↓*Akkermansia muciniphila*
Zang et al. 2023	FinnGen database R8 Pso (n = 8075) Controls (n = 339,050)	16s rRNA sequencing and Mendellian randomization	N/A	Protective Against Pso: *Bacteroidetes*	—	Protective Against Pso: *Prevotella* Causative for Pso: *Eubacterium fissicatena*	—

Table 2.

Complete Differences Across Studies Evaluating the Gut Microbiome in Patients Following the Mediterranean Diet and Other Lifestyle Interventions. Changes in Microbiota Separated by Taxonomic Groupings. A "-" Indicates No Significant Findings in That Taxonomic Grouping for the Study, or the Study Did Not Perform Analysis Within That Grouping. F/B = Firmicutes/Bacteroidetes Ratio. Pso = Psoriasis. WD = Western Diet. MD = Mediterranean Diet. FF = Fast Food. BMI = Body Mass Index. MetS-OB = Metabolic Syndrome and Obesity. NAFLD = non-alcoholic Fatty Liver Disease. VD = Vegetarian Diet. HIV = Human Immunodeficiency Virus.

Authors	Cohort	Methods	Bacterial Changes: Diversity	Bacterial Changes: Phyla	Bacterial Changes: Class/ Family	Bacterial Changes: Genera	Bacterial Changes: Species
Barber et al. 2021	-20 healthy men	MetaPhlAn 2.0 (v2.9.14) and HUMAnN 2.0 (v2.9.0)?	*Increase in beta diversity in FMD compared to western diet*	—	—	*MD*: ↑Agathobaculum	MD: ↑Agathobaculum butyriciproducens ↑Anaerostipes hadrus
	-a 2-week washout period followed by 2-weeks of each diet, Western-type diet and fiber-enhanced MD	-axonomic identification relies on clade-specific marker genes included in the "v296_ChocoPhlAn_201901" database				↑Anaerostipes	
Calabrese et al. 2022	-109 patients with NAFLD -randomized to six different groups based on diet, exercise, and diet and exercise combined	-16S rRNA hypervariable V3 and V4 regions	*No significant difference on alpha diversity*	—	—	MD+aerobic exercise: ↑Akkermansia ↑Alistipes ↑Dialister ↑Eubacterium eligens ↑Oscillospiraceae-UCG002 ↑Oscillospiraceae-UCG005 ↑Ruminococcus ↑Tyzzerella ↑uncultured_Peptococcaceae ↓Collinsella	—
Forteza et al. 2022	-7 adult, active women with no metabolic conditions -compared effect of 7-day MD diet versus Canadian macronutrient diet -16S	-16S rRNA amplification V3 and V4 regions	*No significant difference*	—	MD: ↑Oscillospiraceae family ↑Prevotellaceae *family* ↓Coriobacteriaceae *family*↓Erysipelotrichaceae *family*	—	—

Authors	Cohort	Methods	Bacterial Changes: Diversity	Bacterial Changes: Phyla	Bacterial Changes: Class/ Family	Bacterial Changes: Genera	Bacterial Changes: Species
Gomez-Perez et al. 2023	-297 overweight/ obese patients with NAFLD -participants consumed energy-reduced MD or unrestricted MD for 1 year	-16S rRNA primer set V2–4–8 and primer set V3–6, 7–9	*Beta diversity changed in T1 and T2 Alpha diversity changed only in T1*	↓Lentisphaerae ↓Proteobacteria	↑Alcaligenaceae *family* ↑Bifidobacteriaceae *family* ↓Enterobacteriaceae family	↑Bifidobacterium ↑Coprococcus ↑Desulfovibrio ↑Faecalibacterium ↑Lachnospira ↑Oscillospira ↑Sutterella	—
Gosh et al. 2020	-612 elderly patients of European decent consuming MD for 12—months	-16S rRNA amplification V3 and V4 regions	*No significant difference in MD intervention groups*	—	—	—	↑Anaerostipes hadrus ↑Bacteroides thetaiotaomicron ↑Faecalibacterium prausnitzii ↑Eubacterium. eligens ↑Eubacterium rectale ↑Eubacterium xylanophilum ↑Prevotella copri ↑Roseburia hominis
Haro et al. 2017	-106 subjects, 3 study groups: obese with metabolic disease, obese without metabolic disease, and not obese -participants consumed MD diet for 2-years	-16S rRNA V4 515–806 bp region	*No significant difference*	*MD in MetS-OB ↑*Bacteroidetes* →↓ F/B ratio	—	MD in MetS-OB: ↑*Bacteroides* ↑*Faecalibacterium* ↑*Prevotella* ↑*Roseburia* ↑*Ruminococcus* genus	MD in MetS-OB: ↑*Parabacteroides distasonis* ↑*Prausnitzii*
Illescas et al. 2021	-meta-analysis of public 16S data from people following MD or other diets	-*16S rRNA meta-analysis search*	*No significant difference in alpha diversity Significant difference beta-diversity in MD group compared to other study groups*	*MD*: ↑*Verrucomicrobia* ↓*Candidatus Saccharibacteria* ↓*Proteobacteria* *MD vs. WD*: ↓*Euryarchaeota* ↓*Fusobacteria* ↓*Firmicutes* ↑*Bacteroidetes* →↓ F/B ratio	*MD*: ↑Ruminococcaceae *family* ↑*Veillonellaceae* family ↓Helicobacteraceae *family* ↓Sphingomonadaceae *family*	*MD*: ↑Adlercreutzia ↑Akkermansiat ↑Bifidobacteriumt ↑Coprococcus ↑Dialister ↑Dorea ↑*Slackia* genus ↓ *Lachnospiraceae*	-*MD*: ↓Fusobacterium nucleatum ↓*Methanobrevibacter smithii*
Ismael et al. 2021	-9 patients with T2DM -received counseling on the MD over 12 weeks -16S rRNA	-16S rRNA region V3–V4	*No significant difference*	-MD at 12 weeks: ↑*Bacteroidetes* phylum ↓*Firmicutes* phylum → ↓ F/B ratio	—	-MD at 4 weeks: ↑*Prevotella* ↓*Bacteroides*	—

Authors	Cohort	Methods	Bacterial Changes: Diversity	Bacterial Changes: Phyla	Bacterial Changes: Class/ Family	Bacterial Changes: Genera	Bacterial Changes: Species
Meslier et al. 2020	-82 overweight and obese people over an 8-week period -39 continued their regular diets -43 consumed a MD with the first 4 weeks being high-adherence	-16S rRNA region V3–V4	*Diversity not measured*	—	—	Baseline to 8 weeks: ↑Lachnospiraceae ↑Roseburia	↑*Faecalibacterium prausnitzii* Baseline to 4 weeks: ↓*Flavonifractor plautii* ↓*Ruminococcus gnavus* ↓*Ruminococcus torques* ↓*Ruthenibacterium lactatiformans* ↓*Streptococcus thermophilus*
Pagliai et al. 2019	-23 overweight omnivores with-randomly assigned to VD or MD for 3-month period	-16S rRNA region V3–V4	*No significant difference in alpha diversity.*	—	—	MD: ↑*Enterorhabdus* ↑*Lachnoclostridium* ↓*Parabacteroides*	—
Pastor-Ibanez et al. 2021	-102 HIV positive individuals -received supplemented MD or control diet for 12 weeks	-16S rRNA region V3–V4	*No significant difference in alpha or beta diversity in intervention group*	—	—	high-adherence supplemented MD: ↑Burkholderiales ↑Butyrivibrio ↑Catenibacterium ↑Succinivibrio low-adherence: ↑Bacteroides ↑Bilophila ↑Desulfovibrio ↑Parabacteroides ↑Paraprevotella *high adherence:*↓Bacteroides	—
Rinott et al. 2022	-294 people with obesity/ dyslipidemia -Patient randomized 1:1:1 to healthy diet, MD, or green MD for 6 months	-16S rRNA region V3–V4	*Diversity not measured*	—	—	-green MD and MD: ↑*Bacteroides* ↑*Enterorhabdus* ↑*Lachnospira* MD: ↑*Erysipelotrichaceae* ↑*Gemella* ↑*Granculicatella* green MD: ↑Lachnospiraceae ↓*Collinsella* ↓*Dorea* ↓*Ruminococcaceae*	—
Tagliamonte et al. 2021	-82 overweight and obese people over an 8-week period -39 continued regular diet	-amplified using primers target-ing the 16S rRNA for A. muciniphila	*Diversity not measured*	-	-		↑Akkermansia muciniphila ↑Faecalibacterium prausnitzii ↑Roseburia faecis ↑Roseburia hominis

Authors	Cohort	Methods	Bacterial Changes: Diversity	Bacterial Changes: Phyla	Bacterial Changes: Class/ Family	Bacterial Changes: Genera	Bacterial Changes: Species
	-43 consumed a MD						
Van Soest et al. 2020	-252 healthy older adults -received counseling on MD over a year -16S rRNA	-16S rRNA V1 and V6 hypervariable regions	*Alpha diversity positively correlated with peanuts, nuts, seeds, fresh fruit, vitamin C, plant protein. Alpha diversity negatively correlated with BMI*	*Fresh* fruits, vitamin C, and nuts, seeds and peanuts↑ Bacteroidetes → ↓ F/B ratio		*Fresh* fruits, vitamin C, and nuts, seeds and peanuts: ↑Alistipes ↑Eubacterium rectale ↑Oscillospira guillermondii ↑Parabacteroides ↑Prevotella *Grain*: ↑Dialister	↑Faecalibacterium prausnitzii *Grain*: ↑species related to Clostridium difficile Animal-based food: ↑Collinsella ↑Ruminococcus gnavus ↑*Streptococcus* bovis ↑Streptococcus mitis ↓Akkermansia muciniphila
Vitale et al. 2020	-29 overweight/ obese participants -assigned to MD or control diet over an 8 week-interval	-16S rRNA region V3–V4	*Significant increase in alpha diversity in the MD group*	—	—	—	↑*Akkermansia muciniphila* ↑*Intestinimonas butyriciproducens* ↓*Coprococcus comes* ↓*Flavonifractor plautii* ↓*Ruminococcus torques* ↓*Streptococcus gallolyticus*
Zhu et al. 2020	-10 healthy subjects consumed MD diet for 4 days, followed by a 4-day washout period, followed by 4-days of a fast-food diet	-16S rRNA V4 region	*No significant effect*	MD: ↑*Firmicutes*	MD: ↑Lachnospiraceae family FF: ↑Coriobacteria class ↑Deltaproteobacteria class ↑Porphyromonadaceae family ↑Rikenellaceae family ↓Lachnosporaceae family	-MD: ↑Butyricicoccus FF: ↑Bilophila ↑Collinsella ↑Parabacteroides ↓Butyricicoccus	—