doi: http://dx.doi.org/10.22201/fmvz.24486760e.2023.1205
Vol. 10 | 2023

Veterinaria México OA
Publicación Digital de la Facultad de Medicina Veterinaria y Zootecnia

AMENA

Symposium on
**Biological Causes
and Coping Strategies**

Shimada A (editor)
Asociación Mexicana
de Especialistas en Nutrición
Animal, AC (AMENA). Mexico

The role of gut microbiota in the development of obesity in dogs‡

María del Carmen Camacho-Rea[1]
0000-0002-1858-8071
Diego Alfredo Cardoso Carmona[2]
0009-0003-7475-3654

[1] Instituto Nacional de Ciencias Médicas
y Nutrición Salvador Zubirán,
Departamento de Nutrición Animal
“Fernando Pérez-Gil Romo”,
Ciudad de México, Mexico.

[2] Universidad Nacional Autónoma de México, Facultad
de Estudios Superiores Cuautitlán,
Posgrado en Ciencias de la Producción
y la Salud Animal,
Cuautitlán, México.

***Corresponding author:**
Email address:
carmen.camachor@incmnsz.mx

‡Presented at a Symposium
on Obesity in Dogs: Biological Causes
and Coping Strategies.
2021. Shimada A (editor)
Asociación Mexicana de Especialistas en
Nutrición Animal, AC (AMENA). México

Abstract

The gut microbiota has become the subject of extensive research in the last decades. Intensive research has revealed its role in several functions related to energy metabolism as well as its importance in both health and illness. An imbalance in gut microbiota composition results in dysbiosis, which has been associated with metabolic disorders such as obesity. In the latter context, the gut microbiota appears to mediate the impact of diet on the host body weight. There are many studies in rodents that show profound changes in the composition and metabolic function of the gut microbiota in subjects with obesity, indicating its influence on the development of the problem. Usually, the microbiota of obese dogs has a modified *Firmicutes*: *Bacteroidetes* ratio, which returns to normal values after dietary intervention with diet-induced weight loss. The role of the gut microbiota on the development of dog obesity is a recent topic of research, which has been complex due to most of the studies being carried out using commercial extruded diets, which differ in their nutritional composition, resulting in controversial findings. Nevertheless, it has been shown that macro-nutrients from the diet are the most relevant factors that can modulate the microbiota's composition in a particular way. Moreover, current studies indicate that a personalized nutritional intervention could modify the composition and function of gut microbiota in a positive manner, reducing the development of pathologies such as obesity.

Keywords: Obesity; Dogs; Intestinal microbiota; Nutritional disorders; Metabolic disorders; Environmental factors.

Submitted: 2023-05-23
Accepted: 2023-05-30
Published: 2023-06-21

Additional information and declarations
can be found on page 7

Cite this as:

Camacho-Rea M del C, Cardoso Carmona DA. The role of gut microbiota in the development of obesity in dogs. Veterinaria México OA. 2023;10. doi: 10.22201/fmvz.24486760e.2023.1205.

doi: http://dx.doi.org/10.22201/fmvz.24486760e.2023.1205
Vol. 10 | 2023

Introduction

According to the World Health Organization (WHO), overweight and obesity are defined as abnormal or excessive accumulation of body fat that may impair health.(1) Obesity is the main nutritional disorder not only in humans, but also in companion animals, and the incidence of this condition in them has increased significantly, being a serious concern in veterinary clinic.(2)

Obesity represents a greater risk for developing disturbances such as diabetes, heart disease, high blood pressure, orthopedic disease,(3) urinary tract disease,(4, 5) respiratory dysfunction(6) as well as certain types of cancers that in turn lead to a shorter life span and a decreased quality of life.(7, 8)

In humans as in dogs, obesity has a genetic component that can be influenced by several environmental factors, including diet, lifestyle, and health condition.(9) Moreover, in the last decades the role of gut microbiota on several metabolic functions such as weight gain,(10) energy harvest,(11) fat metabolism,(12) satiety regulation, systemic inflammation,(13) metabolic homeostasis, and nutrient absorption, have been uncovered.

Dog gut microbiota

The scientific community is gaining a greater understanding of bacterial communities as well as the physiology of gut microbiota, in part due to the Human Microbiome Project.(14) In this sense, the mammals' gut microbiota harbors more than 100 billion microorganisms, including fungi, archaea, virus, and bacteria.(15) The latter represent more than 90 % of the microbiota, and belong to either the gram-positive *Firmicutes* (64 %) or the gram-negative *Bacteroidetes* (23 %),(16) being both the most abundant phyla in lean and obese individuals,(17) respectively. In humans as in animals, the gut microbiota plays a significant role in health and disease.(18) In healthy dogs, several studies have shown that fecal microbiota is co-dominated by *Fusobacterium*, *Bacteroidetes*, and *Firmicutes* phyla.(19, 20)

The major taxa belong to *phylum Firmicutes*, where *Clostridia*, *Bacilli*, and *Erysipelotrichi* are the most representative classes. The class *Clostridia* is largely dominated by three *Clostridium* clusters: IV (families *Ruminococcaceae*, *Faecalibacterium prausnitzii*), XI (family *Peptostreptococcaceae*), and XIVa (families *Lachnospiraceae*, *Blautia* spp).(21, 22) Also, class *Bacilli* are formed almost exclusively of the order *Lactobacillales*, dominated by the genera *Streptococcus* and *Lactobacillus*; whereas *Erysipelotrichi* mainly comprises the genera *Coprobacillus*, *Turicibacter*, and *Catenibacterium*.(23) The phylum *Bacteroidetes* comprises the genera *Prevotella*, *Bacteroides*, and *Megamonas*.(19, 23) In addition, the phylum *Fusobacteria* includes the *Fusobacterium* genus, which is increased in dogs with access to the outdoors.(24)

In humans, *Fusobacterium* is associated with gastrointestinal diseases, so the *Fusobacterium* genus could play a different role in the intestinal tract of dog.(22) Additionally, other phyla such as *Proteobacteria* and *Actinobacteria* are typically colonizers of the small intestine and it is possible to find them in smaller numbers in fecal samples.

Dysbiosis

An imbalance in gut microbiota results in dysbiosis, which is caused by different factors such as inflammatory processes, unhealthy eating habits, or sedentary lifestyle. Likewise, dysbiosis has been associated with metabolic syndrome, cardiovascular disease, immune disorders, and obesity.(25) In the obesity context, the gut microbiome mediates the impact of diet on host body weight.(26, 27) In this sense, microbial 16S rRNA gene sequencing of fecal samples from animal models and humans have underlined the importance of the gut microbiota composition on the amount of energy extracted from the diet and the risk of developing obesity.(19, 28)

Previous studies have shown that, at the phylum level, *Firmicutes*, *Bacteroidetes*, *Actinobacteria*, and *Fusobacteria* are significantly different between obese and normal-weight individuals.(29) In obese people, the ratio of *Firmicutes:Bacteroidetes* decreased significantly. In fact, previous research has reported significant changes in the abundance of *Firmicutes* and *Bacteroidetes* in both obese humans and dogs compared with their lean counterparts.(30)

Other studies have reported that the reduction in *Bacteroidetes* with respect to *Firmicutes* in obese individuals can be reverted through diet-induced weight loss, which increases the abundance of phyla that predominate in lean individuals.(31) Moreover, the increase of *Firmicutes* has been thought to cause an increased efficiency in energy extraction from the diet, resulting in higher levels of short-chain fatty acids that are suspected of altering the metabolism of obese individuals.(26, 28) Other studies have confirmed the role of *Proteobacteria* in obesity by producing pro-inflammatory molecules such as lipopolysaccharides, helping to harvest energy, increase host fat storage(32) and promote inflammation.

The role of gut microbiota in dog obesity

Experimental evidence has revealed that obesity has a microbial component. For instance, transplanted gut microbiota from normal mice into germ-free mice recipients resulted in an increased body fat without any increase in food consumption.(10) This evidence raised the possibility that the composition of the microbial community in the gut affects the amount of energy extracted from the diet. A short time later, it was observed that obese subjects had an enriched microbiota that expresses genes encoding enzymes involved in polysaccharide breakdown and metabolism of simple carbohydrates.(26) Further studies confirmed that gut microbiota participates in whole-body metabolism by affecting energy balance, glucose metabolism, and the low-grade inflammation associated with obesity and related metabolic disorders.(33)

The human microbiota consists of two groups of dominant beneficial bacteria: *Bacteroidetes* and *Firmicutes*. In this regard, it has been observed that obese people have a lower relative proportion of *Bacteroidetes* compared with lean individuals.(28) Research has also documented differences in the gut microbiota composition between obese and lean dogs.(19) However, to date, there is limited information about the role of gut microbiota on the development of obesity in canines.

One of the first studies on this subject used high-throughput pyrosequencing and qPCR to compare the microbiota composition of fecal samples from obese (n = 21) and lean (n = 22) dogs, as well as of animals fed a high-fat commercial dry diet either *ad libitum* (n = 6) or restricted (n = 4) for six months.(34) No significant differences were found in the microbiota alpha diversity between obese and lean dogs. However, the abundance of *Actinobacteria* phylum, as well as *Clostridiales*, particularly *Roseburia*, were significantly greater in obese dogs. Conversely, the abundance of *Bacillales* and *Fusobacteriales* was lower in this group. Moreover, there were no differences at the *Firmicutes* level between the dogs fed *ad libitum* or restricted. Nevertheless, *Firmicutes* and the order *Clostridiales* increased throughout the course of the study, whereas the *Bacteroidetes* decreased in dogs under restricted feeding.

The findings in human gut microbiota and its implication in the development of obesity have allowed studies to improve the health and welfare of companion animals, where obesity has increased exponentially in recent times in domestic dogs. Hence, there is a growing interest in assessing the impact of gut microbiota on canine health.

Modulation of gut microbiota

The intestinal microbiota can be modulated by different factors being the diet the most relevant.(35, 36) It has been reported that differences in dietary macronutrients modulate the microbiome profile rather than the source origin of the ingredient composition.(37) For instance, diets with high content of vegetable fiber cause an increase in *Firmicutes* abundance and a reduction in *Fusobacteria* and *Proteobacteria* phyla.(20, 38) Conversely, using plant-based protein sources did not seem to significantly alter the gut microbiota in dogs, compared with a traditional diet based on mixed animal and vegetable protein sources.(39, 40) However, it has been reported that there is a positive correlation between the abundance of *Clostridiaceae* family and dietary protein content.(39)

A recent study in dogs showed that the production of short chain fatty acids (SCFA) is not exclusively dependent on the diet's carbohydrate content.(41) In this trial, there was no difference in the levels of acetate, butyrate, and propionate between high-fat/low-starch and low-fat/high-starch. In other experiments, the addition of minced meat to a conventional kibble diet resulted in a small increase in fecal butyrate and isovalerate.(42)

The effects of probiotics and prebiotics on gut microbiota have also been tested. In this regard, the evidence suggests that these nutritional interventions could modify the composition of gut microbiota in a positive manner, reducing the devel-

doi: http://dx.doi.org/10.22201/fmvz.24486760e.2023.1205
Vol. 10 | 2023

opment of pathologies associated with inflammation,(13) which is the base of most metabolic disorders including those associated to obesity.

In humans, dietary interventions with prebiotics and probiotics not only modulate the composition but also the functionality of gut microbiota.(43) The probiotics might have beneficial effects through the production of metabolites and antimicrobial peptides, which modify local microbiota and interact with the host immune system.(44) In dogs, the probiotics have been used for treating acute uncomplicated diarrhea and inflammatory bowel disease (IBD). Likewise, a dietary intervention with a symbiotic probiotic-prebiotic combination has shown to increase fecal family *Lactobacillaceae* after two weeks of treatment,(45) a time in which the most beneficial bacteria present were *Lactobacillus*, from the *Firmicutes* phylum.(46)

It is important to consider that there are still inconsistencies in several nutritional interventions regarding microbiota modulation. Therefore, in dog research, the results from several studies should be taken into consideration, since most of them have been carried out using commercial extruded diets differing in nutritional composition. Moreover, the reduced number of individuals used in the trials is another limitation of these studies, considering the existence of individual differences in the microbiome profiles.(47) The manipulation of intestinal microbiota via nutritional intervention(48, 49) or even using antibiotics(50) could potentially provide an easily applicable complementary therapy for obesity, which should be deeply studied.

Nutritional approach to obesity control

Different types of dietary interventions have been evaluated for treating or controlling dog obesity. However, they have shown modest positive effects in the short-term as well as poor results in long-term trials.(51, 52) Nevertheless, the effect of weight loss on intestinal microbiota composition have been evaluated in several studies.(30, 53, 54)

Mori et al.(55) reported that a commercial weight-loss diet (high-protein, low-fat, low-carbohydrate, and high-fiber levels), resulted in a significantly decreased proportion of *Actinobacteria* and *Firmicutes* phyla, whereas *Fusobacteria* phylum increased compared with microbiota from dogs fed with an antiallergenic diet (medium-protein, high-fat, medium-carbohydrate, and low-fiber levels). Another study evaluated the effect of a restricted feeding during a 12-weeks period in obese dogs, using a prescription commercial dry diet (high-protein/high-fiber).(56) This study also evaluated the interaction of restricted feeding with exercise, weight-loss, and intestinal microbiota composition.

Results from the study described above showed that the exercise had no influence on total weight loss and gut microbiota. Overall, the most abundant genera in the microbiota were *Fusobacterium* (~20–50 %) and *Bacteroides* (~15–35 %). *Megamonas* genus abundance negatively correlated with a fast weight loss rate, which was considered as ≥1 % per week. Moreover, acetic and propionic acid concentrations decreased in dogs with a fast weight loss rate.

doi: http://dx.doi.org/10.22201/fmvz.24486760e.2023.1205
Vol. 10 | 2023

These findings suggest that weight loss rate may be related to gut microbiota composition, as well as the production of metabolites produced by *Megamonas* and *Ruminococcaceae*. In addition, the *Ruminococcaceae* relative abundance was lower at the end of the study in dogs with a fast weight loss rate. They concluded that microbiota that favors short chain fatty acid production may negatively affect the weight loss rate in dogs. Nevertheless, it is difficult to separate the effects of weight loss from those of energy restriction and macronutrient composition. In addition, it is important to mention that different subpopulations of obese individuals might respond differently to specific weight loss diets.(54, 57)

doi: http://dx.doi.org/10.22201/fmvz.24486760e.2023.1205
Vol. 10 | 2023

Conflicts of interest

The authors have no conflict of interest to declare in regard to this publication.

Author contributions

Conceptualization: MC Camacho-Rea, DA Cardoso-Carmona
Writing-review and editing: MC Camacho-Rea, DA Cardoso-Carmona

References

1. World Health Organization. Obesity and overweight. 2020. https://www.who.int/news-room/fact-sheets/detail/obesity-and-overweight
2. Thiago HA, Vendramini HT, Macedo RV, Zafalon A, Matheus V, Macegoza V, et al. Serum metabolomics analysis reveals that weight loss in obese dogs results in a similar metabolic profile to dogs in ideal body condition. Metabolomics. 2021;17(3):27. doi: 10.1007/s11306-020-01753-4.
3. Kealy RD, Lawler DF, Ballam JM, Lust G, Biery DN, Smith GK, et al. Evaluation of the effect of limited food consumption on radiographic evidence of osteoarthritis in dogs. Journal of the American Veterinary Medical Association. 2000;217(11):1678-1680. doi: 10.2460/javma.2000.217.1678.
4. Lekcharoensuk C, Lulich JP, Osborne CA, Pusoonthornthum R, Allen TA, Koehler LA, et al. Patient and environmental factors associated with calcium oxalate urolithiasis in dogs. Journal of the American Veterinary Medical Association. 2000;217(4):515–519. doi: 10.2460/javma.2000.217.515.
5. Lund EM, Armstrong PJ, Kirk CA, Klausner JS. Prevalence and risk factors for obesity in adult dogs from private US veterinary practices. International Journal of Applied Research in Veterinary Medicine. 2006;4(2):177–186.
6. Bach JF, Rozanski EA, Bedenice D, Chan DL, Freeman LM, Lofgren JLS, et al. Association of expiratory airway dysfunction with marked obesity in healthy adult dogs. American Journal of Veterinary Research. 2007;68(6):670–675. doi: 10.2460/ajvr.68.6.670.
7. Sandøe P, Palmer C, Corr S, Astrup A, Bjørnvad CR. Canine and feline obesity: A one health perspective. Veterinary Record. 2014;175(24):610–616. doi: 10.1136/vr.g7521.
8. Salt C, Morris PJ, Wilson D, Lund EM, German AJ. Association between life span and body condition in neutered client owned dogs. Journal of Veterinary Internal Medicine. 2019;33(1):89-99. doi: 10.1111/jvim.15367.
9. Rafan E, Dennis RJ, O'Donovan CJ, Becker JM, Scott RA, Smith SP, et al. A deletion in the canine POMC gene is associated with weight and appetite in obesity-prone Labrador retriever dogs. Cell Metabolism. 2016;23(5):893–900. doi: 10.1016/j.cmet.2016.04.012.
10. Bäckhed F, Ding H, Wang T, Hooper LV, Koh GY, Nagy A, et al. The gut microbiota as an environmental factor that regulates fat storage. Proceedings of the National Academy of Sciences. 2004;101(44):15718–15723. doi: 10.1073/pnas.0407076101.

doi: http://dx.doi.org/10.22201/fmvz.24486760e.2023.1205
Vol. 10 | 2023

11. Rosenbaum M, Knight R, Leibel RL. The gut microbiota in human energy homeostasis and obesity. Trends in Endocrinology and Metabolism. 2015;26(9):493–501. doi: 10.1016/j.tem.2015.07.002.
12. Ghazalpour A, Cespedes I, Bennett BJ, Allayee H. Expanding role of gut microbiota in lipid metabolism. Current Opinions on Lipidology. 2016;27(2):141-147. doi: 10.1097/MOL.0000000000000278.
13. Boulangé L, Neves AL, Chilloux J, Nicholson JK, Dumas ME. Impact of the gut microbiota on inflammation, obesity, and metabolic disease. Genome Medicine. 2016;8(42):1–12.
14. Turnbaugh PJ, Ley RE, Hamady M, Fraser-Liggett CM, Knight R, Gordon JI. The Human Microbiome Project. Nature. 2007;449(7164):804–810. doi: 10.1038/nature06244.
15. Honneffer JB, Minamoto Y, Suchodolski JS. Microbiota alterations in acute and chronic gastrointestinal inflammation of cats and dogs. World Journal of Gastroenterology. 2014;20(44):16489–16497. doi: 10.3748/wjg.v20.i44.16489.
16. Abenavoli L, Scarpellini E, Colica C, Boccuto L, Salehi B, Sharifi-Rad J, et al. Gut microbiota and obesity: a role for probiotics. Nutrients. 2019;11(11):2690. doi: 10.3390/nu11112690.
17. Gao R, Zhu C, Li H, Yin M, Pan C, Huang L, et al. Dysbiosis signatures of gut microbiota along the sequence from healthy, young patients to those with overweight and obesity. Obesity. 2018;26(2):351–361. doi: 10.1002/oby.22088.
18. Clemente JC, Ursell LK, Parfrey LW, Knight R. The impact of the gut microbiota on human health: an integrative view. Cell. 2012;148(6):1258–1270. doi: 10.1016/j.cell.2012.01.035.
19. Hand D, Wallis C, Colyer A, Penn CW. Pyrosequencing the canine faecal microbiota: breadth and depth of biodiversity. PLoS One. 2013;8(1):e53115. doi: 10.1371/journal.pone.0053115.
20. Middelbos IS, Vester Boler BM, Qu A, White BA, Swanson KS, Fahey GC Jr. Phylogenetic characterization of fecal microbial communities of dogs fed diets with or without supplemental dietary fiber using 454 pyrosequencing. PLoS One. 2010;5(3):e9768. doi: 10.1371/journal.pone.0009768.
21. Handl S, Dowd SE, Garcia-Mazcorro JF, Steiner JM, Suchodolski JS. Massive parallel 16S rRNA gene pyrosequencing reveals highly diverse fecal bacterial and fungal communities in healthy dogs and cats. FEMS Microbiological Ecology. 2011;76(2):301–310. doi: 10.1111/j.1574-6941.2011.01058.x.
22. Vazquez-Baeza Y, Hyde ER, Suchodolski JS, Knight R. Dog and human inflammatory bowel disease rely on overlapping yet distinct dysbiosis networks. Nature Microbiology. 2016;1:16177. doi: 10.1038/nmicrobiol.2016.177.
23. Garcia-Mazcorro JF, Dowd SE, Poulsen J, Steiner JM, Suchodolski JS. Abundance and short-term temporal variability of fecal microbiota in healthy dogs. Microbiology Open. 2012;1(3):340–347. doi: 10.1002/mbo3.36.
24. Switonski M, Mankowska M. Dog obesity–The need for identifying predisposing genetic markers. Research in Veterinary Science. 2013;95(3):831–836. doi: 10.1016/j.rvsc.2013.08.015.

doi: http://dx.doi.org/10.22201/fmvz.24486760e.2023.1205
Vol. 10 | 2023

25. Bäckhed F, Fraser CM, Ringel Y, Sanders ME, Sartor RB, Sherman PM, et al. Defining a healthy human gut microbiome: current concepts, future directions, and clinical applications. Cell Host and Microbe. 2012;12(5):611–622. doi: 10.1016/j.chom.2012.10.012.
26. Turnbaugh PJ, Ley RE, Mahowald MA, Magrini V, Mardis ER, Gordon JI. An obesity-associated gut microbiome with increased capacity for energy harvest. Nature. 2006;444:1027–1031. doi 10.1038/nature05414.
27. David LA, Maurice CF, Carmody RN, Gootenberg DB, Button JE, Wolfe BE et al. Diet rapidly and reproducibly alters the human gut microbiome. Nature. 2014;505:559–563. doi: 10.1038/nature12820.
28. Ley RE, Turnbaugh PJ, Klein S, Gordon JI. Microbial ecology: human gut microbes associated with obesity. Nature. 2006;444:1022–1023. doi: 10.1038/4441022a.
29. Duan M, Wang Y, Zhang Q, Zou R, Guo M, Zheng H. Characteristics of gut microbiota in people with obesity. PLoS One. 2021;16(8). eNumber: e0255446. doi: 10.1371/journal.pone.0255446.
30. Ley RE, Bäckhed F, Turnbaugh P, Lozupone CA, Knight RD, Gordon JI et al. Obesity alters gut microbial ecology. Proceedings of the National Academy of Sciences. 2005;102(31):11070–11075. doi: 10.1073/pnas.0504978102.
31. Turnbaugh PJ, Bäckhed F, Fulton L, Gordon JI. Diet-induced obesity is linked to marked but reversible alterations in the mouse distal gut microbiome. Cell Host and Microbe. 2008;3(4):213–223. doi: 10.1016/ j.chom.2008.02.015.
32. Rizzatti G, Lopetuso LR, Gibiino G, Binda C, Gasbarrini A. Proteobacteria: a common factor in human diseases. BioMed Research International 2017;2017:9351507. doi: 10.1155/2017/9351507.
33. Cani PD, Osto M, Geurts L, Everard A. Involvement of gut microbiota in the development of low-grade inflammation and type 2 diabetes associated with obesity. Gut Microbes. 2012;3(4):279-288. doi: 10.4161/gmic.19625.
34. Handl S, German AJ, Holden SL, Dowd SE, et al. Faecal microbiota in lean and obese dogs. FEMS Microbiology Ecology. 2013;84(2):332–343. doi: 10.1111/1574-6941.12067.
35. Benson AK, Kelly SA, Legge R, Ma F, Low SJ, Kim J, Zhang M, et al. Individuality in gut microbiota composition is a complex polygenic trait shaped by multiple environmental and host genetic factors. Proceedings of the National Academy of Sciences. 2010;107(44):18933–18938. doi: 10.1073/pnas.1007028107.
36. Xu Z, Knight R. Dietary effects on human gut microbiome diversity. British Journal of Nutrition. 2015;113(Suppl 1):S1–S5. doi: 10.1017/S0007114514004127.
37. Suchodolski JS, Ruaux CG, Steiner JM, Fetz K, Williams DA. Assessment of the qualitative variation in bacterial microflora among compartments of the intestinal tract of dogs by use of a molecular fingerprinting technique. American Journal of Veterinary Research. 2005;66(9):1556–1562. doi: 10.2460/ ajvr.2005.66.1556.
38. Alexander C, Cross TL, Devendran S, Neumer F, Theis S, Ridlon JM, et al. Effects of prebiotic inulin-type fructans on blood metabolite and hormone concentra-

doi: http://dx.doi.org/10.22201/fmvz.24486760e.2023.1205
Vol. 10 | 2023

tions and faecal microbiota and metabolites in overweight dogs. British Journal of Nutrition. 2018;120(6):711–720. doi: 10.1017/S00071145180 01952.

39. Bermingham EN, Maclean P, Thomas DG, Cave NJ, Young W. Key bacterial families (*Clostridiaceae*, *Erysipelotrichaceae* and *Bacteroidaceae*) are related to the digestion of protein and energy in dogs. PeerJ. 2017;5:e3019. doi: 10.7717/peerj.3019.
40. Bresciani F, Minamoto Y, Suchodolski JS, Galiazzo G, Vecchiato CG, Pinna C, et al. Effect of an extruded animal protein-free diet on fecal microbiota of dogs with food-responsive enteropathy. Journal Veterinary Internal Medicine. 2018;32(6):1903–1190. doi: 10.1111/jvim.15227.
41. Schauf S, de la Fuente G, Newbold CJ, Salas-Mani A, Torre C, Abecia L, et al. Effect of dietary fat to starch content on fecal microbiota composition and activity in dogs. Journal of Animal Science. 2018;96(9):3684–3698. doi: 10.1093/jas/sky264.
42. Herstad KMV, Gajardo K, Bakke AM, Moe L, Ludvigsen J, Rudi K, et al. A diet change from dry food to beef induces reversible changes on the faecal microbiota in healthy, adult client-owned dogs. BMC Veterinary Research. 2017;13(147):1-13. doi: 10.1186/s12917-017-1073-9.
43. Marchesi JR, Adams DH, Fava F, Hermes GDA, Hirschfield GM, Hold G, et al. The gut microbiota and host health: a new clinical frontier. Gut. 2016;65(2):330–339. doi: 10.1136/gutjnl-2015-309990.
44. Schmitz S, Suchodolski J. Understanding the canine intestinal microbiota and its modification by pro-, pre- and synbiotics- what is the evidence? Veterinary Medicine and Science. 2016;2(2):71–94. doi: 10.1002/vms3.17.
45. Gagné JW, Wakshlag JJ, Simpson KW, Dowd SE, Latchman S, Brown DA, et al. Effects of a synbiotic on fecal quality, short-chain fatty acid concentrations, and the microbiome of healthy sled dogs [PDF]. BMC Veterinary Research. 2013;9(246):1–10. doi: 10.1186/1746-6148-9-246.
46. Maynard C, Weinkove D. The gut microbiota and ageing. In: J Harris, V Korolchuk, editors. Biochemistry and Cell Biology of Ageing: Part I Biomedical Science. Subcellular Biochemistry. Vol. 90. Singapore: Springer; 2018. pp. 351-371. doi: 10.1007/978-981-13-2835-0_12.
47. Guard BC, Suchodolski JS. Horse Species Symposium: Canine intestinal microbiology and metagenomics: from phylogeny to function. Journal of Animal Science. 2016;94(6):2247–2261. doi: 10.2527/jas.2015-0029.
48. Cani PD, Amar J, Iglesias MA, Poggi M, Knauf C, Bastelica D, et al. Metabolic endotoxemia initiates obesity and insulin resistance. Diabetes. 2007;56(7):1761-1772. doi: 10.2337/db06-1491.
49. Everard A, Lazarevic V, Derrien M, Girard M, Muccioli GG, Neyrinck AM, et al. Responses of gut microbiota and glucose and lipid metabolism to prebiotics in genetic obese and diet-induced leptin-resistant mice. Diabetes. 2011;60(11):2775-2786. doi: 10.2337/db11-0227.
50. Murphy EF, Cotter PD, Hogan A, O'Sullivan O, Joyce A, Fouhy F, et al. Divergent metabolic outcomes arising from targeted manipulation of the gut micro-

doi: http://dx.doi.org/10.22201/fmvz.24486760e.2023.1205
Vol. 10 2023

biota in diet-induced obesity. Gut. 2013;62(2):220-226. doi: 10.1136/gutjnl-2011-300705.

51. Fildes A, Charlton J, Rudisill C, Littlejohns P, Prevost AT, Gulliford MC. Probability of an obese person attaining normal body weight: cohort study using electronic health records. American Journal of Public Health. 2015;105(9):e54-e59. doi: 10.2105/AJPH.2015.302773.
52. German AJ, Titcomb JM, Holden SL, Queau Y, Morris PJ, Biourge V. Cohort study of the success of controlled weight loss programs for obese dogs. Journal of Veterinary Internal Medicine. 2015;29(6):1547–1555. doi: 10.1111/jvim.13629.
53. Duncan S, Lobley G, Holtrop G. Ince J, Johnstone AM, Louis P, et al. Human colonic microbiota associated with diet, obesity and weight loss. International Journal of Obesity. 2008;32(11):1720–1724. doi: 10.1038/ijo.2008.155.
54. Cotillard A, Kennedy S, Kong L, Prifti E, Pons N, Le Chatelier E, et al. Dietary intervention impact on gut microbial gene richness. Nature. 2013;500:585–588. doi: 10.1038/nature12480.
55. Mori A, Goto A, Kibe R, Oda H, Kataoka Y, Sako T. Comparison of the effects of four commercially available prescription diet regimens on the fecal microbiome in healthy dogs. Journal of Veterinary Medical Science. 2019;81(12):1783-1790. doi: 10.1292/jvms.19-0055.
56. Kieler IN, Kamal S, Vitger AD, Nielsen DS, Lauridsen C, Bjornvad CR. Gut microbiota composition may relate to weight loss rate in obese pet dogs. Veterinary Medicine and Science. 2017;3(4):252-262. doi: 10.1002/vms3.80.
57. Santacruz A, Marcos A, Wärnberg J, Martí A, Martin-Matillas M, Campoy C, et al. Interplay between weight loss and gut microbiota composition in overweight adolescents. Obesity. 2009;17(10):1906-1915. doi: 10.1038/oby.2009.112.