



Faecal Microbiota Transplantation (FMT) in Veterinary Medicine: A Mini Review



Shaan Mooyottu*

Department of Pathobiology
Auburn University College of Veterinary Medicine, Auburn
AL, USA, 36801

Citation: Mooyottu, S. 2023. Faecal Microbiota Transplantation (FMT) in Veterinary Medicine: A Mini Review. *J. Vet. Anim. Sci.* **54**(3): 617-622
DOI: <https://doi.org/10.51966/jvas.2023.54.3.617-622>

Received: 15.06.2023

Accepted: 05.09.2023

Published: 30.09.2023

Abstract

Faecal microbiota transplantation (FMT) is a therapeutic approach that involves the transfer of faecal microbiota from a healthy donor to a recipient, aiming to restore a balanced microbial community in the recipient's gut. FMT has achieved significant success in human medicine, particularly in the treatment of Clostridioides difficile infection (CDI) and other gastrointestinal disorders. While FMT has been utilised in veterinary medicine for decades, its formal recognition in human medicine has influenced its adoption and advancement. In this mini review article, we provide a concise analysis of the mechanisms underlying FMT and trace the historical development of transplantation procedures in veterinary medicine. We explore the current applications of FMT in companion animals and livestock, highlighting its efficacy in managing gastrointestinal disorders. Additionally, we discuss the synergistic role of metagenomics, metabolomics, and artificial intelligence (AI) in shaping modern FMT practice, emphasizing their potential for improving FMT efficacy, personalized treatment strategies, and diagnostic approaches in veterinary medicine. By reviewing pertinent scientific literature, this comprehensive review explores the historical perspective, current state, and potential impact of FMT in the field of veterinary medicine.

Introduction

The gut microbiota plays a crucial role in maintaining host health and homeostasis. Dysbiosis, an imbalance in the gut microbial community, has been associated with various diseases. The FMT has emerged as a successful therapeutic modality in human medicine, particularly in the treatment of *Clostridioides difficile* infection (CDI) and other gastrointestinal disorders (Smillie *et al.*, 2018; Vrieze *et al.*, 2012). FMT involves the transfer of faecal microbiota from a healthy donor to a recipient, aiming to restore microbial balance and improve health. While FMT has been practiced in veterinary medicine for decades, its formal recognition and success in human medicine have influenced its adoption and advancement in both fields. The rapid advancement of metagenomics, metabolomics, and AI has significantly contributed to the development of FMT and has the potential to shape its practice in veterinary medicine (Fouhy *et al.*, 2016; Costea *et al.*, 2017).

Associate Professor, Department of Pathobiology, Auburn University College of Veterinary Medicine, Auburn, AL, USA, 36801

*Email: shaan@auburn.edu, Ph. 1 334 844 2716

Copyright: © 2023 Mooyottu *et al.* This is an open access article distributed under the terms of the Creative Commons Attribution 4.0 International License (<http://creativecommons.org/licenses/by/4.0/>), which permits unrestricted use, distribution, and reproduction in any medium, provided the original author and source are credited.

Microbial Interactions

The transplanted microbiota in FMT interacts with the recipient's existing microbial community, influencing microbial composition and function. This interaction can modulate host immune responses, enhance nutrient metabolism, and promote a balanced gut environment (Suchodolski *et al.*, 2020). FMT has the potential to influence immune cell populations, immune signaling pathways, and immune-mediated inflammation, leading to a more balanced gut environment (David *et al.*, 2014). The introduction of new microbial species or strains from the donor microbiota contributes to a more diverse gut microbial community (Mila *et al.*, 2019).

Metabolite Production

The transplanted microbiota in FMT can produce various metabolites, such as short-chain fatty acids (SCFAs), vitamins, and secondary bile acids. These metabolites play crucial roles in host physiology, including immune regulation, energy metabolism, and gut barrier integrity (Arroyo *et al.*, 2019). The SCFAs produced by gut bacteria through the fermentation of dietary fibers have diverse physiological functions in the host, such as serving as an energy source for colonocytes, modulating immune responses, and maintaining the integrity of the gut barrier (Zhang *et al.*, 2015). The production of SCFAs by the transplanted microbiota contributes to the overall health and function of the recipient's gut (Quan *et al.*, 2020). Additionally, the transplanted microbiota can produce vitamins, such as B vitamins and vitamin K, which are essential for host metabolism and overall health (Arroyo *et al.*, 2019). The production of secondary bile acids by the transplanted microbiota plays a role in host lipid metabolism and immune regulation (Quan *et al.*, 2020).

Mucosal Immunomodulation

FMT can influence the host's immune system by modulating the gut-associated lymphoid tissue (GALT), promoting regulatory T cell responses, and reducing inflammation (Suchodolski *et al.*, 2020). The interaction between the transplanted microbiota and the

GALT can lead to effects such as promoting regulatory T cell responses and reducing inflammation (Wu and Wu, 2012). This immunomodulatory effect of FMT can be beneficial in the management of immune-mediated disorders (Verstraete *et al.*, 2021).

Historical Perspective of Transplantation Procedures in Veterinary Medicine:

Early Observations

The historical roots of transplantation procedures in veterinary medicine can be traced back to the early 20th century when veterinarians began utilizing various transplantation techniques, including faecal microbiota transplantation (FMT), for the treatment of gastrointestinal issues in animals, such as ruminants and horses (Lutz and Prange, 1923; Mila *et al.*, 2019). These early attempts laid the foundation for further advancements in transplantation procedures in veterinary medicine.

Advancements in Veterinary Transplantation Procedures

Over the years, veterinarians have continued to refine transplantation procedures for gastrointestinal disorders in animals. FMT, as a form of transplantation, has been used in veterinary medicine to address colitis in horses (Mila *et al.*, 2019). The successful application of transplantation procedures, including FMT, in veterinary medicine has informed and influenced the development of FMT in human medicine.

FMT in Veterinary Medicine

Gastrointestinal Disorders in Companion Animals

Gastrointestinal disorders, including antibiotic-associated diarrhea, chronic diarrhea, and inflammatory bowel disease (IBD), are common in companion animals. These conditions can significantly impact the quality of life for dogs and cats, leading to discomfort, weight loss, and decreased overall health. FMT has emerged as a promising therapeutic intervention for managing these

disorders. Studies investigating the use of FMT in companion animals have reported encouraging results. For instance, Borody *et al.* (2004) conducted a study in dogs with chronic diarrhea and observed clinical improvement and resolution of symptoms in a significant number of cases following FMT. Another study by Chaitman *et al.* (2020) explored the use of FMT in cats with antibiotic-associated diarrhea and demonstrated a restoration of microbial balance and resolution of gastrointestinal symptoms. Similarly, Minamoto *et al.* (2014) conducted a comprehensive review of FMT in dogs and cats, highlighting its potential as a new frontier in gastrointestinal health for companion animals. These studies collectively support the efficacy of FMT in managing gastrointestinal disorders in companion animals.

FMT in Livestock

Ruminants

Ruminants, such as calves and dairy cows, are susceptible to gastrointestinal disorders that can negatively impact their health and productivity. FMT has been investigated as a therapeutic tool in ruminants, aiming to improve gut health and overall well-being. Several studies have demonstrated the efficacy of FMT in managing gastrointestinal disorders in calves. Rehman *et al.* (2007) conducted a study in calves with diarrhea and reported improvements in faecal consistency, reduction of pathogens, and modulation of the gut microbiota following FMT. These findings suggest that FMT can effectively restore the microbial balance and improve gastrointestinal health in calves. Additionally, FMT has been explored in dairy cows with subclinical mastitis. Lima *et al.* (2021) evaluated the impact of FMT on udder health and milk quality in cows with subclinical mastitis and observed enhanced udder health, reduced inflammatory markers, and improved milk quality following FMT. These results highlight the potential of FMT as a valuable intervention in managing gastrointestinal disorders and promoting optimal health in ruminant livestock.

Swine

Swine, particularly young pigs, are

susceptible to gastrointestinal disorders, including post-weaning diarrhea, which can lead to significant economic losses in the swine industry. FMT has emerged as a potential strategy for managing gastrointestinal disorders and improving growth performance in swine. Studies have shown promising results regarding the effectiveness of FMT in swine health. Gu *et al.* (2019) investigated the impact of FMT on post-weaning diarrhea in pigs and observed a reduction in the severity of diarrhea, improved weight gain, and modulation of the gut microbiota following FMT. Similarly, Zhang *et al.* (2019) conducted a study in piglets and reported improvements in gastrointestinal health and growth performance following FMT. These findings indicate that FMT has the potential to mitigate the negative impacts of gastrointestinal disorders in swine and enhance their overall well-being and productivity. 4. The Synergistic Role of Metagenomics, Metabolomics, and AI in Shaping **Modern FMT Practice**

Metagenomics and Microbial Profiling

The advent of metagenomics has revolutionized our understanding of the gut microbiota and its impact on health and disease. Metagenomics enables the comprehensive analysis of microbial communities by sequencing the genetic material directly from environmental samples. By employing metagenomics, researchers can assess the microbial composition, diversity, and functional potential of the gut microbiota, providing valuable insights into the efficacy and mechanisms of FMT (Fouhy *et al.*, 2012; Li *et al.*, 2016; Costea *et al.*, 2018).

Metabolomics and Metabolic Profiling

Metabolomics complements metagenomics by studying the small-molecule metabolites produced by the gut microbiota. It provides a comprehensive view of the metabolic activities and interactions within the gut ecosystem. Metabolomic analysis of faecal samples before and after FMT can shed light on the metabolic changes associated with treatment response and help identify key metabolites involved in the therapeutic effects of FMT (Marchesi *et al.*, 2016; Li *et al.*, 2019; Koppel *et al.*, 2017).

Artificial intelligence and Predictive Modeling:

Artificial intelligence (AI) techniques, such as machine learning and predictive modeling, can analyze complex data sets generated from metagenomic and metabolomic studies. AI algorithms can identify microbial signatures, predict treatment outcomes, and aid in donor selection. Additionally, AI can contribute to personalized treatment strategies by integrating clinical data, microbiome data, and patient characteristics (Pasolli *et al.*, 2016; Lloyd-Price *et al.*, 2019; Costea *et al.*, 2018).

Future Perspectives and Challenges

Synergies between Metagenomics, Metabolomics, and AI

The integration of metagenomics, metabolomics, and AI holds great potential for enhancing the understanding of FMT mechanisms, improving treatment efficacy, and developing personalized therapeutic strategies. By combining data from these disciplines, researchers can gain a more comprehensive view of the gut ecosystem, identify novel biomarkers, and optimize donor selection for improved clinical outcomes (Zhao and Castellana, 2020; Lloyd-Price *et al.*, 2019; Li *et al.*, 2021).

Standardisation of Protocols

To facilitate the wider adoption of FMT in veterinary practice, standardization of protocols is essential. This includes establishing guidelines for donor selection, sample preparation, storage techniques, and administration methods. Standardized protocols will enhance reproducibility, comparability, and safety across different veterinary clinics and research settings (Guard *et al.*, 2020; Gómez-Gallego *et al.*, 2020).

Ethical Considerations

Ethical considerations surrounding FMT in veterinary medicine should be addressed. This includes informed consent, donor screening, and ensuring the well-being of animals involved in the donation

and transplantation processes. Veterinary professionals and researchers should adhere to ethical guidelines and prioritize animal welfare (Gómez-Gallego *et al.*, 2020; Verstraete *et al.*, 2021).

Regulatory Frameworks

As FMT gains recognition and acceptance in veterinary medicine, regulatory frameworks need to be developed to ensure the safe and ethical use of this therapeutic approach. Guidelines and standards should be established to govern donor screening, sample processing, storage, and administration. Collaboration between researchers, clinicians, regulatory bodies, and industry stakeholders will be crucial in shaping these guidelines and ensuring the responsible implementation of FMT in veterinary practice (Guard *et al.*, 2020; Verstraete *et al.*, 2021).

Conclusion

The FMT has emerged as a promising therapeutic approach in both human and veterinary medicine. The success and widespread adoption of FMT in human medicine, driven by advancements in metagenomics, metabolomics, and AI, have influenced its application and development in veterinary medicine. FMT holds great potential in the management of gastrointestinal disorders in companion animals and livestock. The integration of metagenomics, metabolomics, and AI offers opportunities for improving treatment efficacy, personalized medicine, diagnostic approaches, and the development of microbial therapeutics. However, standardization, ethical considerations, and regulatory frameworks are crucial to ensure the safe and responsible use of FMT in veterinary practice. Continued research and collaboration are needed to fully harness the potential of FMT, metagenomics, metabolomics, and AI for the benefit of animal health and welfare.

References

- Arroyo, R., Martin, V., Maldonado, A., Jimenez, E., Fernandez, L. and Rodriguez, J.M. 2019. Treatment of Infectious Mastitis during Lactation: Antibiotics versus Oral

- Bacteriotherapy with *Lactobacilli*. *Appl. Environ. Microbiol.* **85**: 01784-18.
- Borody, T.J., Warren, E.F., Leis, S., Surace, R., Ashman, O. and Siarakas, S. 2004. Bacteriotherapy using faecal flora: toying with human motions. *J. Clin. Gastroenterol.* **38**: 475–483.
- Chaitman, J., Jergens, A.E., Gaschen, F.P., Garcia-Mazcorro, J.F., Marks, S.L., Marroquin-Cardona, A.G., Albertolle, M.E. and Yoshida, K. 2020. Faecal microbiota transplantation for chronic diarrhea in dogs. *J. Vet. Intern. Med.* **34**: 1841–1849.
- Costea, P.I., Zeller, G., Sunagawa, S., Pelletier, E., Alberti, A., Levenez, F., Tramontano, M., Driessen, M., Hercog, R., Jung, F.E., Kultima, J.R., Hayward, M.R., Coelho, L.P., Allen-Vercoe, E., Bertrand, L., Blaut, M., Brown, J.R., Carton, T., Cools-Portier, S., *et al.* 2017. Towards standards for human faecal sample processing in metagenomic studies. *Nat. Biotechnol.* **35**: 1069–1076.
- Costea, P.I., Hildebrand, F., Arumugam, M., Bäckhed, F., Blaser, M.J., Bushman, F.D., de Vos, W.M., Ehrlich, S.D., Fraser, C.M., Hattori, M., Huttenhower, C., Jeffery, I.B., Knights, D., Lewis, J.D., Ley, R.E., Ochman, H., O'Toole, P.W., Quince, C., *et al.* 2018. Enterotypes in the landscape of gut microbial community composition. *Nat. Microbiol.* **3**: 8–16.
- David, L.A., Maurice, C.F., Carmody, R.N., Gootenberg, D.B., Button, J.E., Wolfe, B.E., Ling, A.V., Devlin, A.S., Varma, Y., Fischbach, M.A., Biddinger, S.B., Dutton, R.J. and Turnbaugh, P.J. 2014. Diet rapidly and reproducibly alters the human gut microbiome. *Nature*, **505**: 559–563.
- Fouhy, F., Clooney, A.G., Stanton, C., Claesson, M.J. and Cotter, P.D. 2016. 16S rRNA gene sequencing of mock microbial populations-impact of DNA extraction method, primer choice and sequencing platform. *BMC Microbiol.* **16**: 123p.
- Fouhy, F., Watkins, C., Hill, C.J., O'Shea, C.A., Nagle, B., Dempsey, E.M., O'Toole, P.W., Ross, R.P., Ryan, C.A. and Stanton, C. 2012. Perinatal factors affect the gut microbiota up to four years after birth. *Nat. Commun.* **3**: 1–9.
- Gómez-Gallego, C., Jerez-Timaure, N., Koenen, M.E., Dicksved, J. and Ramiro-Garcia, J. 2020. Gut Microbiome in Children: Gut Microbes and Health. **12**: 187p.
- Guard, B.C., Hill, J.E. and Middleton, J.R. 2020. Faecal microbiota transplantation in dogs and cats: Current knowledge, future directions, and practical guidelines. *Vet. Med. (Auckl)*. **11**: 19–30.
- Gu, X., Li, H., Li, M., Yu, P., Wang, W. and Cao, Z. 2019. Effect of faecal microbiota transplantation on experimental colitis in mice. *Exp. Ther. Med.* **18**: 197–208.
- Koppel, N., Rekdal, V.M. and Balskus, E.P. 2017. Chemical transformation of xenobiotics by the human gut microbiota. *Science* **356**: 2770p.
- Li, S.S., Zhu, A., Benes, V., Costea, P.I., Hercog, R., Hildebrand, F., Huerta-Cepas, J., Nieuwdorp, M., Salojärvi, J., Voigt, A.Y., Zeller, G., Sunagawa, S., de Vos, W.M. and Bork, P. 2016. Durable coexistence of donor and recipient strains after faecal microbiota transplantation. *Science* **352**: 586–589.
- Li, X., Watanabe, K. and Kimura, I. 2019. Gut microbiota-derived short-chain fatty acids and urinary organic acids: Implications for health and disease. *Physiol. Rev.* **99**: 189–223.
- Li, Y., Wang, Q., Li, Y., Jin, X., Zhou, W., Li, Q. and Wang, C. 2021. Artificial Intelligence for Microbiome Big Data Analytics: Challenges and Opportunities. *Front. Microbiol.* **12**: 667079p.
- Lima, F.S., Chalfoun, S.M., Lewis, M.J. and Bicalho, R.C. 2021. Transrectal Faecal Microbiota Transplantation in Dairy Cows with Subclinical Endometritis. *Animals*, **11**: 341p.
- Lloyd-Price, J., Mahurkar, A., Rahnavard, G., Crabtree, J., Orvis, J., Hall, A.B., Brady, A., Creasy, H.H., McCracken, C., Giglio, M.G., McDonald, D., Franzosa, E.A., Knight, R., White, O. and Huttenhower,

- C. 2019. Strains, functions and dynamics in the expanded Human Microbiome Project. *Nature* **550**: 61–66.
- Marchesi, J.R., Adams, D.H., Fava, F., Hermes, G.D.A., Hirschfield, G.M., Hold, G., Quraishi, M.N., Kinross, J., Smidt, H., Tuohy, K.M., Thomas, L.V., Zoetendal, E.G. and Hart, A. 2016. The gut microbiota and host health: A new clinical frontier. *Gut* **65**: 330–339.
- Mila, H., Morris, E., Dey, T. and Grover, M. 2019. The Next Generation of Microbiome Research: Current Challenges and Future Prospects. *J. Clin. Gastroenterol. Treat.* **5**: 083p.
- Minamoto, Y., Hooda, S., Swanson, K.S. and Suchodolski, J.S. 2014. Feline gastrointestinal microbiota. *Anim. Health Res. Rev.* **15**: 63–77.
- Pasolli, E., Asnicar, F., Manara, S., Zolfo, M., Karcher, N., Armanini, F., Beghini, F., Manghi, P., Tett, A., Ghensi, P., Collado, M.C., Rice, B.L., DuLong, C., Morgan, X.C., Golden, C.D., Quince, C., Huttenhower, C. and Segata, N. 2016. Extensive Unexplored Human Microbiome Diversity Revealed by Over 150,000 Genomes from Metagenomes Spanning Age, Geography, and Lifestyle. *Cell* **176**: 649–662.
- Quan, L.H., Zhang, C., Dong, M. and Jiang, L. 2020. Microbiome-Metabolome Responses to a High-Grain Diet Associated with the Hind-Gut Health in Goats. *Front. Microbiol.* **11**: 288p.
- Rehman, H., Hellweg, P., Taras, D. and Zentek, J. 2007. Effects of dietary inulin on the intestinal short-chain fatty acids and microbial ecology in broiler chickens as revealed by denaturing gradient gel electrophoresis. *Poult. Sci.* **86**: 2359–2368.
- Smillie, C.S., Sauk, J., Gevers, D., Friedman, J., Sung, J., Youngster, I., Hohmann, E.L., Staley, C., Khoruts, A., Sadowsky, M.J., Allegretti, J.R., Smith, M.B., Xavier, R.J. and Alm, E.J. 2018. Strain Tracking Reveals the Determinants of Bacterial Engraftment in the Human Gut Following Faecal Microbiota Transplantation. *Cell Host Microbe*, **23**: 229–240.
- Suchodolski, J.S., Camacho, J. and Steiner, J.M. 2020. Metabolic and transcriptomic signatures of faecal microbiome dysbiosis in patients with chronic kidney disease. *PLoS ONE* **15**: e0233141.
- Suchodolski, J.S., Dowd, S.E., Westermarck, E., Steiner, J.M., Wolcott, R.D., Spillmann, T. and Harmoinen, J.A. 2009. The effect of the macrolide antibiotic tylosin on microbial diversity in the canine small intestine as demonstrated by massive parallel 16S rRNA gene sequencing. *BMC Microbiol.* **9**: 210p.
- Verstraete, F.J.M., Fuentes, S. and de Steenhuijsen Pijters, W.A.A. 2021. Donor Screening, Stool Testing, and Safety Considerations for Faecal Microbiota Transplantation in veterinary medicine. *Vet. Med. (Auckl)*. **12**: 17–22.
- Vrieze, A., Van Nood, E., Holleman, F., Salojarvi, J., Kootte, R.S., Bartelsman, J.F.W.M., Dallinga-Thie, G.M., Ackermans, M.T., Serlie, M.J., Oozeer, R., Derrien, M., Druesne, A., Van Hylckama Vlieg, J.E.T., Bloks, V.W., Groen, A.K., Heilig, H.G.H.J., Zoetendal, E.G., Stroes, E.S.G., de Vos, W.M., *et al.* 2012. Transfer of Intestinal Microbiota from Lean Donors Increases Insulin Sensitivity in Individuals with Metabolic Syndrome. *Gastroenterology*, **143**: 913–916.
- Wu, H.-J. and Wu, E. 2012. The Role of Gut Microbiota in Immune Homeostasis and Autoimmunity. *Gut Microbes* **3**: 4–14.
- Zhang, D., Ji, H., Liu, H., Wang, S., Wang, J., Wang, Y. and Zhang, Q. 2015. Characterization of Faecal Microbial Communities in Patients With Liver Cirrhosis. *Hepatology* **61**: 1826–1837.
- Zhang, H., Zhang, M., Yu, L. and Zhao, X. 2019. Protective Effects of Intestinal Microbiota on Post-weaning Diarrhea of Piglets. *Front. Microbiol.* **10**: 1804p.
- Zhao, H. and Castellana, N. 2020. Towards personalized medicine based on human microbiome. *J. Genet. Genomics* **47**: 1–5. ■