Decoding the canine faecal microbiome: insights into health and disease

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1. Introduction

The gut microbiome is increasingly recognized as a critical regulator of host health, influencing not only gastrointestinal function but also systemic physiology, including immune, metabolic, and neurological pathways. In dogs, as in humans, the study of the microbiome is offering promising insights into diagnostics, disease mechanisms, and therapeutic interventions. Three key concepts underpin much of this emerging research:

- *Dysbiosis*: an imbalance in microbiota composition/function, linked to conditions from chronic enteropathies to epilepsy.
- *Faecal Microbiota Transplantation (FMT)*: the transfer of stool from healthy donors to restore balance in diseased recipients.
- *Microbiota-gut-brain axis*: a bidirectional network linking gut microbes to brain function via immune and neurochemical pathways.

To date, canine microbiome research has focused primarily on metrics (diagnostic tools) and modifiers (therapeutic interventions), while mechanistic insights remain limited. This lecture highlights how emerging findings are translating into clinical practice, featuring examples from my own research.

2. Investigating the effects of antimicrobials on dysbiosis and AMR development

Microbiome research can be used to assess the impact of antimicrobials on gut microbiota. We investigated the impact of two widely used aminopenicillin formulations, amoxicillin (AMX) and amoxicillin–clavulanic acid (AMC), on the faecal microbiota of dogs [1]. Both treatments caused a significant but temporary reduction in microbial richness and diversity during the treatment period, with partial recovery within one week of cessation. However, while AMC had a broader impact on the microbial community, reducing the abundance of beneficial taxa such as *Roseburia*, *Dialister*, and *Lachnospiraceae*, which are typically associated with gut health and SCFA production, AMX displayed a narrower spectrum of disruption, with less pronounced alterations in the abundance of these health-associated genera. Furthermore, AMC also induced a relative enrichment of *Escherichia coli*, suggesting that clavulanic acid may exacerbate the selective pressure on microbial populations despite not increasing overall resistance levels beyond those seen with amoxicillin alone. These findings emphasize that not all antibiotics, even chemically related drugs within the same class, affect the microbiota equally, and highlight the usefulness of microbiome research for evidence-based antimicrobial stewardship in veterinary practice.

3. Predicting gut health by microbiota composition

In recent years, there has been growing interest in the development of diagnostic tools that allow clinicians to assess gut health based on microbiota composition—what we refer to as metrics. One of the most impactful contributions in this area for canine medicine is the development of a quantitative Dysbiosis Index [2]. Using faecal samples from over 95 healthy dogs and 106 dogs with chronic inflammatory enteropathy (CE), a quantitative PCR was developed to measure the abundance of key microbial taxa, including beneficial bacteria such as *Faecalibacterium*, *Clostridium hiranonis*, and *Fusobacterium*, as well as potentially harmful bacteria like *E. coli* and streptococci. Using this dataset, the authors developed the *Dysbiosis Index*—a single score indicating gut health. Negative values reflect normobiosis; positive values suggest dysbiosis, as seen in chronic enteropathy (CE). The model showed 74% sensitivity and 95% specificity, demonstrating how microbiome metrics can translate research into clinical tools. Similar indices may support diagnosis in other areas, including behavioural and neurological disorders.

4. Exploring the role of gut microbiota on non-enteric disease

Beyond gastrointestinal disease, the gut microbiota is increasingly linked to extra-intestinal conditions affecting the brain, immune system, and cardiovascular health. This connection is mediated by the microbiota–gut–brain axis, which integrates microbial metabolites (e.g. SCFAs), immune signalling, and neural pathways. In one of our recent studies [3], we provided new evidence of this link in dogs with idiopathic epilepsy. Using 16S rRNA sequencing, wey compared 19 drug-naïve epileptic dogs to 17 healthy controls. While overall community composition (β-diversity) was similar, epileptic dogs showed significantly reduced microbial richness and lower levels of SCFA-producing bacteria such as *Faecalibacterium*, *Prevotella*, and *Blautia*, along with increased *E. coli*, *C. perfringens*, and *Bacteroides*. These shifts suggest a functional dysbiosis that may contribute to neuroinflammation and seizure susceptibility. These findings align with a recent review of the associations between microbiota composition and behavioural traits such as anxiety and aggression in dogs [4]. Together, this growing body of evidence suggests that neurological and behavioural disorders in dogs may be modulated by gut microbiota. However, inconsistencies across taxa highlight the complexity of the gut-brain axis and the need to study microbial function, not just taxonomy.

5. Modulating gut microbiota to improve dog health

While metrics such as the Dysbiosis Index help assess gut health, microbiota-targeted interventions—or modifiers—aim to restore or enhance the microbiome to prevent or treat disease. Such strategies include probiotics, prebiotics, synbiotics, and FMT. Originally developed for recurrent *Clostridioides difficile* infections in humans, FMT is now being adopted in veterinary medicine. FMT's benefits are multifactorial: it restores SCFA production, reintroduces keystone beneficial taxa, modulates immunity, and improves bile acid metabolism. The Companion Animal FMT Consortium has recently published practical guidance for implementing FMT in small animal veterinary practice as an adjunctive therapy for parvovirus enteritis, acute diarrhoea, and chronic enteropathy [5]. FMT is safe, well-tolerated, minimally invasive, and feasible in general practice with proper donor screening. Fresh faeces are preferred, and donor selection should consider health history and lifestyle.

Beyond FMT, the gut microbiota is responsive to dietary nutrients, particularly macronutrients like fibre, starch, and protein [6]. Significant shifts in microbiome and metabolome composition occur mainly with major dietary changes, driven by substrate availability. Due to microbial redundancy, key metabolites like butyrate can be produced from different sources, such as fibre or protein, though optimal levels remain unclear. In healthy dogs and cats, the microbiome is resilient and returns to baseline after reverting to a regular diet, indicating that lasting changes require long-term dietary interventions.

6. Conclusions

Microbiome research is already impacting canine medicine by improving diagnostics and expanding therapeutic options. Yet the field's future lies in uncovering mechanisms: how microbes influence host physiology. This will require integrating metabolomics, immune profiling, and longitudinal studies. Such approaches will help move from descriptive studies to personalized, evidence-based care that leverages the microbiome to improve outcomes across a range of canine conditions.

References

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