

The faecal microbiome: a reservoir of antimicrobial resistance in dogs

A UCD research team led by Monica Augusto aims to investigate the short-term effect of antibiotics on the faecal bacterial population and resistance to antimicrobial drugs in dogs

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MICROBIOME

Disturbance of the natural microbiome is a contemporary health topic both in human and veterinary medicine. The intestinal microbiome is defined as the collection of all living microorganisms (bacteria, fungi, protozoa, and viruses) that occupy the gastrointestinal tract. With the development of new molecular techniques (such as bacterial 16S rRNA gene sequencing), it is currently recognised that the microbiome is highly diverse, containing several hundred to over a thousand bacterial phylotypes¹, and it plays an important role in the development and regulation of the host immune system, but also in the pathogenesis of multiple medical conditions².

ANTIBIOTIC USE

The administration of antibiotics can lead to the appearance of resistant bacteria either to a specific antibiotic or potentially others within the same or a different group. As a result, the number



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of antibiotics that are effective to treat a certain disease may become limited

or even non-existent. Moreover, this resistance is not restricted to bacteria that cause disease as it may also develop in non-harmful bacteria that are exposed to the antibiotic, such as the intestinal microbiome (as represented in the faecal microbiota). In companion animals, this is of particular concern due to the frequent direct contact between people and their pets and their often-shared living space. And it is not known if the changes induced by antibiotics persist, and for how long, following completion of antibiotic therapy.

If the intestinal microbiome is altered, dysbiosis occurs. Antibiotic treatment is an important cause of dysbiosis because it can radically alter the composition





New UCD research aims to help determine the degree to which antibiotic administration perturbs the canine faecal microbiome and to what extent this promotes AMR.

of the intestinal microbiome³ and increase the risk of developing infections⁴. Since the intestinal microbiome plays a crucial role in immunity, metabolism and endocrinology, the effects of antibiotics on the faecal microbiota may lead to further health complications².

OBJECTIVES

The aims of this study are to determine if administration of antibiotics to dogs causes an effect on the overall faecal bacterial population (faecal microbiota) and/or induces antimicrobial resistance (AMR) in the faecal bacterial microbiota.

METHODOLOGY

Faecal samples will be collected from dogs prior to the oral administration of amoxicillin-clavulanate or a fluoroquinolone. Both antibiotics are defined by the World Health Organisation (WHO) as critically important and of highest priority for human medicine. Part of the fresh faecal sample will be submitted for routine culture of *Escherichia coli* (used as an indicator organism) and susceptibility testing. The remaining faecal material will be aliquoted and stored at -80°C for microbiome analysis. Faecal samples will also be collected one to two weeks after discontinuation of

therapy. Microbiota composition profiling of the canine faecal population will be performed by 16S rRNA amplicon sequencing as well as culture and susceptibility testing.

The emergence of AMR is considered one of the major threats to human and animal health. The results of this study will be important in determining the degree to which antibiotic administration perturbs the canine faecal microbiome and to what extent this promotes AMR.

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