

The prevalence of obesity is rapidly increasing worldwide, constituting an important health problem. Similarly, as occurs in human, the number of pets with obesity is increasing notably, being the most common metabolic disorder in companion animals. Apart from genetic susceptibility, sedentary lifestyle and increased food consumption, environment factors such as changes in the gut microbiota seem to play a role in the development of this metabolic disease.

In addition, studies in humans, animal models and dogs have revealed that the fecal microbiota of subjects with obesity is different from that of lean subjects, and changes after weight loss. However, the impact of weight loss on the fecal microbiota in dogs with obesity has not been fully characterized, existing discrepancies between different studies that aimed to investigate the effect of weight loss on the fecal microbiota of dogs.

This study reviews the current knowledge about the role of the gut microbiota in the maintenance of energy homeostasis in mammalian hosts. Focusing on dogs and humans, and describing the mechanism proposed to explain how the gut bacteria can contribute to the development of obesity.

Furthermore, to evaluate the possible changes in the gut microbiota of obese dogs associated to weight loss, 16S rRNA gene sequencing was performed in fecal samples of 20 dogs with obesity and after weight loss with a high-fiber-high-protein diet. The endpoint of the weight loss program was individually tailored to the ideal body weight of each dog.

The results obtained showed that after weight loss, the fecal microbiota of dogs with obesity changed significantly. This shift in the fecal microbiota composition was characterized

by an increase in bacterial diversity, a decrease in Firmicutes, and increase in Bacteroidetes and Fusobacteria.

Taxonomic analysis of the gut microbial communities is the first approach to understand the composition of gut microbiota in obese individuals and detect gut microbiota signatures in the obese phenotype. However, methodological approaches such as metagenomic and metabolomic analyses are needed to elucidate the functions of these bacteria that can affect the host and also to understand the role of gut microbiota in obesity.