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**Oral microbiome in domestic cats with feline chronic gingivitis.****Valéria Maria Lara<sup>1</sup>, Mariel Dalmedico Policano<sup>1</sup>, Camila Aparecida Cruz Reis<sup>1</sup>, Márcia de Oliveira Sampaio Gomes<sup>1</sup>, Aline Rodrigues Hoffman<sup>2</sup>, Raquel Silveira Pedreira<sup>3</sup>, Adriano Bonfim Carregaro<sup>1</sup> and Carlos Eduardo Ambrósio<sup>1</sup>**<sup>1</sup>University of São Paulo, SP 13635-900, Brazil<sup>2</sup>Texas A&M University, TX 77843, USA<sup>3</sup>Instituto PremieR Pet, SP 04548-005, Brazil

Feline chronic gingivitis (FCG) is still considered one of the most challenging conditions to be treated of all oral inflammatory diseases. The etiopathogenesis of FGC has not been elucidated and it is known to be a multifactorial disease in which bacteria, viruses, nutritional, environmental and management conditions associated with genetic factors are likely to contribute to the development and chronicity of this condition. These factors can directly or indirectly initiate the inflammatory process by imbalance of the oral bacterial microbiota and the immune response as well. Although bacteria play a major role on FCG, few studies have investigated their role. Therefore, this project aimed to assess and describe the bacterial microbiota of the oral cavity in domestic cats with clinical signs of chronic gingivitis. Oral microbiome composition was assessed by amplifying the V4 region of the 16S gene from DNA extracted from oral swabs from 20 domestic cats. These amplicons were sequenced using Illumina technology. The majority of the sequences belonged to six phyla; Firmicutes, Bacteroidetes, Proteobacteria, Actinobacteria, Spirochaetae and Fusobacteria. The most taxa were as follow: an unclassified *Clostridiales* (2,21%), *Bacteroides* (3,7%), *Clostridium* (2,13%), *Porphyromonas* (1,44%), *Corynebacterium* (1,32%), *Fusobacterium* (1,23%), *Treponema* (0,93%), *Campylobacter* (0,75%), *Moraxella* (0,64%) and *Pasteurella* (0,58%). Results suggest that the feline oral microbiota even in cats with chronic feline gingivitis is similar to that observed in healthy animals, which reflects a large conservation at the phylum level and that the bacterial population is highly diverse, rich and even.

**Biography**

I'm Valéria Maria Lara. I have been a veterinary doctor and PhD in microbiology for more than 13 years. During my doctorate, I developed a study on the phylogeny of the feline immunodeficiency virus (FIV). Currently, I do postdoctoral studies at the University of São Paulo and develop a study with oral microbioma of domestic cats with chronic gingivitis and its association with FIV infection. I has published 20 papers in reputed journals.

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