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BACTERIAL CHARACTERIZATION OF THE ORAL CAVITY OF THE DOMESTIC CAT POPULATION IN THE CITY OF CAMPO GRANDE, MS, BRAZIL

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ABSTRACT

Owing to the high incidence of domestic animal bites and resultant bacterial infections, this study aimed to identify the main bacteria isolated from the oral microbiota of 50 domestic cats. This is the first study to identify the genus *Pseudomonas* as the most frequently isolated agent, corresponding to 45% of the samples, followed among the gram-negative bacteria by *Acinetobacterlwoffi* (8.33%), *Achromobacter group F* (6.66%), *CDC group IIj* (5%), *Moraxella* spp.(3.33%), *CDC Group IIF*(3.33%), *Burkholderia mallei* (3.33%), *Flavobacterium* spp. (1.66%), *Kingella* spp. (1.66%), *Escherichia coli*(1.66%), *Eikenellacorrodens*(1.66%), *Serratiarubiaceae* (1.66%), and*Klebsiella* spp. (1.66%). The gram-positive bacteria isolated consisted of *Bacillus* spp. (6.66%), *Streptococcus* spp. (3.33%), *Staphylococcus* spp. (3.33%), and *Micrococcus* spp. (1.66%). This study demonstrates the diversity of the domestic feline oral cavity microbiota and discusses the variation of the generaidentified in studies carried out in different geographic regions.It is also of importance not only to veterinarians, but also to health care professionals involved in the medical treatment of humans with animal bite wounds.

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INTRODUCTION

Thousands of people seek medical attention every year due to bite wounds from pets. Such wounds not only cause pain, but can also result in bacterial infections, which incur costs and are a public health problem (Viaro 2004). Therefore, the microbiology of the wounds caused by animal bites has been studied in human medicine to identify the microbiological and epidemiological aspects (Viaro 2004). Although dog bites are more common and account for approximately 80% of all reported bites (Patronek and Slavinski 2009), infection rates are higher in bite wounds from cats, due to the deep punctate lesions caused by theirsharperteeth (Westling *et al*. 2006). Infection is estimated to occur in 20 to 80% of lesions caused by cat bites, while infection occurs in less than 18% of those from dog bites (Talan *et al*. 1999). The microorganisms isolated from cat bites include bacteria of the genera *Streptococcus, Staphylococcus, Fusobacterium, Bacteroides, Porphyromonas, Moraxella,* and, most commonly, *Pasteurella*, which are known for causing various infections in humans (Kalchbrenner 2017). Considering the increasing preference for cats as pets, with numbers surpassing those of dogs in some countries (AVMA 2012), and the lack of knowledge regarding the geographic diversity of the oral microbiota and its dynamics in bite-infection processes in humans, the objective of this study was to characterize the oral microbiota of the domestic cat population in the city of Campo Grande, Mato Grosso do Sul, Brazil.

MATERIALS AND METHODS

This study evaluated 50 cats that were brought to the Zoonoses Control Center (CCZ) of Campo Grande, Mato Grosso do Sul for neutering and spaying between September 2012 and April 2013. Each animal's owner answered the anamnesis questionnaire, and all physical examination parameters were recorded. After the animals were anesthetized for surgery following the institution's protocol (CCZ), the oral cavity was

exposed, and a sterile swab was rubbed on the gums. Subsequently, the swab was inserted into a tube containing Brain Heart Infusion (BHI) broth. The sample was labeled and immediately sent for bacterial culture at the Laboratory of Bacteriology (LABAC) of the School of Veterinary Medicine and Animal Science of the Federal University of Mato Grosso do Sul (UFMS). The samples were seeded on BHI agar and incubated in an aerobic environment for up to 72 hours. Cultures were identified using biochemical tests, according to the scheme proposed by Koneman (2008), and statistical probabilistic identification software for non-fermentative gram-negative bacterial genera (Bryant 2004). This study was part of a research project approved by the Ethics Committee for Animal Experimentation, UFMS, protocol number 296.

RESULTS

Of the 50 animals sampled, 21 were female, and 29 were male. They were between 6 months and 4 years of age;48 were of an undefined breed, one was a Persian, and one was a Siamese.
In this study, 20% of the samples had bacterial growth of more than one species, totaling 60 microorganisms,comprising 17 different bacterial agents. For the gram-negative bacteria (Table 1), the genus *Pseudomonas* was the most frequent, accounting for 45% of the total isolates. Forthe gram-positive bacteria (Table 1), the genus *Bacillus*was the most frequent, accounting for 6.66% of the total isolates.

Table 1. Aerobic gram-negative and gram-positive bacteria isolated from 50 oral microbiota samples from healthy cats in the city of Campo Grande, MS

Bacteria	Frequency (%)	Number of Samples
Gram-negative		
Pseudomonas spp.	45	27
Acinetobacterlwoffi	8.33	5
Achromobacter group F	6.66	4
CDC groupIIj	5.00	3
Burkholderia mallei	3.33	2
CDC group IIF	3.33	2
Moraxella spp.	3.33	2
Escherichia coli	1.66	1
Eikenellacorrodens	1.66	1
*Flavobacterium*spp.	1.66	1
*Kingella*spp.	1.66	1
*Klebsiella*spp.	1.66	1
Serratiarubiaceae	1.66	1
Gram-positive		
Bacillus sp.	6.66	4
Staphylococcus spp.	3.33	2
Streptococcus spp.	3.33	2
Micrococcus spp.	1.66	1
Total	100	60

DISCUSSION

Although none of the individuals in this study had evident lesions of periodontal disease, a dental evaluation using specific instrumentsand laboratory testing for viral diseases were not performed. Therefore, the results refer to the characterization of the oral cavity microbiota of domestic cats considered clinically healthy. A large variety of bacterial species was identified in the oral cavity of the sampled cats, as has beenreported in other studies (Dolieslager *et al*. 2011, Perez-Salcedo *et al*. 2011, Sturgeon *et al*. 2014, Harris *et al*. 2015,Weese *et al*. 2015, Whyte *et al*.,unpublished data). The clinical interpretation and relevance of such microbiological diversity remains obscure, and there is no definite conclusion, since variation in important methodological aspects is observed among studies, such as inclusion of patients with viral comorbidities (Weese *et al*. 2015, Sturgeon *et al*. 2014),use of different methods to define periodontal disease (Dolieslager *et al*. 2011, Harris *et al*. 2015), and different objectives (Magaji *et al*. 2008, Perez-Salcedo *et al*. 2011), which makes it impossible to compare results directly. One of the few commonalitiesamong studies is the observation that regardless of the culture technique (Dolieslager *et al*. 2011, Perez-Salcedo *et al*. 2011, Whyte *et al*., unpublished data) or molecular biology (Dolieslager *et al*. 2011, Harris *et al*. 2015), the bacterial diversity found in healthy oral cavities is greater than that found in oral cavities that present some type of clinical alteration. However, it is still uncertain whether this alteration is primarilycaused by bacteria or is secondary to previous lesions in the oral mucosa. Although the diversity of the oral feline microbiota isreportedly related to sex, no significant difference was found in this study, in contrast to Whyte *et al*. (unpublished data), who reported a higher frequency (p=0.009) of females with more than two bacterial genera per sample (70.8%),when compared to samples of males. Furthermore, there are no significant discussions about the effect of age on the microbiota, and this information may be absent in some studies (Mallonee *et al*. 1988, Magaji *et al*. 2008, Dolieslager *et al*. 2011). This may be due to the higher prevalence of studies that correlate bacterial diversity with oral cavity diseases (periodontal disease and/or gingivitis-stomatitis complex) (Healey *et al*. 2007), which intrinsically involve older patients.

Another frequent result is the higher prevalence of *Pasteurella* spp.in oral cavity samples (Dolieslager *et al*. 2011) and bite lesions (Westling *et al*. 2006). However, as in the study by Perez-Salcedo *et al*. (2011), no samples of this genus were identified from oral cavities sampled in our study. The isolation of *Pseudomonas* as the most prevalent genus (45%) is unprecedented, both in results previously reported on the direct evaluation of the oral cavity (Sturgeon *et al*. 2014, Harris *et al*. 2015,Weese *et al*. 2015, Whyte *et al*.,unpublished data), and in research on the microbiota of bitewounds (Westling *et al*. 2006, Abrahamian and Goldstein 2011, Lau *et al*. 2016). Due to the variability observed in the oral microbiota of each individual, the importance of regional microbiological characterization is indicated, as knowledge of the specific bacterial agent involved in an infectious process prior to the completion of laboratory isolation can aid in preventing severe complications, as was already reported for *Pasteurella* spp. (Jones and Lockton 1987, Al-Allaf *et al*. 2001) and *Pseudomonas* spp.infections (Bodey *et al*. 1983, McCarthy and Paterson 2017). Unreasonable use of antimicrobial agents has been reported in veterinary medicine, and *in vitro* antimicrobial resistant strains of *Staphylococcus*have been isolated from the oral cavity of domestic cats(Muniz *et al*. 2013, Rossi *et al*. 2017). In spite of the fact that *Staphylococcus* and *Streptococcus*spp. each representedonly 3.33% of the total samples in this study, they have been isolated at higher frequencies by other authors (Magaji *et al*. 2008, Whyte *et al*., unpublished data).

Conclusions

This is the first report demonstrating *Pseudomonas* as the main bacterial genus isolated from the oral cavity of domestic cats. Therefore, this study presents information that supports the importance of updated local epidemiological knowledge, as organisms of the genus *Pseudomonas,* like those

ofPasteurella, Staphylococcus, and Streptococcus, can be responsible for severe complications ofinfections in humans and animals.

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