J Med Microb Diagn 2017, 6:2(Suppl)
DOI: 10.4172/2161-0703-C1-006

Evaluation of domestic dogs and cats oral flora in relationship of oral hygiene and detection of multi resistant bacterial strains

Ka Tik Cheung
Tung Wah College, China

Recently, human-animal interaction has occurred more frequently, animal bite injuries have become a serious and high-risk problems as the result. Oral flora can be transferred by close oral contact and through bites. While most of the bites do not require medical progress, only some bites would become an infection. The resultant infection is typically a poly-microbial infection; consist of common environmental flora and the oral flora in animals. As oral hygiene is an important method to reduce the number of bacteria of human oral cavities, but there are only a few articles demonstrated in domestic dogs and cats. To evaluate the effectiveness of oral hygiene in domestic dogs and cats, this study compared the complexity of isolates from the oral cavities and the frequencies of performing oral hygiene. The age of domestic dogs and cats was compared to the number of isolates from the flora as well. Besides, the oral flora was identified and the frequency of occurrence was evaluated, in order to attempt the bacteriology of domestic dogs and cat's oral cavity and the causative agent of human infection. In this study, gram stain, a series of biochemical tests and Matrix-assisted Laser Desorption Ionization-Time of Flight Mass Spectrometry (MALDI-TOF-MS) were used in identification. *Pasteurella* species and *Streptococcus* species were isolated in high frequency. *Neisseria* species, *Pseudomonas* species, Enterobacteriaceae family, *Corynebacterium diphtheriae, Achromobacter xylosoxidans/denitrificans* and *Sphingomonas paucimobilis* were also identified in the samples as well. Moreover, detection of multiple antibiotic resistant bacteria was also carried out in this study as well. It was used to provide more evidence-based information on antibiotic therapy in dog bite wounds and related infections. In which, multi-resistant organisms and extended-spectrum beta-lactamase (ESBL) positive Enterobacteriaceae were found in the oral cavity of sample dogs. Antibiotic susceptibility patterns for some bacteria were evaluated in this study.

ktcheung@twc.edu.hk

Expression discrimination of STAT3, NF-κB3 in the Uygur and Han asthma patients in Xinjiang Urumqi

Yao Li-Min, Jiang Xiao-fang, Delixiati Yimiti and Gao Li
Xinjiang Medical University, China

Background: The STAT3 and NF-κB3 transcription factor is critical for cytokine signaling and the acute phase response, but its role in allergic asthma is largely undefined.

Aim: Aim of this study is to investigate the expression levels of STAT3 and NF-κB3 in Xinjiang Uygur and Han population of asthma and healthy individuals.

Method: Peripheral Blood Mononuclear Cells (PBMCs) were isolated from Xinjiang Uygur asthma (n=25), Han population asthma (n=115) and healthy individuals (n=121). The expressions of STAT3mRNA and NF-κB3 (P65) mRNA were quantified through the RT-PCR.

Results: The distribution of expression of STAT3mRNA and NF-κB3mRNA was significantly different between asthma group and healthy controls. The distribution of expression of STAT3mRNA was significantly different between Xinjiang Uygur asthma group and Han population asthma group. There was no difference of distribution of expression of NF-κB3mRNA between Xinjiang Uygur asthma group and Han population asthma group.

Conclusions: It is indicated that the STAT3 and NF-κB3 might be involved in the etiology of asthma.

~~**ktcheung@twc.edu.hk**~~