Oral presentations

METHODS

A retrospective epidemiological study was performed on the results of canine BAL submissions to three referral veterinary laboratories between July 2013 and July 2018. Data on signalment, microbial culture, and cytological findings were collected. Cases were excluded if insufficient information was available. Data was collated using Microsoft Excel and descriptive statistics were performed using GraphPad Prism.

RESULTS

2501 cases were collected from a 5 year period. Cases ranged in age from 1 to 17 years with a mean age of 7.87 years. 1735 (69%) of those cases had microbial culture performed, with 767 yielding a positive culture. 405 cases

(16.2%) had a cytological diagnosis of neutrophilic inflammation with sepsis, 237 of which had a concurrent positive microbial culture result. 1100 cases had findings of neutrophilic inflammation with no overt signs of sepsis found. *Bordetella* spp., Beta haemolytic *Streptococcus*, Coagulase-positive *Staphylococcus*, Coliform spp., and *Pasteurella* spp. were the most frequent bacterial species isolated in cases of sepsis. Oropharyngeal contamination was found in 308 submissions, and 315 proved non-diagnostic. There was no significant difference in age or sex between disease groups.

STATEMENT (CONCLUSIONS)

Bacterial infection of the lower respiratory tract is a frequent finding, more commonly made via cytological signs of sepsis, rather than microbial culture.

Core outcomes in feline Chronic Kidney Disease: what should we be measuring?

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OBJECTIVES

Over 100 different parameters are measured in the published treatment efficacy studies for cats with Chronic Kidney Disease (CKD), making it impossible to compare or combine the results of studies. Developing an agreed Core Outcome Set (COS) would resolve some of the issues as all future studies can use these when assessing treatment efficacy. The overall aim of this study was to create a COS for CKD in cats.

METHODS

Using a Delphi methodology, an anonymous, international panel of 73 stakeholders, including clinical experts, journal editors, regulatory agencies and cat owners, completed a series of online questionnaires to build consensus on the most important parameters to measure when treating cats with CKD. They were asked to rate the importance of parameters using Likert scales (1–9). Consensus was defined a priori as 80% of participants rating the parameter as 8 or 9. The study contained 3 rounds in total.

RESULTS

Response rate was between 78 and 95% across the first questionnaires, with 14 parameters reaching consensus for inclusion within the first round of the study. These included specific parameters from urine and serum tests, quality of life, survival time/renal survival end-point, IRIS stage and clinical examination.

STATEMENT (CONCLUSIONS)

This research highlights the outcomes which all stakeholders consider important when making treatment decisions for cats with CKD. Including this COS in future clinical trials will ensure results will be relevant to both first opinion and referral practice, strengthening the evidence base available for decision making.

A cat and mouth game: Investigation of odontoclast dysregulation in feline tooth resorption

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OBJECTIVES

Feline tooth resorption (TR) is a painful and progressive clinical condition that affects at least 30% of adult cats. Recently, a RNA sequencing study (unpublished data)

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identified >1000 differentially expressed (DE) genes between TR negative (TR-) and TR positive (TR+) teeth. Many of the DE genes were involved in pathways relating to TR, odontoclast differentiation, and tooth remodeling processes. From this data, six genes (MMP9, P2XR4, SPI.1, OPG, RANK, RANKL) were chosen for closer inspection. The objectives of this study were: 1. To confirm if these six genes are truly differentially expressed between TR+ and TR- teeth, and 2. To localize protein expression from these genes in feline dental tissues.

METHODS

A case-control study was conducted on feline teeth collected from clinical samples and at post mortem with owner consent. Quantitative-PCR using the delta-delta method was used to validate the selected genes, followed by immunohistochemical staining to label the proteins in tissue samples. H&E-stained tooth sections

were also evaluated to investigate the histological features of TR+ teeth.

RESULTS

Quantitative-PCR analysis revealed increased MMP9 and P2XR4 expression in TR+ teeth. The RANKL/OPG expression ratio did not change significantly between paired teeth. H&E and immunohistochemical staining of feline tooth sections identified the presence of odontoclasts, strong MMP9 expression, and ankylosis at sites of TR.

STATEMENT (CONCLUSIONS)

Identification of specific genetic factors involved in feline tooth resorption could have important implications for the development of therapeutic treatments for the condition.