were also three times more likely to contain *Staphylococcus spp.* compared with post-wash scrubs.

73 out of 78 (93.6%) of participants responded to the questionnaire. 61.6% did not wear a clean scrub top every day, whilst 53.4% did not wear clean scrub trousers every day. Additionally 60.3% left the hospital in their uniform after the working day.

STATEMENT (CONCLUSIONS)

Clinicians and nurses should be aware that bacterial contamination occurs during a shift and that home laundry detergent is effective at reducing bacterial count. A minority of veterinary professionals wear clean scrubs daily.

Detection of Feline Immunodeficiency Virus and Feline Leukemia Virus in tissue samples of domestic cats with *in situ* hybridization

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OBJECTIVES

The aim of the project was to detect Feline Immunodeficiency Virus (FIV) and Feline Leukemia Virus (FeLV) in various types of tissues of infected domestic cats with a method of RNAscope®.

METHODS

Multiple tissues from cats were harvested using a standard protocol at the Department of Pathology of

University of Veterinary Medicine, Budapest. Tissues were fixed in 8% neutral buffered formalin for 16–48 hours. Fixed samples were dehydrated in a graded series of ethanol and xylene, followed by infiltration of melted paraffin at 56°C. Sections were cut at a thickness of 5 µm and mounted on the SuperFrost® Plus slides. Ready-to-use reagents from RNAscope® 2.5 HD Reagent Kit-RED were used on our slides and control slides with target and positive/negative control probes as per manufacturers' instructions, in a manual assay workflow. Sections were evaluated with Olympus CX21 light microscope, images were acquired using Nikon imaging system. RNA markers were analyzed based on the average RNA dot number per cell.

RESULTS

FIV and FeLV can be visualized with RNAscope® *in situ* hybridization in various tissue types (spleen, lymph node, kidney, lung, intestine, bone marrow) and also in neoplastic tissues.

STATEMENT (CONCLUSIONS)

In future studies these results with *in situ* hybridization can be compared with other diagnostic methods (e.g. polymerase chain reaction, PCR) to learn more about the pathogenesis of these viruses, and refine data in individual clinical cases.

Investigating expression of proteins associated with glomerular endothelial cell fenestrations in diabetic cats and dogs

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OBJECTIVES

To evaluate expression of proteins that play a role in glomerular endothelial cell fenestration formation (Eps homology domain 3&4 [EHD 3&4], moesin and vascular endothelial growth factor [VEGF]) in glomeruli from diabetic compared to control cats and dogs.

METHODS

Kidney tissue was obtained at post-mortem from 11 diabetic dogs (DD), seven diabetic cats (DC), four dogs with glomerulonephritis (GD), three cats with glomerulonephritis (GC) and five cats with normal kidney structure and function (NC). Samples were paraffin-embedded and protein staining using immunohistochemistry was optimised. A standard immunohistochemistry protocol was followed and primary antibodies and dilutions trialled. Glomerular protein expression was evaluated by scoring

Poster presentations

staining intensity under light microscopy, using a 0–3 scale by two independent scorers and objective quantification using an image-processing program. Staining intensity was compared between groups using T-testing.

RESULTS

An immunohistochemistry protocol for EHD 3&4, moesin and VEGF staining was successfully optimised for kidney tissue from dogs and cats. Expression of VEGF was significantly increased in DC ($P=0.016$) and GC ($P=0.028$) compared to NC. Moesin expression was also significantly

increased in GC compared to NC ($P=0.038$). No significant difference in expression of EHD 3&4 was found. There was no significant difference in protein expression between DD and GD.

STATEMENT (CONCLUSIONS)

Increased VEGF and moesin expression in DC and GC may suggest glomerular endothelial cell fenestration number is changed in these diseases thus affecting renal filtration function. The non-significant results in dogs could be due to lack of an appropriate control group.

Network analysis of multiple brain morphometric features in dogs to isolate key driving factors for syringomyelia

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OBJECTIVES

Syringomyelia (SM) is an extremely painful condition that commonly affects the Cavalier King Charles Spaniel (CKCS) and represents one of the most important welfare issues currently present in veterinary neurology. Much controversy exists surrounding the development of SM; historically, diagnosis has focused on Magnetic Resonance Imaging (MRI) features of the spinal cord and Chiari-like malformation (CLM) at the skull-neck junction, overlooking potentially relevant features of the brain. This study set out to test whether any MRI-derived

morphometric features of the brain may explain the predisposition of dogs to SM.

METHODS

An unbiased approach was taken using network analysis software (Miru) to evaluate enrichment within 8,432 data points, incorporating clinical data and blinded retrospective measurements of brain MRI features in 246 dogs, including 22 CKCSs.

RESULTS

Key preliminary findings included a significant correlation between brain ventricle morphometry and breed type in terms of length of the skull. CKCS dogs clustered independently based on median age at MRI, brain length-to-volume ratio, cerebellar volume and sulcus depth. To date, this study has generated the most comprehensive analysis of MRI-based brain morphometry in dogs, highlighting candidate measures to explore further as putative drivers of SM.

STATEMENT (CONCLUSIONS)

Preliminary analysis has clustered brachycephalic breeds on the basis of ventricular morphology, and a proportion of CKCS dogs due to a combination of factors, including ventricular morphology. Further analysis of this data is ongoing and will focus on parameters that isolate CKCS dogs independently of features associated generally with brachycephaly and parameters that isolate dogs with SM irrespective of breed.