The occurrence of mycoplasma felis infection in Feline BAL samples and its association with cytological patterns of inflammation

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A number of *Mycoplasma* species, including *M. felis*, have been identified from the upper respiratory tracts of healthy cats; however, *Mycoplasma* spp. are not generally considered to be present in the lower airways of healthy cats. *Mycoplasma* spp. are too small to be commonly identified with routine light microscopy and require special microbial culture conditions to grow. Therefore increasingly, detection relies upon PCR techniques, which are often not routinely performed on BAL samples. However, *M. felis* infection may be associated with particular patterns of inflammation, which

when present, could act as a trigger for pursuing further investigation with PCR. The purpose of the current study was twofold. Firstly, to investigate how commonly *M. felis* is present, detected using quantitative PCR (qPCR), in feline BAL samples submitted to a commercial diagnostic laboratory from cases with clinical signs of respiratory disease; and secondly, to examine the relationship between cytological patterns of inflammation and the presence of *M. felis* DNA. Feline BAL samples were prospectively collected and a cytospin preparation was made, Wright's stained and examined cytologically. Samples without respiratory epithelium or containing oropharyngeal contamination were excluded from the study. A 100 inflammatory cell differential count was performed to identify the pattern of inflammation in each case. Fluid from each case was assessed for the presence of *M. felis* using qPCR. *M. felis* DNA was detected in 38.3% (23/60) of samples examined. The cytological pattern of inflammation could not be used to accurately predict positive cases. Using a cut off of 10% or more eosinophils provided the highest sensitivity (78.3%) but specificity was poor (48.6%). Given the lack of accuracy of the inflammatory pattern in predicting infection with *M. felis*, and the high incidence of *M. felis* infection in feline BALs, the results of this study indicate that routine PCR investigation for the presence of *M. felis* in cats presenting with respiratory signs seems justified.

Lab-based surveillance of toxoplasmosis in pets in the UK

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Toxoplasmosis is a zoonotic disease caused by the protozoan parasite *Toxoplasma gondii* with cats being the definitive host. Recently, efforts have been made to enhance the surveillance system for human toxoplasmosis in the UK. However, companion animals lack coordinated toxoplasmosis national surveillance.

Here we use data from commercial diagnostic laboratories, gathered by SAVSNET – The Small Animal Veterinary Surveillance Network to estimate the proportion and spatial distribution of positive *T. gondii* samples in dogs and cats. We also investigate both space-time clusters of infections with *T. gondii* and samples in which a diagnosis was not reached.

The study was performed using results of immunofluorescence assays conducted between January 2012 and May 2014. A retrospective space-time permutation scan statistic

model which requires only case data was used to investigate clusters of *T. gondii* infections. Clusters of samples tested negative were investigated using a space-time Bernoulli (i.e. case/control study) scan statistic model. The maximum size of the spatial and temporal windows for the clusters was assumed to be 50% of the study area and study period, respectively. Models were run 999 times using a Monte Carlo sampling method using SaTScan software version 9.2. Results were mapped using Quantum GIS (version 1.8.0-Lisboa).

In dogs and cats, the mean percentage of samples testing positive to *T. gondii* was 9.0% (95% CI = 8.1% – 9.9%) and 12% (95% CI = 10.3% – 13.9%) respectively. Samples for *T. gondii* testing were submitted to the labs from 30 (24.8%) UK postcode areas. Edinburgh was the area where the highest percentage of samples tested positive (mean = 15.5%, 95% CI = 11.4% – 20.7%). However, no significant ($P < 0.05$) space-time infection clusters were identified. Significant space-time clusters of negative samples were located: in dogs in northern and southern regions of the UK during the first half of the year 2012, and in cats in the southeast of the country between April and October 2012.

This is the first time lab-based surveillance has been used to generate national maps of distribution for *T. gondii* infection in dogs and cats. In the future, any significant hotspot of infection in cats may be used to target human health interventions. In addition, identifying clusters of samples in which a diagnosis is not reached could help identify the emergence of new strains or new diseases over space and time.