

PREVALENCE IN VET-VISITING DOGS IN THE UK

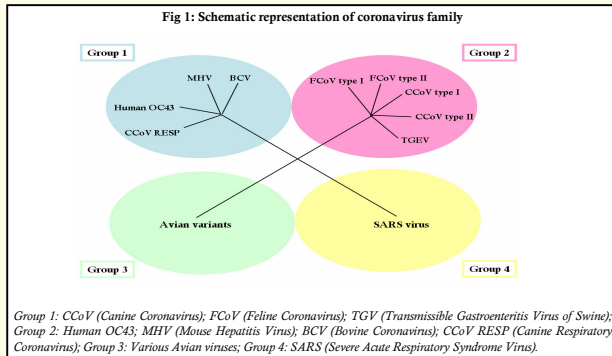
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Canine coronavirus

Canine coronavirus (CCoV) is a member of the coronavirus family, a diverse group of viruses which includes the causative agents of Severe Acute Respiratory Syndrome (SARS) in humans, and Feline Infectious Peritonitis (Fig 1)

This study concerns the (Group 1) enteric CCoV. This exists as two subtypes; the original, designated CCoV Type II, and the recently recognised Type I¹. A (Group 2) respiratory CCoV also exists, but will not be further discussed here.



Clinical Disease

Enteric CCoV most typically presents as diarrhoea, sometimes associated with vomiting, inappetence and pyrexia. Disease is generally mild and self-limiting; however there have been occasional reports of severe gastrointestinal disease, neurological signs and even sporadic fatalities attributed to CCoV infection^{2,3}.



In outbreaks in closely confined environments such as rescue shelters and boarding and working kennels, morbidity can be very high, with reports of up to 95% of dogs in a kennel being affected⁴.

Asymptomatic carriage of the virus appears to occur in healthy dogs, and this may be important epidemiologically. However, there is relatively little known either about the prevalence of CCoV in healthy dogs or the current status of the disease in the UK

Study Aims

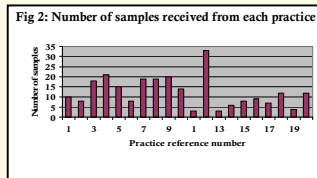
- To determine the prevalence of CCoV carriage among healthy dogs in the UK.
- To ascertain the genetic variation in types of CCoV present among UK dogs.

Methods

Dogs visiting veterinary practices were selected as the target population. One practice was recruited randomly from each of the 23 regions of the UK (regions as defined by the Royal College of Veterinary Surgeons). Each practice was requested to obtain a faecal sample from 25 dogs. Dogs could be visiting the surgery for any reason, including routine checks, neutering or illness; however practitioners were requested to neither specifically select nor exclude dogs with enteric disease, but to include a number which reflected their representation in the general population. For each sampled dog, owner consent was obtained, along with details of signalment and vaccinal and health status. All of these samples were tested for the presence of CCoV by RT-PCR targeting the conserved M region of the genome⁵. The PCR product was sequenced for each of the positive samples in order to explore their genetic relatedness.

Results – 1: Practice responses (Fig 2)

- Of 23 regions, three were excluded as they had no eligible practices willing to participate.
- Of the 20 remaining practices, all returned some samples, a response rate of 100%.
- Total number of samples received 249 (50% return rate).
- Mean number of samples returned 12.45 per practice (Minimum three; maximum 28).

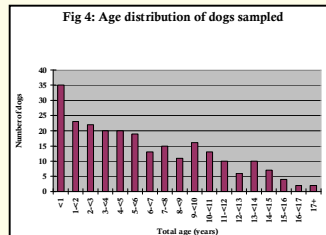


Results – 2: Questionnaire data (Figs 3 & 4)

Of the 249 dogs sampled, 111 (44.8%) were male; 134 (54%) were female, and 3 (1.2%) were not specified. 101 (40.7%) were visiting for a routine reason (including booster vaccination, parasite treatment, elective surgery and nail clip); 114 were visiting for a non-routine reason, and for 33 (13.3%) data was not available.

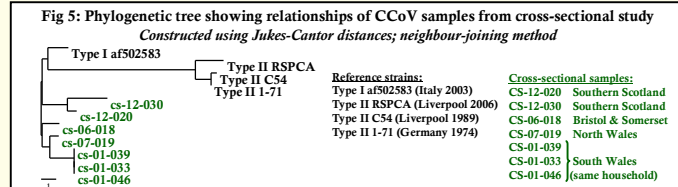
Fig 3: Demographic and clinical responses from questionnaire

	Yes	No	Don't know/unspecified
Is the dog a pedigree?	172 (69.4%)	72 (29%)	4 (1.6%)
Is the dog neutered?	167 (67.3%)	72 (29%)	9 (3.6%)
Has the dog had diarrhoea in the past month?	66 (26.6%)	181 (73%)	1 (0.4%)
Has the dog had any vomiting in the past month?	39 (15.7%)	208 (83.9%)	1 (0.4%)
Is the dog specifically presented for vomiting and/or diarrhoea?	14 (5.6%)	200 (80.6%)	34 (13.7%)



Results – 3: Prevalence of Coronavirus

Seven samples were positive for CCoV, a prevalence of 2.8% (95% confidence intervals 1.1, 5.7). These seven samples were from four different regions. Three of the samples came from healthy dogs in a single household. Of the other four positive samples, three had a history of diarrhoea within the previous month.



Results – 4: Sequence analysis (Fig 5)

All of these isolates cluster with type I CCoV in the M gene region. Apart from the three dogs from the same household, all of the sequences exhibited distinct base polymorphisms, eliminating the possibility of contamination.

Conclusions:

CCoV is circulating at a low prevalence among the general dog population in the UK. Isolates of the newly-emerged Type I CCoV were found at several locations in the UK. This represents the first report of type I CCoV in the UK. Further investigations are planned, including sample analysis by fluorogenic ('real-time') PCR, and a case-control study of dogs with enteritis. It is hoped that these will elucidate the role of this pathogen in canine enteric disease.

Acknowledgements:

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