Spatial Distribution of Feline Calicivirus Strains From a Sample of the UK Vet-visiting Cat Population

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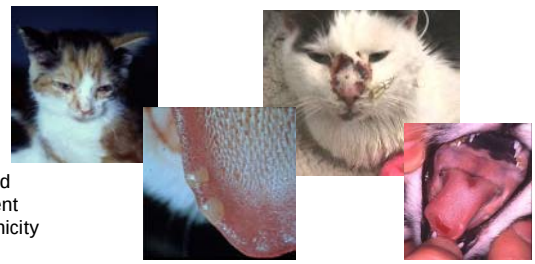
BACKGROUND and AIMS

Feline calicivirus (FCV) is a highly infectious RNA pathogen of domestic cats, belonging to the *Caliciviridae* family, which includes other important pathogens of man.



FCV infection is generally associated with mild acute oral and respiratory disease. More recently, outbreaks of severe systemic calicivirus disease with high mortality have also been reported (1)

FCV is a highly variable virus, both genetically and antigenically. There are a large number of different strains of FCV, with varying antigenicity pathogenicity circulating in the general cat population.

FCV vaccines do not prevent infection, and both vaccinated and unvaccinated cats may become asymptomatically persistently infected, with FCV prevalence rates as high as 91% being reported (2, 3).

The variability of feline calicivirus represents a major challenge to its control.

It is crucial to understand how such viruses are transmitted and how they persist in the wider population: Disease will ultimately only be controlled if we can control virus spread.

Here we have used a sample of the UK veterinary-visiting cat population to determine the prevalence and genetic diversity of FCV.

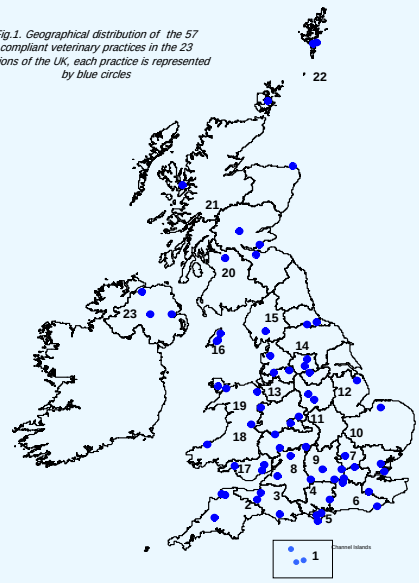
METHODS and RESULTS

Three veterinary practices were randomly chosen from each of 23 regions of the UK, as defined in the Royal College of Veterinary Surgeons register of practices (2004).

A total of 69 practices were asked to take oropharyngeal (OP) swabs from 30 consecutive, compliant cats presented at their surgery between September and December 2006.

For each sampled cat, owner consent was obtained and a simple questionnaire, detailing the cats postcode and basic demographic and clinical details was completed. All OP samples were batched and sent to our laboratory for virus isolation and sequencing of the viral capsid using standard protocols (2)

Fig.1. Geographical distribution of the 57 compliant veterinary practices in the 23 regions of the UK, each practice is represented by blue circles



Cross sectional study September - December 2006	
Practice compliance	83% (57/69)
Total number of samples returned	1466
Mean number of samples per practice (Range per practice, min – max)	26.5 (3 – 34)
Overall UK prevalence (Range per practice, min – max)	9% (135/1466) (0 – 33%)

Table 1: Summary of compliance and prevalence

A practice compliance rate of 83% and an FCV isolation rate of 9%, was achieved *(Table 1).*

Univariable analysis identified a number of individual cat predictor variables that were associated with FCV carriage including: current mouth ulcers, current URTD, past mouth ulcers and past URTD. In addition, cats that had been vaccinated were less likely to be FCV positive *(Table 2).*

FCV isolates were obtained from each of the 23 geographical regions *(Fig. 1*). Region 23 had the highest prevalence (20%), and region 21 had the lowest prevalence (1%).

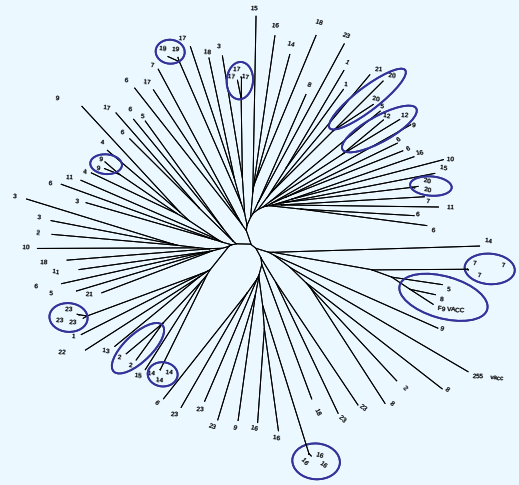
Variable	Odds Ratio	95% C.I	P value
Current vaccination			
No	1		
Yes	0.53	0.37 – 0.78	P = 0.001
Current mouth ulcers			
No	1		
Yes	11.69	6.64 – 20.58	P <0.001
Current URTD			
No	1		
Yes	3.15	1.8 – 5.52	P <0.001
History of mouth ulcers			
No	1		
Yes	5.14	2.59 – 10.19	P <0.001
History of URTD			
No	1		
Yes	2.47	1.41 – 4.33	P <0.001

Table 2: Univariable analysis of FCV carriage

A wide range of genetic diversity of FCV was observed with phylogenetic analysis identifying **76** distinct strains of FCV circulating in the UK *(Fig. 2).*

Some evidence of geographical clustering was identified, where viruses isolated from different cats from the same practice clustered together (outlined in blue) as variants of a single strain.

Figure 2: Genetic diversity of 94 of the 135 FCV isolates obtained from regions 1 -23). Clusters, outlined in blue, represent variants of the same strain isolated from the same practice within a region.



CONCLUSIONS

FCV is endemic in the UK cat population

A wide range of different strains appear to be circulating in the UK cat population, with some geographical clustering of variants of the same strain. This suggest that transmission and evolution of FCV may be occurring at the local level.

Future work will include analysis of strain variability within and between practices , and investigation of correlation between the precise geographical location of a virus isolate and its genotype

References: 1. Coyne, et al (2006). Lethal outbreak of disease associated with feline calicivirus infection in cats. *Vet Rec* **158**, 544 - 550.2. Coyne et al., (2006) Long term analysis of feline calicivirus prevalence and viral shedding patterns in naturally infected colonies of domestic cats. *Ver. Micro.* **118**, 12-25. 3. Coyne et al., (2007) Evolutionary mechanisms of persistence and diversification of a calicivirus within endemically infected natural host populations. *J Virol* **81**, 1961-1971.