A mRNA PCR for the diagnosis of feline infectious peritonitis

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Abstract

A reverse transcriptase polymerase chain reaction (RT-PCR) for the detection of feline coronavirus (FCoV) messenger RNA in peripheral blood mononuclear cells (PBMCs) is described. The assay is evaluated as a diagnostic test for feline infectious peritonitis (FIP). It is based on a well-documented key event in the development of FIP: the replication of virulent FCoV mutants in monocytes/macrophages. To detect most feline coronavirus field strains, the test was designed to amplify subgenomic mRNA of the highly conserved M gene. The test was applied to 1075 feline blood samples (424 from healthy, 651 from sick cats suspected of FIP) and returned 46% of the diseased cats as positive for feline coronavirus mRNA in their peripheral blood cells; of the healthy cats, 5% tested positive. Of a group of 81 animals in which FIP had been confirmed by post-mortem examination, 75 (93%) tested positive, whereas 17 cats with different pathologies (non-FIP cases) all tested negative. In view of the low rate of false-positive results (high specificity) the mRNA RT-PCR may be a valuable addition to the diagnostic arsenal for FIP.

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1. Introduction

Coronaviruses are enveloped, positive-stranded ssRNA viruses, a genus in the family Coronaviridae, order Nidovirales. They are ubiquitous in cat populations, with particularly high prevalence in catteries and multiple-cat households. Feline coronaviruses (FCoVs) show a bimodal pathogenicity distribution, with subclinical or mild enteric infections in young kittens at one extreme and the deadly feline infectious peritonitis (FIP) at the other. The low virulence strains are referred to as feline enteric coronaviruses (FECoV), the highly virulent ones as FIP viruses (FIPV). Though occurring only sporadically (i.e. not causing epidemics), FIP is an important disease: it is mostly fatal, its biology is still poorly understood and prevention is difficult, to say the least. FIP is an immune mediated, progressive polyserositis and pyogranulomatosis. It occurs worldwide, affecting both domestic and wild felids (Holzworth, 1973; Horzinek and Osterhaus, 1979). Antibodies against FCoVs are found in 80-90% of the animals living in catteries or multiple-cat households and in up to 50% of solitary cats; however, only some 1–5% of the seropositive cats eventually come down with FIP. The reason for this discrepancy became clear when the biological and genetic properties of FECoV and FIPV isolates had been studied (Addie and Jarrett, 1992; Hohdatsu et al., 1992; Horzinek and Osterhaus, 1979): the avirulent FECoV strains causing inconspicuous infections are responsible for the high sero-
prevalence; in cats experiencing some immunosuppressive event, expansion of the quasispecies cloud and mutations in the FCoV genome lead to virulent variants that induce FIP (Vennema et al., 1998).

At present, there are no routine serological and virological assays available for an aetiological diagnosis of FIP, and to distinguish avirulent from virulent FCoVs. Although serology is still used in the diagnosis of FIP, it is of very limited value. Results can only be interpreted in correlation with clinical symptoms. Currently the presumptive diagnosis of FIP is based on clinical data and characteristic changes in some blood parameters (Cammarata Parodi et al., 1993; Gouffeux et al., 1975). A definite diagnosis can only be made on the basis of histological examination of biopsy material or post-mortem (Sparkes et al., 1991, 1992).

Our PCR technique using primers targeted to conserved regions of the viral genome, the 3′-UTR (Lai and Cavanagh, 1997), and its modifications (using the S gene (Gamble et al., 1997)) became a valuable tool for the detection of FCoV in body fluids and tissue samples. Unfortunately, the technique detects also avirulent FCoVs in healthy cats. Although the percentage of PCR-positive healthy animals is much lower when compared to FIP cats, a positive PCR result alone does not allow a definite diagnosis (Egberink et al., 1995; Gunn-Moore et al., 1998).

An important event in FIP pathogenesis is the infection of monocytes and macrophages (Stodart and Scott, 1989). Originally, it was thought that the avirulent FECVs would remain confined to the digestive tract and not spread beyond the intestinal epithelium and regional lymph nodes. Virulent FIPVs, on the other hand, would leave the gut, enter the bloodstream, generalize and reach different organ parenchymas via infected monocytes. Not unexpectedly, however, FCoV were detected in blood samples of healthy cats that never developed FIP, and also after experimental FCoV infection (Gamble et al., 1997; Zhang et al., 1994) would detect the macrophage-tropic sequences in cell culture. FIPV UCD3 was obtained from tissue cell culture from infected feline feces (Pedersen et al., 1981b). FECV UCD was acquired from feline feces as described by Pedersen (1987) and grown to low titers in fcfv cells. FIPV Dahlberg was obtained from brain of a mouse inoculated with homogenate as described by Osterhaus et al. (1978). FIPV Wellcome was derived from feline embryonic lung cells as described by O’Reily et al. (1979).

Blood samples were collected from diseased cats suspected of having FIP based on clinical symptoms (n = 651) as well as from healthy cats (n = 424). The healthy cats were mainly animals living in the same household or cattery as the cats suspected of having FIP. These samples were obtained from different veterinary clinics in The Netherlands.

2.2. Sample preparation for RT-PCR

Blood: A maximum of 1 ml of non-coagulated EDTA blood was centrifuged for 10 min at 2500 rpm. Plasma was separated from the cell pellet and stored at −20 °C. One volume of PBS was added to the blood cells and total RNA was isolated following the Total Quick RNA Blood Kit Protocol (Talent).

As a control to check the efficiency of the RNA isolation from all the blood samples and the subsequent reverse transcriptase reaction, a glyceraldehyde-3-phosphate dehydrogenase (GAPDH) RT-PCR was performed for every clinical sample (primers 1180 and 1181).

### 2. Materials and methods

#### 2.1. Virus and clinical specimens

The FCoV reference strains and their sources are listed in Table 1. Strains FIPV 79-1146, FECV 79-1683, and FIPV UCD1 were grown in felis catus whole fetus (fcfw) cells. FIPV UCD3 was obtained from tissue cell culture from infected fcfv cells (Pedersen et al., 1981b). FECV UCD was acquired from feline feces as described by Pedersen (1987)

| Strain          | Source           | Reference                  |
|-----------------|------------------|----------------------------|
| FECV UCD        | Feline feces     | Pedersen (1987)            |
| FECV RM         | Feline feces     | Hickman et al. (1995)      |
| FIPV Dahlberg   | Mouse brain      | Osterhaus et al. (1978)    |
| FIPV UCD1       | Fcfv cells       | Pedersen et al. (1981b)    |
| FIPV UCD3       | Fcfv cells       | Pedersen and Flood (1985)  |
| FECV 79-1683    | Fcfv cells       | Evermann et al. (1981)     |
| FIPV 79-1146    | Fcfv cells       | McKeehan et al. (1981)     |
| FIPV Wellcome   | Feline embryonic | O’Reily et al. (1979)      |
|                 | lung cells       |                            |
| CCV K78         | Vennema et al.   | (1992)                     |
| TGEV Pernice    | Kapke and Brian  | (1986)                     |

2.3. Primer selection

The oligonucleotide primers were chosen from the highly conserved M gene sequence (primer 1124) of the FCoV genome combined with a primer aiming at the leader sequence of the FCoV-genome (primer 1179). Primer sequences are shown in Table 2.

### 2.4. Reverse transcriptase reaction

The reverse transcriptase (RT) reactions, 10 μl of the RNA solution and 2 μl of reverse primer 212 or 1181 (each
5 mM) were mixed and incubated for 2 min at 95 °C and immediately cooled on ice. Subsequently, a mix consisting of 4 μl RT-Buffer (10×; GibcoBRL Life Technologies), 2 μl dithiothreitol (DTT) (100 mM; GibcoBRL Life Technologies), 1 μl deoxyribonucleotide triphosphates (dNTPs) mix (25 mM each dNTP; GibcoBRL Life Technologies), 0.5 μl RNAguard/RNase inhibitor (40 U/μl; Pharmacia Biochemicals) and 0.5 μl Moloney Murine Leukaemia virus (MMLV) reverse transcriptase (200 U/μl; GibcoBRL Life Technologies) was added. The reaction mixture was spun down and incubated for 60 min at 37 °C. The enzyme was inactivated by incubation at 95 °C for 5 min. Samples were stored at −20 °C before using it in the mRNA RT-PCR assay.

### 2.5. Polymerase chain reaction

Following reverse transcription, 3 μl of the RT reaction mixture was added to 27 μl of the PCR reaction mixture. The PCR mix consisted of 3 μl PCR Buffer 2 (10×; Perkin Elmer USA), 1 × 10 μM Tris–HCl, pH 8.3, 50 mM KCl), 2.5 μl magnesium chloride (25 mM; GibcoBRL Life Technologies), 1 μl dNTPs (25 mM each dNTP; GibcoBRL Life Technologies), 1 μl primer 212 (5 mM), and 1 μl primer 1179 (5 mM) (both Invitrogen), 0.25 μl Taq Polymerase (5 U/μl; GibcoBRL Life Technologies) and 0.5 μl primer 1180 (5 mM), and 1 μl primer 1181 (5 mM) (both Invitrogen). For the GAPDH RT-PCR reaction the same PCR mix was used but with different primers: 1 μl primers 1180 and 1181 (each 5 mM) (both Invitrogen).

The reaction mixture was placed in a thermal cycler (Biozym). The temperature cycling protocol consisted of 10 min incubation at 95 °C followed by 30 cycles of 1 min denaturation at 95 °C, 1 min primer annealing at 62 °C and 1 min primer extension at 72 °C. The 30 cycles were followed by 10 min at 72 °C and finally the reaction mixture was cooled to 4 °C.

### 2.6. Analysis of amplified products

Twenty microliters of each PCR sample was analysed by electrophoresis using a 1.5% TAE agarose gel (GibcoBRL Life Technologies) for 45 min at 100 V. A 100 bp molecular weight marker (Invitrogen) was used to control the size of the amplified PCR product. Amplification products were visualised using ethidium bromide staining and UV radiation. Samples revealing a 295 bp fragment for the primers 212 and 1179 and another fragment of 195 bp for the primers 1180 and 1181 were considered positive for coronavirus. Amplification products were photographed using the BioRad GelDoc 1000.

Twenty-three of the obtained PCR products were sequenced to confirm the RT-PCR product.

In order to avoid contamination due to carry-over of amplification products several precautions were taken including physical separation of the pre- and post-PCR procedures, the use of aerosol resistant filter tips (Biozym), and during each step from RNA isolation to reverse transcriptase and amplification, negative controls of RNase free water were included to try to rule out any false positives.

### 2.7. Necropsy

If possible, necropsy of the cat was performed to confirm or rule out a clinical diagnosis of FIP. A total of 98 cats were subjected to post-mortem examination. When macroscopic observations were inconclusive, sections of different organs like liver, kidney, spleen etc. were prepared and examined histopathologically.

### 3. Results

#### 3.1. Primer sensitivity

To determine if a RT-PCR for M gene mRNA detects different coronavirus isolates, several laboratory isolates were subjected to this assay (Table 1). RNA from FIPV serotype I (strains UCD1, UCD3), and serotype II (strains 79-1146, NOR15, Wellcome), FECV serotype I (UCD, RM), FECV serotype II (79-1683), FIPV Wellicome, CCV-K378 and TGEV Purdue could all be detected in cell culture and faecal material or tissue homogenates. After amplification, fragments of the expected size of 295 bp were obtained with all isolates, as shown in Fig. 1.

In all samples tested, GAPDH amplicons were demonstrated. The GAPDH gene, which is constitutively expressed at high levels in most tissues, was used for reference as a positive result in the GAPDH RT-PCR will rule out any failure of sample RNA isolation or reverse transcription. An example of a positive mRNA RT-PCR assay and GAPDH control is shown in Fig. 2.
3.2. Detection of FCoV in the blood of healthy cats

Blood samples from 424 healthy cats were assessed for the presence of FCoV in peripheral blood cells. These animals had been living in catteries or multiple cat households, where other cats with FIP-related clinical signs were living. Twenty-three cats out of the 424 cats (5%) indeed tested positive for FCoV in the mRNA RT-PCR test. Two cats from the 23 PCR-positive animals became sick within 2 months, both showing different clinical symptoms, one of them indicative of FIP. Unfortunately, the cause of death could not be assessed by necropsy.

3.3. Detection of FCoV in blood of diseased cats

Veterinary practitioners had submitted 651 samples from cats they suspected to suffer from FIP. The animals had shown one or several of the following symptoms: fever, anorexia, weight loss, diarrhea, poor growth, enlarged abdomen, presence of ascitic or thoracic fluid, uveitis and neurological signs. Of these, 301 samples (46%) were positive for FCoV mRNA in blood cells. A summary of the PCR results is shown in Table 3.

3.4. Detection of FCoV in blood of cats with FIP confirmed by necropsy

Microscopy was performed on 98 cats tested for FCoV mRNA in the blood. In 81 cases FIP was confirmed. Of these, 75 cats (93%) were found to have FCoV mRNA in their peripheral blood cells (e.g. heart failure, neoplasia, and bacterial infections). The obtained results were statistically significant when controlled by a chi-square (Table 5).

4. Discussion

This report describes an RT-PCR assay to detect FCoV mRNA in blood samples of cats. Our approach was based on the assumption that during the pathogenesis of FIP, the mutant virus would replicate in monocytes and macrophages. We postulated that detection of FCoV mRNA in blood samples would correlate with the development of FIP. There are several observations that led to this assumption.

Infection of monocytes and macrophages is considered as the most important pathogenetic event in FIP. The mutant virus has acquired a new tropism and replicates to high titers in monocytes and macrophages (Stoddart and Scott, 1989; Kipar et al., 1999). In vitro, the virulence of FCoV strains...
correlated with their ability to infect macrophages: avirulent FCoVs infected fewer cells and produced lower titers than virulent FCoVs. The avirulent FCoVs were also inferior in susceptibility to FIP virus. Vet. Microbiol. 62, 193–205.

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