Full Title: Clinicopathologic features of a feline SARS-CoV-2 infection model

parallel acute COVID-19 in humans

Short Title: SARS-CoV-2-induced acute respiratory distress syndrome in domestic cats: a

model to study COVID-19

Authors: Jennifer M. Rudd[1], Miruthula Tamil Selvan[1], Shannon Cowan[1], Yun-Fan Kao[1], Cecily

C. Midkiff[2], Jerry W. Ritchey[1], Craig A. Miller[1*]

Affiliations:

[1] Department of Veterinary Pathobiology, College of Veterinary Medicine, Oklahoma State

University; Stillwater, OK, USA

[2] Division of Comparative Pathology, National Primate Research Center, Tulane University;

Covington, LA, USA

* Corresponding author. Email: craig.miller@okstate.edu (CAM)

Keywords: COVID-19, SARS-CoV-2, Domestic Cats, Feline, Animal Model, ARDS, Pathology

Abstract: The emergence and ensuing dominance of COVID-19 on the world stage has emphasized the urgency of efficient animal models for the development of therapeutics and assessment of immune responses to SARS-CoV-2 infection. Shortcomings of current animal models for SARS-CoV-2 include limited lower respiratory disease, divergence from clinical COVID-19 disease, and requirements for host genetic modifications to permit infection. This study validates a feline model for SARS-CoV-2 infection that results in clinical disease and histopathologic lesions consistent with severe COVID-19 in humans. Intra-tracheal inoculation of concentrated SARS-CoV-2 caused infected cats to develop clinical disease consistent with that observed in the early exudative phase of COVID-19. A novel clinical scoring system for feline respiratory disease was developed and utilized, documenting a significant degree of lethargy, fever, dyspnea, and dry cough in infected cats. In addition, histopathologic pulmonary lesions such as diffuse alveolar damage, hyaline membrane formation, fibrin deposition, and proteinaceous exudates were observed due to SARS-CoV-2 infection, imitating lesions identified in people hospitalized with ARDS from COVID-19. A significant correlation exists between the degree of clinical disease identified in infected cats and pulmonary lesions. Viral loads and ACE2 expression were quantified in nasal turbinates, distal trachea, lung, and various other organs. Natural ACE2 expression, paired with clinicopathologic correlates between this feline model and human COVID-19, encourage use of this model for future translational studies.

Author Summary: Identifying an ideal animal model to study COVID-19 has been difficult, and current models come with challenges that restrict their potential in translational studies. Few lab animals naturally express the receptors necessary for viral infection (ACE2), and many fail to manifest clinical signs or pathology similar to that seen in humans. Other models (non-human primates, mink) are ideal for disease and transmission studies, but are restricted by cost,

husbandry challenges, and scarce availability. Alternatively, cats naturally express ACE2

receptors, are naturally infected with SARS-CoV-2 and can transmit virus from cat-to-cat. Prior

to this study, cats infected by oral/nasal routes have not displayed significant clinical disease or

lung pathology. However, we demonstrate that direct inoculation of concentrated SARS-CoV-2

virus in the trachea of cats induces analogous clinical and pathologic features to hospitalized

patients with acute COVID-19. Our results show that infected cats exhibit significant clinical

signs during experimental infection (coughing, increased respiratory effort, lethargy, and fever)

and exhibit extensive lung lesions that mimic severe COVID-19 pathology such as diffuse

alveolar damage and hyaline membrane formation – highlighting the immeasurable potential for

this feline model to address translational approaches for COVID-19 and to better understand the

role of cats in transmission and disease.

53 INTRODUCTION

Since the emergence of severe acute respiratory syndrome coronavirus-2 (SARS-CoV-2)

in late 2019, Coronavirus Disease 2019 (COVID-19) has swept across the globe resulting in

nearly 3 million deaths worldwide as of March 2021 (1). Although a wide range of clinical

symptoms are reported, mortality of COVID-19 patients is closely correlated with progression of

viral infection to severe lung disease (pneumonia) and respiratory failure due to acute respiratory

distress syndrome (ARDS), which is further complicated by immune cell dyscrasias and

hyperinflammation (cytokine storm) in critically ill patients (2-4). Features of pulmonary

pathology that are hallmarks of severe COVID-19 (i.e., diffuse alveolar damage with hyaline

membrane formation, type II pneumocyte hyperplasia, vascular thrombi, fibrin and serous

exudation) have been difficult to reproduce in animal models, making it impossible to

completely understand the pathophysiology of disease and to test efficacy of new therapeutics

and vaccines (5, 6). Identification of a translational animal model that parallels clinical and

pathologic features of disease in addition to route of infection, replication, and transmission

kinetics is of paramount importance.

SARS-CoV-2 viral infection and replication within a host requires the presence and

distribution of angiotensin-converting enzyme 2 (ACE2) receptors similar to humans (7). Natural

SARS-CoV-2 infections in animals are documented to occur in a diverse range of species,

including domestic and exotic cats, dogs, mink, and Golden Syrian hamsters (8-11), and this

diverse host range is largely due to natural expression of ACE2 receptors and host tropism of this

receptor with the S protein of SARS-CoV-2 (12, 13). Due to the natural availability of ACE2

receptors and confirmed host susceptibility and transmission (10, 14-17), domestic cats offer an

exciting advantage as experimental models for SARS-CoV-2 infection (18, 19). Comorbidities

that exacerbate COVID-19 disease, such as hypertension, diabetes, renal disease, and obesity, are

readily adapted to feline models (20-25). Furthermore, establishing a SARS-CoV-2 infected

feline model is prudent to better understand zoonotic transmission potential from domestic cats

back to people in close contact.

Previous studies have successfully infected cats with SARS-CoV-2 via intra-nasal (1-

3.05×10^5 PFU) and/or intra-oral routes (5×10^5 $TCID_{50}$/ml) and have confirmed cat-to-cat

transmission through both respiratory droplets and aerosolization (16, 26-28). However, these

studies failed to produce clinical signs in infected cats, and evidence of lower respiratory

pathology mirroring severe COVID-19 in humans was not observed (16, 26-28), potentially due

to concentration of the viral inoculum and/or inoculation route. Interestingly, pulmonary disease

with diffuse alveolar damage was previously documented in cats intra-tracheally infected with

1×10^6 TCID$_{50}$ SARS-CoV-1, which also resulted in efficient transmission of virus to uninfected

animals (29, 30).

Based on outcomes of these former studies, we hypothesized that inoculation with a

higher concentration of SARS-CoV-2 via the intra-tracheal route would result in pulmonary

pathology and clinical disease in domestic cats similar to COVID-19 in human patients. The

experiments reported in this study provide the first feline model of SARS-CoV-2 infection with

significant lower respiratory disease that displays features of diffuse alveolar damage seen in the

early exudative phase of human COVID-19. In addition, SARS-CoV-2 infected cats exhibited

clinical signs of lower respiratory disease characterized by increased respiratory effort and

coughing in addition to signs of systemic involvement such as pyrexia and lethargy. While the

role of cats in zoonotic transmission is still under investigation, the applicability of a clinically

significant SARS-CoV-2 feline model with pathological lesions that mirror severe COVID-19 is

of high impact for future studies.

RESULTS

SARS-CoV-2 infected cats exhibit clinical signs of lower respiratory disease

In order to clinically assess the feline model in Animal Biosafety Level-3 conditions, a

novel clinical scoring system for feline respiratory disease was developed by integrating features

of previously utilized systems (31-33) (Table 1). Each cat was assigned a score from 0 to 2 for

each of the following categories: body weight loss, activity levels, behavioral changes, body

temperature, respiratory effort, ocular or nasal discharge, and coughing. Scores were then

summated to assign an overall clinical score for each day.

SARS-CoV-2-infected cats exhibited a significant increase in clinical disease scores

starting on 4 days post-inoculation (dpi) and then on 5, 6, and 8 dpi when compared to sham-

inoculated controls (Fig 1A). Clinical disease peaked on 4 dpi and continued through the study

endpoint at day 8. The most prominent clinical signs noted were lethargy and increased

respiratory effort, which were observed in 100% (12/12) of SARS-COV-2-infected cats during

this study. Both lethargy and respiratory effort increase significantly between 3 and 4 dpi

($p=0.0027$; $p=0.0027$) and remained elevated with significantly higher scores through 8 dpi when

compared with day 0 (Fig 1B). Coughing was noted in 4 of 12 infected cats with peak clinical

signs occurring at 4 dpi. Pyrexia (temperature > 39.2°C) was documented in 8 of 12 SARS-CoV-

2 infected cats over the course of the study, while 7 infected cats displayed altered behavior

(reduced interest in food or attention) and 5 had measurable weight loss. No cats had ocular or

nasal discharge (S1 Table). Sham-inoculated cats did not exhibit clinical signs except for one cat

with mild weight loss on day 4.

	0 (Healthy)	1	2
Body Weight	No weight loss	0 to 5% weight loss	> 5% weight loss
Temperature	37.2 to 39.1° C	39.2 to 39.7° C	> 39.7° C
Respiratory Effort	Normal resting respiratory rate and normal effort	Mild tachypnea, but no overt increase in effort	Marked increase in both respiratory rate and effort; dyspnea
Activity	Normal	Reduced activity when disturbed* (lethargy)	Little to no activity disturbed*; reduced activity stimulated**
Behavior	Normal	Reduced interest in food and/or attention	Anorexia and lack of interest
Ocular/Nasal Discharge	None	Mild discharge noted	Discharge evident from both nasal and ocular regions
Coughing/ Wheezing	None	Mild wheezing, but no coughing	Coughing and/or marked wheezing

***Disturbed**: observer in the room, but kennel unopened
****Stimulated**: kennel open
Table 1. Clinical Scoring System for Feline Respiratory Disease. A scoring system was

designed to assess clinical lower respiratory and systemic disease in the feline model. Each cat

was scored daily at the same time point (morning) by a small animal clinician (JMR). Cats were

assigned a score from 0 to 2 for each clinical parameter: body weight, temperature, respiratory

effort, activity, behavior, ocular/nasal discharge, coughing/wheezing. The parameter scores were

summed to assign an overall score per cat per day. Potential scores can range from 0 (healthy

with no signs of disease) to 14 on any given day. Resting respiratory rate was considered normal

if <36 breaths per minute. Marked increases in rate were >50 breaths per minute at rest.

Temperatures were obtained via thermal microchips, and body weights were obtained last to

limit stress affecting clinical scoring.

Feline SARS-CoV-2 infection pathology mirrors acute COVID-19

Complete post-mortem evaluation was performed for all sham-inoculated control animals (n=6) and SARS-CoV-2-infected cats euthanized on day 4 (n=6) and day 8 (n=6) post-inoculation. Necropsy tissues from SARS-CoV-2-infected cats (including lung, trachea, nasal turbinates, and tracheobronchial lymph node (TBLN)) were grossly examined and compared to those from sham-inoculated cats (Fig 2 A-C). At 4 dpi, the lungs of SARS-CoV-2-infected cats were grossly heavy and wet, with large multifocal to coalescing regions of dark red consolidation that exuded a moderate amount of edema upon cut section (Fig 2 B). Gross lung lesions were similar at 8 dpi in SARS-CoV-2-infected cats, although the degree of pulmonary edema was moderately more pronounced (Fig 2 C). The TBLN of all SARS-CoV-2-infected cats were diffusely enlarged 4-5 times normal at both 4 dpi (n=6) and 8 dpi (n=6).

Microscopic evaluation of selected necropsy tissues (lung, trachea, nasal turbinates, TBLN, and kidney) was performed for all study animals. Tissue sections from all sham-inoculated animals (n=6) were histologically unremarkable (Fig 2 D and S2 Table). In contrast, histopathologic features of feline SARS-CoV-2 infection exhibited striking similarities to documented pathologic features of the acute (exudative) and organizing phases of human COVID-19 (34-37). At 4 dpi, 100% (6/6) of SARS-COV-2 -infected cats exhibited a significant degree of lung pathology (interaction, $p<0.0001$) and prominent histologic features consistent with diffuse alveolar damage (DAD) (Fig 2 E-F). Pulmonary edema (5/6 cats), multifocal alveolar damage and necrosis (5/6 cats), perivascular lymphocytic and neutrophilic infiltrates (6/6 cats), and increased intra-alveolar macrophages (5/6 cats) were significantly elevated in SARS-CoV-2-infected cats at 4 dpi (Supporting Information). These changes were occasionally

accompanied by multifocal areas of hyaline membrane formation (3/6 cats), mild to moderate

amounts of intra-alveolar fibrin (2/6 cats), type II pneumocyte hyperplasia (2/6 cats), and intra-

alveolar syncytial cells (2/6 cats). One SARS-CoV-2 infected cat exhibited severe inflammation

in the distal trachea at 4 dpi characterized by multifocal areas of submucosal necrosis and

fibrinoid vasculitis with multifocal areas of mucosal ulceration and diphtheritic membrane

formation (Fig 2 G).

Similar histologic features of DAD were also observed in the lungs of SARS-CoV-2-infected

cats at 8 dpi, however, the overall pattern of lung injury appeared exhibited more prominent

features of vascular injury compared to day 4 (Fig 2 H). A significant degree of pulmonary

edema/exudate, perivascular inflammatory infiltration, and alveolar histiocytosis was present in

100% of SARS-CoV-2 animals (6/6 cats) at 8 dpi (Supporting Information). Alveolar damage

and necrosis (4/6 cats) and intra-alveolar fibrin (3/6 cats) were also prominent features at this

time point. Moreover, histologic evidence of fibrinoid vasculitis (2/6 cats) and vascular

thrombosis (2/6 cats) was also observed at 8 dpi, in addition to occasional viral syncytia (1/6

cats) (Fig 2H). In 2 of these cats, the tracheal submucosa was multifocally expanded and effaced

by moderate to severe lymphoplasmacytic, histiocytic, and neutrophilic inflammation with

necrosis (Fig 2 I).

A positive linear correlation exists between peak clinical scores and histopathology scores of

the lungs in SARS-CoV-2 infected cats (p=0.0002; R^2=0.5884) indicating that severe clinical

signs of disease correlate with pulmonary pathology (S1 Fig). Mild, multifocal lymphofollicular

inflammation was observed in the nasal turbinates of all SARS-CoV-2-infected cats (6/6) at 4 dpi

and in 4/6 cats at 8 dpi, with variable neutrophilic infiltration (Supporting Information). All

SARS-CoV-2-infected animals (12/12) exhibited mildly increased lymphoid hyperplasia in

TBLN at 4 and 8 dpi characterized by increased medullary cords and extranodal proliferations

(Supporting Information), but overall changes were not statistically significant. No significant

histopathologic findings were observed in renal tissues at either time point. Fluorescent

immunohistochemistry was performed to detect SARS-CoV-2 positive cells in lung and TBLN

of 2 SARS-CoV-2 infected cats (n=1 at 4 dpi, n=1 at 8 dpi). At both time points, low numbers of

mononuclear cells positive for SARS-CoV-2 nucleoprotein were detected within the medulla of

the TBLN, however, no positive cells were observed in lungs of these animals. (Fig 3).

ACE2 expression and viral RNA in feline tissues during SARS-CoV-2 infection

SARS-CoV-2 viral RNA and fACE2 RNA expression was quantified in the nasal

turbinates, TBLN, distal trachea, kidneys and lungs of all SARS-CoV-2-infected cats (n=12) and

sham-inoculated controls (n=6) using ddPCR (Fig 4 and S3 Table). Viral RNA was detected in

100% of tissues collected on 4 dpi from SARS-CoV-2-infected cats (Fig 4 A). At 8 dpi, viral

RNA was also detectable in the lung, TBLN, and kidney tissues of all (6/6) infected cats, and in

5/6 cats in the nasal turbinates and 5/6 cats in the distal trachea. No SARS-CoV-2 viral RNA was

detected in tissues collected from sham-inoculated cats at either time point (S3 Table). SARS-

CoV-2 viral RNA copies were elevated in the TBLN at 8 dpi compared with day 4 samples,

although this trend was not significant (p=0.0567). In contrast, SARS-CoV-2 viral load in lung

samples was significantly lower at 8 dpi than at 4 dpi (p=0.0007) (Figure 4 A). A positive linear

correlation was observed between SARS-CoV-2 RNA in the lung and pulmonary histopathology

scores of SARS-CoV-2 infected cats (p=0.0183; R^2=0. 3012) (S1 Fig). SARS-CoV-2 RNA was

not reliably detected in nasal swabs or plasma of infected cats at either time point.

In sham-inoculated cats, Kruskal Wallis test revealed that fACE2 RNA in the nasal

turbinates was significantly higher than in the lung (p=0.0093) and TBLN (p=0.0049). fACE2

RNA was also higher in the kidney when compared to lung (p=0.0003), trachea (p=0.0034), and

TBLN (p=0.0001). These findings were similar in SARS-CoV-2-infected animals at 4 and 8 dpi,

with fACE2 RNA levels being significantly higher in the nasal turbinates and kidney versus

other tissues (p<0.05) (S4 Table). Overall, fACE2 RNA in the kidney was significantly increased

in SARS-CoV-2 infected cats on 4 dpi when compared to both sham-inoculated controls, as well

as SARS-CoV-2 infected cats on 8 dpi (ANOVA, p<0.0001) (Figure 4 B). No other significant

changes in ACE2 RNA were observed over time.

DISCUSSION

The potential of this feline model for future evaluation of COVID-19 is extensive.

Challenges with earlier feline models of SARS-CoV-2 infection included a lack of clinical

disease and/or pathology of the lower respiratory tract that resembles lesions seen in patients

with COVID-19. The differences in clinical presentation between previous feline models and the

model described here are likely attributed to modifications in routes and concentration of

inoculation. In this study, SARS-CoV-2 was inoculated through an intra-tracheal route and at a

higher concentration than previously reported (16, 26, 27). Route of inoculation is an important

consideration when establishing an animal model for disease, and previous studies have

exhibited marked differences in primary disease severity and distribution based on route of

inoculation (38, 39).

While previous feline models offer value for study of asymptomatic infections, viral

shedding, and transmission of SARS-CoV-2, cats infected through an intra-tracheal route exhibit

clinical disease that aligns with that seen in early phases of acute COVID-19. Clinical

assessment of infectious lower respiratory disease in a cat can be challenging, and it is not

uncommon for cats with confirmed histologic infectious pneumonia to have limited clinical

respiratory signs (40). Therefore, the clinical signs of respiratory disease induced in this model

are highly significant. A novel clinical scoring system was designed that could be applied in the

Animal Biosafety Level-3 facility to carefully assess for clinical disease. Interestingly, the

disease noted in the SARS-CoV-2 infected cats was similar to that described in hospitalized

patients with COVID-19. Clinical disease of hospitalized human COVID-19 patients is

characterized by fever (70-90%), dry cough (60-86%), shortness of breath (53-80%), and fatigue

(38%) (41) while predominant clinical sings in SARS-CoV-2 infected cats consisted of fever,

cough, lethargy and increased respiratory effort, with lethargy and increased respiratory effort

being the most notable clinical signs (Fig 1).

In addition to clinical signs of lower respiratory and systemic disease, SARS-CoV-2

infected cats also exhibited conspicuous pulmonary lesions of diffuse alveolar damage (DAD) by

4 dpi, and additional evidence of vascular damage by 8 dpi (Fig 2). Specific histopathological

lesions align closely with those reported in human COVID-19 patients (34-36, 42-44), including

DAD resulting in hyaline membrane formation, type II pneumocyte hyperplasia, occasional

intra-alveolar syncytial cells, and the development of fibrinous exudate and vascular thrombi. To

the author's knowledge, this is the first report of hyaline membrane formation and type II

pneumocyte hyperplasia in feline SARS-CoV-2 infection. Peak clinical disease scores positively

correlated with severity of histologic lesions in the lungs (S1 Fig), which further support that cats

with marked pulmonary histologic damage also had more severe clinical signs of disease.

Surprisingly, intra-tracheal inoculation of SARS-CoV-2 did not produce high viral RNA

loads in the lungs as compared with other studies in which the inoculate was delivered via the

intranasal route (26). However, despite by-passing the upper airway, virus was still detected in

the nasal turbinates by 4 and 8 dpi, suggesting the virus may utilize the mucociliary escalator to

travel up the respiratory tree and establish infection intra-nasally even without intra-nasal

inoculation. Although seemingly lower quantities of SARS-CoV-2 RNA were recovered from

lungs of intra-tracheally inoculated cats, the damage to lung tissues was highly evident,

indicating that extensive pulmonary damage will occur even without high levels of viral

replication within the pulmonary tissue at 4 and 8 dpi. Viral migration from lung to the TBLN

occurred quickly (by 4 dpi) and this TBLN involvement is a novel finding to the feline model of

SARS-CoV-2, including detection of viral antigen within the TBLN via fluorescent

immunohistochemistry.

Similar to humans, fACE2 RNA expression varied by tissue location, but were relatively

low in the lungs of both infected and uninfected cats. It is important to note that RNA

measurements indicate an upregulation or downregulation of production of proteins, but do not

necessarily indicate an absolute number of receptors available. However, it is possible that

inefficient replication and rapid clearance of SARS-CoV-2 in the lungs is related to lower

expression of ACE2 receptors as compared with nasal turbinate ACE2. Histopathology shows

that cells regularly expressing ACE2 are damaged in the lung and this viral-induced pulmonary

epithelial pathology may contribute further. ACE2 RNA copies in the feline kidney are

significantly higher than that of other assessed tissues, and viral infection resulted in a significant

upregulation of ACE2 RNA by 4 dpi and then a subsequent reduction by 8 dpi. Hypertension and

activation of the renin-angiotensin system may have driven this rise in ACE2 in order to

counterbalance system effects on infection, and future studies should include blood pressure

evaluation in conjunction with other clinical parameters such as oxygen saturation, chemistry

panels, and imaging. Further studies are needed to fully understand the role of ACE2 in SARS-

CoV-2 viral replication kinetics and disease.

Limitations to this study include sample sizes as well as sampling time points. Further

studies are needed to try and better identify peak viral loads in various tissues as well as ACE2

expression in order to investigate when viral clearance occurs and when this feline model moves

from early exudative disease to more organized, fibrotic disease. A better delineation of these

events would add value to the model and its potential for use at other stages of disease. In

addition, transmission and viral shedding after intra-tracheal inoculation of SARS-CoV-2 should

be evaluated and compared with that of intra-nasal inoculation and spread. Expansion of in depth

diagnostics was limited due to animal biosafety level requirements and availability of resources,

but future studies will seek to evaluate other clinical parameters, such as oxygen saturation,

thoracic imaging and complete blood counts, chemistry panels and urine analysis to better assess

damage to other organ systems and further compare with human disease.

This feline model of SARS-CoV-2 infection offers an animal model that closely mirrors

both clinical disease and pathology identified in hospitalized patients with severe COVID-19,

making the model a potential option for future studies addressing novel therapeutics for COVID-

19. Therapeutic measures can be thoroughly assessed for improvement in pathology and

mitigation of clinical disease in cats before being validated in human trials, and more thorough

evaluation of the feline immune response to infection may elucidate other options for COVID-19

treatments that could mitigate disease and improve clinical outcomes. The continued emergence

of novel variants, circulating globally, ceaselessly contributes to the complexity and duration of

this pandemic. This animal model offers an ease of use, which can positively impact further

vaccination and control strategies necessary to achieve an end to the rapid spread of COVID-19.

This model also offers utility in a One Health approach to the role of companion animals in

disease transmission, antigenic drift, and more thorough evaluation of the potential for feline

contributions to the spread of SARS-CoV-2.

MATERIALS AND METHODS

Ethics Statement. This study was approved by the Oklahoma State University Institutional

Animal Care and Use Committee; IACUC-20-48, Validation of a naturally occurring animal

model for SARS-CoV-2 infection. Oklahoma State University's animal care and use program is

licensed by the United States Department of Agriculture (USDA), and accredited by the

Association for Assessment and Accreditation of Laboratory Animal Care (AAALAC). In

accordance with the approved IACUC protocol, animals were monitored at least once daily for

evidence of morbidity and discomfort by trained animal care staff. Prior to experimental

procedures, all study animals were anesthetized to minimize animal suffering and distress.

Human euthanasia procedures were conducted by phenobarbital overdose in accordance with

IACUC protocols and American Veterinary Medical Association (AVMA) Guidelines for the

Euthanasia of Animals. Prior to euthanasia, all study animals were anesthetized by intramuscular

injection of ketamine (4 mg/kg), dexmedetomidine (0.02 mg/kg), and butorphanol (0.4 mg/kg).

No animals died without euthanasia during this study.

Virus. SARS-CoV-2 virus isolate USA-WA1/2020 was obtained from BEI Resources, passaged

up to 6 times in Vero E6 cells in Vero E6 cell growth medium. Virus stock was titrated and

quantified on Vero E6 cells using a standard MERS-CoV quantification assay (45). $TCID_{50}$ was

calculated using the Reed and Muench method.

Animals. Eighteen adult (9 males, 9 females, all 9 months-old) specific pathogen free (SPF) cats

were obtained from Marshall BioResources (North Rose, NY). Animals intended for SARS-

CoV-2 inoculation were housed within Biosafety Level 3 (BSL-3) barrier animal rooms at

Oklahoma State University, individually housed and fed dry/wet food with access to water *ad*

libitum. Animals intended for sham-inoculation were group-housed within the AAALAC

International Accredited animal facility at Oklahoma State University. Animals were allowed 30

days for acclimation prior to initiation of the study. Temperature-sensing microchips (Bio Medic

Data Systems, Seaford, DE) were implanted subcutaneously in the dorsum after 30 days.

Baseline weights, body temperatures, clinical evaluation, and nasal swab sampling were obtained

prior to inoculation. All animals were in apparent good health at the onset of the study.

Virus Challenge. Cats were lightly anesthetized with ketamine (4 mg/kg), dexmedetomidine (20

μg/kg), and butorphanol (0.4 mg/kg) intramuscularly. Cats were then positioned in ventral

recumbency and intubated so that the end of an endotracheal tube is positioned within the distal

trachea as described (46). In twelve cats, a 3-cc syringe was used to inoculate 1 mL $9x10^5$ PFU

(1.26x10^6 TCID$_{50}$) per mL SARS-CoV-2, isolate USA-WA1/2020 in Dulbecco's Modified Eagle

Medium (DMEM), followed by 2 mL of air from an empty syringe. The remaining six cats were

sham-inoculated using sterile PBS via the same method. Viral inoculum dosage was confirmed

through virus back-titration on E6 cells immediately following inoculation.

Sampling. Blood and nasal swab samples were collected under sedation (described above) from

all study animals (n=18) at day 0 to serve as baseline for ddPCR analysis. Blood samples (6 mL)

were obtained from all cats via cephalic or medial saphenous venipuncture and processed

immediately for viral quantification. Nasal swab samples obtained from the nares of all cats

using ultrafine flocked swabs (Puritan) were placed in 2 mL microcentrifuge tubes containing

RNAlater solution (Ambio, Austin, TX) and stored at -80°C until processed. At day 4 and day 8

post-inoculation, a subset of SARS-CoV-2 infected cats (n=6 per time point) and sham-

inoculated control cats (n=3 per time point) were anesthetized for blood and nasal swab

collection then humanely euthanized (pentobarbital >80mg/kg) and necropsied to collect tissue

samples. Necropsied tissues were processed for histologic examination, immunohistochemistry

(IHC), and RNA analysis as described below.

Clinical Observations and Scoring. Animals were monitored at least once daily for evidence of

morbidity and discomfort by a licensed veterinary practitioner. Body weights and temperatures

(thermal microchips) were documented daily every morning for the duration of the study. Full

clinical scoring included evaluation of body weight, body temperature, activity levels, behavior,

respiratory effort, evidence of ocular/nasal discharge, and recognition of coughing or wheezing.

Each factor was assigned a score of 0 (normal), 1 (mild-moderate), or 2 (severe) as described in

Table 1. Each clinical factor parameter was added to assign an individual animal a summed

clinical score every 24 hours for the duration of the study. Cats were observed at rest for

respiration rates, activity levels and other notable clinical signs before stimulation.

Histopathology. Necropsy was performed on six (n=6) SARS-CoV-2-infected cats at 4 dpi and

the remaining six (n=6) SARS-CoV-2-infected cats at 8 dpi. Three (n=3) sham-inoculated cats

were necropsied at each time point (4 dpi and 8 dpi) to provide control samples. Tissue

collection included: lung, tracheobronchial lymph nodes, nasal turbinates, distal trachea, and

kidney. Necropsy tissues were halved and then placed into either 1 mL tubes and frozen at -

80°C, or into standard tissue cassettes that were then fixed in 10% neutral-buffered formaldehyde

for 96 hours prior transferring to 70% ethanol for 72 hours. Tissues were then trimmed and

processed for histology. Five μm paraffin sections were collected onto charged slides, and one

slide of each tissue was stained with hematoxylin and eosin (H & E) for microscopic evaluation.

Necropsy tissues were evaluated for evidence of inflammation and/or aberrations in lymphoid

populations as reported in human COVID-19 patients (34-37). Lung tissues were specifically

evaluated for the following pathology: alveolar damage (pneumocyte necrosis, hyaline

membrane formation,) alveolar fibrin deposition (± organization), serous exudate/edema,

perivascular infiltrates, alveolar histiocytes, type II pneumocyte hyperplasia, syncytia,

thrombosis, and fibrinoid vasculitis. All tissues were assigned a quantitative histologic score

based on previously documented criteria (47, 48): 0 = no apparent pathology/change; 1 =

minimal change (minimally increased numbers of inflammatory cells); 2 = mild change (mild

inflammatory infiltrates, alveolar damage/necrosis, fibrin deposition and/or exudation); 3 =

moderate change (as previously described, but more moderately extensive); 4 = marked changes

(as previously described, but with severe inflammation, alveolar damage, hyaline membrane

formation, necrosis, exudation, vasculitis and/or thrombosis). All tissues were evaluated and

scored by a board-certified veterinary pathologist blinded to study groups to ensure scientific

rigor and reproducibility.

Viral RNA Analysis. Viral RNA analysis was performed on samples from nasal swabs,

collected plasma, and tissues. Nasal swabs were immediately broken off into 1.5 mL

microcentrifuge tubes containing 200 μL RNAlater Solution (Ambion, Austin, TX) and stored at

-20°C. The nasal swabs were vortexed for 15 seconds, then inverted and centrifuged at 1500 rpm

for 10 minutes. RNA was extracted from frozen necropsy tissues using a QIAamp Viral RNA

Mini Kit (Qiagen, Germantown, MD) and tissue homogenizer. SARS-CoV-2 viral RNA was

quantified by droplet digital PCR (ddPCR) as previously described (49). Briefly, ddPCR was

performed according to manufacturer's instructions for the 2019-nCoV CDC ddPCR Triplex

Probe Assay (Bio-Rad, Hercules, California, USA). PCR reaction mixtures were as follows: 5.5

μl One-Step RT-ddPCR Advanced Kit for Probes Supermix (no dUTP's) (Bio-Rad), 2.2 μl

reverse transcriptase, 1.1 μl 300 mM Dithiothreitol (DTT), 1.1 μl triplex probe assay (for N1,

N2, RPP30 detection), 2.2 μl RNase free water, and 9.9 μl RNA template in a final volume of 22

μl per sample. Duplicate 20 μl samples were partitioned using a QX200 droplet generator (Bio-

Rad, Hercules, California, USA) and then transferred to a 96-well plate and sealed. Samples

were processed in a C1000 touch Thermal Cycler (Bio-Rad) under the following cycling

protocol: 50 °C for 60 min for reverse transcription, 95 °C for 10 min for enzyme activation,

94°C for 30 s for denaturation and 55 °C for 60 s for annealing/extension for 45 cycles, 98 °C 10

min for enzyme deactivation, 4 °C for 30 min for droplet stabilization followed by infinite 4 °C

hold. The amplified samples were read in the FAM and HEX channels using the QX200 reader

(Bio-Rad). Each experiment was performed with a negative control (no template control, NTC)

and a positive control (RNA extracted from SARS-CoV-2 viral stock and diluted 1:12,000). Data

were analyzed using QuantaSoft™ v1 AnalysisPro Software (Bio-Rad) and expressed as Log_{10}

(copies/mL).

Feline ACE2 Analysis. Feline angiotensin converting enzyme 2 (fACE2) RNA was quantified

by ddPCR using methods similar to the above assay for CoV. RNA was extracted from frozen

necropsy tissues as outlined above. cDNA was synthesized as previously published (48). Design

of primers and probe targeting fACE2 was performed according to manufacturer's

recommendation, namely keeping GC content between 50–60 % for primers and 30–80 % for

probes, and melting temperatures between 50–65 ∘C for primers and 3–10 ∘C higher for probes.

Oligoes were synthesized by Integrated DNA Technologies (IDT, Coralville, Iowa, USA). The

sequences are as follows: Forward: 5′- ACGGAGGCGTAAGGATTT -3′ , Reverse: 5′ -

GTGTGGTAGTGGTTGGTATTG -3′ , probe: 5′ - CGGGATCAGAAATCGAAGGAAGAA -

3′. BLAST analysis (50) of the primer and probe sequences against the domestic cat (*Felis catus*)

genome was performed to ensure no similar sequences could be amplified. ddPCR reactions

were prepared by adding 11 µl Supermix for Probes (no dUTP) (Bio-Rad), 1.1 µl of primer/probe

mix (final concentration is 500nM for primers and 250 nM for probe) and 8.8 µl of cDNA

template containing 110 ng RNA equivalent. Droplets were partitioned and PCR executed as

above using the following cycling conditions: 95 °C for 10 min, 95 °C 30 s for denaturation and

58.8 °C for 60 s for annealing/extension for 45 cycles, 98 °C 10 min for enzyme deactivation.

Droplets were read and analyzed as described above.

Immunohistochemistry. 5µm sections of formalin-fixed, paraffin-embedded lung were

mounted on charged glass slides, baked for one hour at 60°C, and passed through Xylene, graded

ethanol, and double distilled water to remove paraffin and rehydrate tissue sections. A

microwave was used for heat induced epitope retrieval. Slides were heated in a high pH solution

(Vector Labs H-3301), rinsed in hot water and transferred to a heated low pH solution (Vector

Labs H-3300) where they were allowed to cool to room temperature. Sections were washed in a

solution of phosphate-buffered saline and fish gelatin (PBS-FSG) and transferred to a humidified

chamber, for staining at room temperature. Tissues were blocked with 10% normal goat serum

(NGS) for 40 minutes, followed by a 60-minute incubation with a guinea pig anti-SARS

antibody (BEI NR-10361) diluted 1:1000 in NGS. Slides were washed and transferred to the

humidified chamber for a 40-minute incubation with a goat anti-guinea pig secondary antibody

(Invitrogen A11073) tagged with Alexa Fluor 488 and diluted 1:1000 in NGS. Following

washes, DAPI (4',6-diamidino-2-phenylindole) was used to label the nuclei of each section.

Slides were mounted using a homemade anti-quenching mounting media containing Mowiol

(Calbiochem#475904) and DABCO (Sigma #D2522) and imaged at 20X with a Zeiss Axio Slide

Scanner.

Statistical Analyses. When applicable, data were expressed as mean ± SEM and statistically

analyzed using GraphPad Prism 9.0 software (La Jolla, CA). Kruskal–Wallis test, Pearson

correlations, and ANOVA were used to compare differences in clinical score, histopathology,

SARS-CoV-2 viral load, and ACE2 RNA among uninfected and SARS-CoV-2-infected

individuals, between sample type, for each tissue individually, and between tissues. For all

significant results, pair-wise comparisons were made by post-hoc analysis. P-values < 0.05 were

considered significant.

Acknowledgments: The authors would like to thank Girish Patil, Akhilesh Ramachandran, and

Sai Narayanan with the Oklahoma Animal Disease Diagnostic Lab for their assistance in viral

RNA extraction and technical advisement. We would also like to acknowledge Curtis Andrew

for assistance with slide preparation and coordination of immunohistochemistry from the

Immunopathology Core Laboratory at Oklahoma State College of Veterinary Medicine.

References

1. WHO. World Health Organization Coronavirus (COVID-19) Dashboard: World Health

Organization; 2021 [cited 2021. Available from: https://covid19.who.int.

2. Wu C, Chen X, Cai Y, Zhou X, Xu S, Huang H, et al. Risk factors associated with acute

respiratory distress syndrome and death in patients with coronavirus disease 2019 pneumonia

in Wuhan, China. JAMA internal medicine. 2020.

3. Chen G, Wu D, Guo W, Cao Y, Huang D, Wang H, et al. Clinical and immunologic features

in severe and moderate Coronavirus Disease 2019. The Journal of Clinical Investigation.

2020.

4. Pedersen SF, Ho Y-C. SARS-CoV-2: a storm is raging. The Journal of Clinical Investigation.

2020.

5. Kumar S, Yadav PK, Srinivasan R, Perumal N. Selection of animal models for COVID-19

research. Virusdisease. 2020;31(4):1-6.

6. Gretebeck LM, Subbarao K. Animal models for SARS and MERS coronaviruses. Curr Opin

Virol. 2015;13:123-9.

7. Hikmet F, Méar L, Edvinsson Å, Micke P, Uhlén M, Lindskog C. The protein expression

profile of ACE2 in human tissues. Mol Syst Biol. 2020;16(7):e9610.

8.   Kiros M, Andualem H, Kiros T, Hailemichael W, Getu S, Geteneh A, et al. COVID-19

pandemic: current knowledge about the role of pets and other animals in disease

transmission. Virol J. 2020;17(1):143.

9.   Oreshkova N, Molenaar RJ, Vreman S, Harders F, Oude Munnink BB, Hakze-van der

Honing RW, et al. SARS-CoV-2 infection in farmed minks, the Netherlands, April and May

2020. Euro Surveill. 2020;25(23).

10.   Newman A, Smith D, Ghai RR, Wallace RM, Torchetti MK, Loiacono C, et al. First

Reported Cases of SARS-CoV-2 Infection in Companion Animals - New York, March-April

2020. MMWR Morb Mortal Wkly Rep. 2020;69(23):710-3.

11.   Molenaar RJ, Vreman S, Hakze-van der Honing RW, Zwart R, de Rond J, Weesendorp E, et

al. Clinical and Pathological Findings in SARS-CoV-2 Disease Outbreaks in Farmed Mink

(Neovison vison). Vet Pathol. 2020;57(5):653-7.

12.   Luan J, Lu Y, Jin X, Zhang L. Spike protein recognition of mammalian ACE2 predicts the

host range and an optimized ACE2 for SARS-CoV-2 infection. Biochem Biophys Res

Commun. 2020;526(1):165-9.

13.   Liu Y, Hu G, Wang Y, Ren W, Zhao X, Ji F, et al. Functional and genetic analysis of viral

receptor ACE2 orthologs reveals a broad potential host range of SARS-CoV-2. Proc Natl

Acad Sci U S A. 2021;118(12).

14.   Hayashi T, Abiko K, Mandai M, Yaegashi N, Konishi I. Highly conserved binding region of

ACE2 as a receptor for SARS-CoV-2 between humans and mammals. Vet Q.

2020;40(1):243-9.

15. McAloose D, Laverack M, Wang L, Killian ML, Caserta LC, Yuan F, et al. From People to

Panthera: Natural SARS-CoV-2 Infection in Tigers and Lions at the Bronx Zoo. mBio.

2020;11(5).

16. Shi J, Wen Z, Zhong G, Yang H, Wang C, Huang B, et al. Susceptibility of ferrets, cats,

dogs, and other domesticated animals to SARS-coronavirus 2. Science. 2020.

17. Zhang Q, Zhang H, Gao J, Huang K, Yang Y, Hui X, et al. A serological survey of SARS-

CoV-2 in cat in Wuhan. Emerg Microbes Infect. 2020;9(1):2013-9.

18. Lakdawala SS, Menachery VD. The search for a COVID-19 animal model. Science.

2020;368(6494):942-3.

19. Hernández M, Abad D, Eiros JM, Rodríguez-Lázaro D. Are Animals a Neglected

Transmission Route of SARS-CoV-2? Pathogens. 2020;9(6).

20. Van de Velde H, Janssens GP, de Rooster H, Polis I, Peters I, Ducatelle R, et al. The cat as a

model for human obesity: insights into depot-specific inflammation associated with feline

obesity. Br J Nutr. 2013;110(7):1326-35.

21. Nelson RW, Reusch CE. Animal models of disease: classification and etiology of diabetes in

dogs and cats. J Endocrinol. 2014;222(3):T1-9.

22. Samaha G, Beatty J, Wade CM, Haase B. The Burmese cat as a genetic model of type 2

diabetes in humans. Anim Genet. 2019;50(4):319-25.

23. Hoenig M. The cat as a model for human obesity and diabetes. J Diabetes Sci Technol.

2012;6(3):525-33.

24. Wallner M, Eaton DM, Berretta RM, Borghetti G, Wu J, Baker ST, et al. A Feline HFpEF

Model with Pulmonary Hypertension and Compromised Pulmonary Function. Sci Rep.

2017;7(1):16587.

25. Prat V, Rozec B, Gauthier C, Lauzier B. Human heart failure with preserved ejection versus

feline cardiomyopathy: what can we learn from both veterinary and human medicine? Heart

Fail Rev. 2017;22(6):783-94.

26. Gaudreault NN, Trujillo JD, Carossino M, Meekins DA, Morozov I, Madden DW, et al.

SARS-CoV-2 infection, disease and transmission in domestic cats. Emerg Microbes Infect.

2020;9(1):2322-32.

27. Bosco-Lauth AM, Hartwig AE, Porter SM, Gordy PW, Nehring M, Byas AD, et al.

Experimental infection of domestic dogs and cats with SARS-CoV-2: Pathogenesis,

transmission, and response to reexposure in cats. Proc Natl Acad Sci U S A.

2020;117(42):26382-8.

28. Gaudreault NN, Carossino M, Morozov I, Trujillo JD, Meekins DA, Madden DW, et al.

Experimental re-infected cats do not transmit SARS-CoV-2. Emerg Microbes Infect.

2021;10(1):638-50.

29. van den Brand JM, Haagmans BL, Leijten L, van Riel D, Martina BE, Osterhaus AD, et al.

Pathology of experimental SARS coronavirus infection in cats and ferrets. Vet Pathol.

2008;45(4):551-62.

30. van den Brand JM, Haagmans BL, van Riel D, Osterhaus AD, Kuiken T. The pathology and

pathogenesis of experimental severe acute respiratory syndrome and influenza in animal

models. J Comp Pathol. 2014;151(1):83-112.

31. Huet O, Ramsey D, Miljavec S, Jenney A, Aubron C, Aprico A, et al. Ensuring animal

welfare while meeting scientific aims using a murine pneumonia model of septic shock.

Shock. 2013;39(6):488-94.

32. Hartmann AD, Helps CR, Lappin MR, Werckenthin C, Hartmann K. Efficacy of

pradofloxacin in cats with feline upper respiratory tract disease due to Chlamydophila felis or

Mycoplasma infections. J Vet Intern Med. 2008;22(1):44-52.

33. Steagall PV, Monteiro BP. Acute pain in cats: Recent advances in clinical assessment. J

Feline Med Surg. 2019;21(1):25-34.

34. Polak SB, Van Gool IC, Cohen D, Jan H, van Paassen J. A systematic review of pathological

findings in COVID-19: a pathophysiological timeline and possible mechanisms of disease

progression. Modern Pathology. 2020;33(11):2128-38.

35. Tian S, Xiong Y, Liu H, Niu L, Guo J, Liao M, et al. Pathological study of the 2019 novel

coronavirus disease (COVID-19) through postmortem core biopsies. Modern Pathology.

2020;33(6):1007-14.

36. von der Thüsen J, van der Eerden M. Histopathology and genetic susceptibility in COVID-19

pneumonia. European journal of clinical investigation. 2020;50(7):e13259.

37. Xu Z, Shi L, Wang Y, Zhang J, Huang L, Zhang C, et al. Pathological findings of COVID-19

associated with acute respiratory distress syndrome. The Lancet respiratory medicine.

2020;8(4):420-2.

38. Bodewes R, Kreijtz JH, van Amerongen G, Fouchier RA, Osterhaus AD, Rimmelzwaan GF,

et al. Pathogenesis of Influenza A/H5N1 virus infection in ferrets differs between intranasal

and intratracheal routes of inoculation. Am J Pathol. 2011;179(1):30-6.

39. Rimmelzwaan GF, van Riel D, Baars M, Bestebroer TM, van Amerongen G, Fouchier RA, et

al. Influenza A virus (H5N1) infection in cats causes systemic disease with potential novel

routes of virus spread within and between hosts. Am J Pathol. 2006;168(1):176-83; quiz 364.

40. Macdonald ES, Norris CR, Berghaus RB, Griffey SM. Clinicopathologic and radiographic

features and etiologic agents in cats with histologically confirmed infectious pneumonia: 39

cases (1991-2000). J Am Vet Med Assoc. 2003;223(8):1142-50.

41. Wiersinga WJ, Rhodes A, Cheng AC, Peacock SJ, Prescott HC. Pathophysiology,

Transmission, Diagnosis, and Treatment of Coronavirus Disease 2019 (COVID-19): A

Review. Jama. 2020;324(8):782-93.

42. Xu Z, Shi L, Wang Y, Zhang J, Huang L, Zhang C, et al. Pathological findings of COVID-19

associated with acute respiratory distress syndrome. Lancet Respir Med. 2020;8(4):420-2.

43. Fox SE, Akmatbekov A, Harbert JL, Li G, Quincy Brown J, Vander Heide RS. Pulmonary

and cardiac pathology in African American patients with COVID-19: an autopsy series from

New Orleans. Lancet Respir Med. 2020;8(7):681-6.

44. Borczuk AC, Salvatore SP, Seshan SV, Patel SS, Bussel JB, Mostyka M, et al. COVID-19

pulmonary pathology: a multi-institutional autopsy cohort from Italy and New York City.

Mod Pathol. 2020;33(11):2156-68.

45. Coleman CM, Frieman MB. Growth and quantification of MERS-CoV infection. Current

protocols in microbiology. 2015;37(1):15E. 2.1-E. 2.9.

46. Ritchey JW, Levy JK, Bliss SK, Tompkins WA, Tompkins MB. Constitutive expression of

types 1 and 2 cytokines by alveolar macrophages from feline immunodeficiency virus-

infected cats. Vet Immunol Immunopathol. 2001;79(1-2):83-100.

47. Miller C, Bielefeldt-Ohmann H, MacMillan M, Huitron-Resendiz S, Henriksen S, Elder J, et

al. Strain-specific viral distribution and neuropathology of feline immunodeficiency virus.

Veterinary immunology and immunopathology. 2011;143(3):282-91.

48. Miller C, Boegler K, Carver S, MacMillan M, Bielefeldt-Ohmann H, VandeWoude S.

Pathogenesis of oral FIV infection. PloS one. 2017;12(9):e0185138.

49. Deiana M, Mori A, Piubelli C, Scarso S, Favarato M, Pomari E. Assessment of the direct

quantitation of SARS-CoV-2 by droplet digital PCR. Scientific reports. 2020;10(1):1-7.

50. O'Driscoll A, Belogrudov V, Carroll J, Kropp K, Walsh P, Ghazal P, et al. HBLAST:

Parallelised sequence similarity--A Hadoop MapReducable basic local alignment search tool.

J Biomed Inform. 2015;54:58-64.

51. Blair RV, Vaccari M, Doyle-Meyers LA, Roy CJ, Russell-Lodrigue K, Fahlberg M, et al.

Acute Respiratory Distress in Aged, SARS-CoV-2–Infected African Green Monkeys but Not

Rhesus Macaques. The American journal of pathology. 2021;191(2):274-82.

Funding: Research reported in this publication was supported by the National Institute of

General Medical Sciences of the National Institutes of Health under Award Number

P20GM103648 (CAM). The content is solely the responsibility of the authors and does not

necessarily represent the official views of the National Institutes of Health. The funders had no

role in study design, data collection and analysis, decision to publish, or preparation of the

manuscript. https://www.nih.gov/

Author Contributions:

Conceptualization: CAM, JMR, JWR

Methodology: CAM, JMR, JWR, SC, CCM

Investigation: CAM, JMR, MTS, SC, JWR, CCM

Visualization: CAM, JMR, MTS

Funding Acquisition: CAM

Writing – original draft: JMR, CAM

Writing – review and editing: JWR, CCM, SC, MTS

Competing Interests: The authors have declared that no competing interests exist.

Data and materials availability: All relevant data associated with this study has been deposited

in a public repository: 10.6084/m9.figshare.14449773

Figures

Fig 1. Intra-tracheal SARS-CoV-2 inoculation results in clinical disease. Clinical parameters

were assessed using the feline respiratory disease clinical scoring system (see Table 1). **(A)**

Clinical parameters summated to provide an overall clinical score per cat per day. Clinical

disease severity peaked on 4 dpi and was significantly higher than sham-inoculated cats on 4 dpi

(p=0.0054), 5 dpi (p=0.0257), 6 dpi (p=0.0004), and 8 dpi (p=0.0453). A noticeable trend in

severity was also noted on 7 dpi as compared with sham-inoculated controls (p=0.0654). **(B)**

Lethargy and increased respiratory effort were the most prominent clinical signs observed in

SARS-CoV-2-infected cats; both of which were significantly increased between days 3 and 4

(p=0.0027; p=0.0027) and remained significantly elevated in infected cats after 4 dpi as

compared to day 0. Coughing was most prominent on 4 dpi and was identified in 4/12 infected

cats. Pyrexia was noted in 8/12 cats over the course of the study. Data are expressed as means ±

SEM. Statistical comparisons made via mixed effects analysis. *p<0.05; **p<0.01; ***p<0.001;

****p<0.0001.

Fig 2. Pathologic features of acute SARS-CoV-2 infection in cats are analogous to the exudative phase of COVID-19. Compared to lungs from healthy sham-inoculated cats **(A)**, the lungs of SARS-CoV-2-infected cats were diffusely consolidated, dark red and edematous at both 4 dpi **(B)** and 8 dpi **(C)**. The lungs of healthy, uninfected cats **(D)** were histologically normal, with open alveoli and minimal atelectasis. At 4 dpi, the lungs of SARS-CoV-2-infected cats **(E)** exhibited discrete foci of alveolar inflammation and necrosis with fibrin deposition (✱), increased alveolar macrophages (arrowhead), perivascular lymphocytes (☆), and type II pneumocyte hyperplasia (arrows). The alveoli in these cats' lungs were frequently filled with large amounts of edema and fibrin strands **(E inset)**, and there were multifocal areas of hyaline membrane formation **(F)** (✱). The distal trachea of 1 SARS-CoV-2 infected cat **(G)** was multifocally ulcerated at 4 dpi (arrow) with diphtheritic membrane formation (arrowhead) and multifocal areas of submucosal necrosis and fibrinoid vasculitis (✱). At 8 dpi **(H)**, fibrinoid vasculitis, vascular thrombosis (arrow), and occasional syncytial cells **(H inset)** were observed in addition to the histopathologic changes described above. Tracheal lesions observed at 8 dpi **(I)** were characterized by varying degrees of lymphoplasmacytic, histiocytic, and neutrophilic inflammation with multifocal areas of submucosal necrosis. Magnification: (D, H) 10x, scale bar = 100μm; (E) 20x, scale bar = 50μm; (E inset, G, H inset, I) 40x, scale bar = 25μm; (F) 60x, scale bar = 17μm

Fig 3. Fluorescent immunohistochemistry for SARS-CoV-2 nucleoprotein identifies

mononuclear cells in tracheobronchial lymph node of intratracheally-infected cats. Low

numbers of SARS-CoV-2 positive cells (green, white arrows) are detected in **(A)** positive control

tissue (lung) from an African Green Monkey infected with SARS-CoV-2 (51), and within **(B)**

mononuclear cells in the TB LN of SARS-CoV-2 infected cats (green, white arrow). White =

DAPI/nuclei; green = CoV-2. Magnification (A-B) 40x, scale bar = 20 μm.

Fig 4. fACE2 RNA and SARS-CoV-2 viral RNA quantification in feline tissues. Extraction of SARS-CoV-2 and ACE2 RNA was performed as described from tissues samples collected on either 4 or 8 dpi. Tissue samples included nasal turbinates, tracheobronchial lymph node (TB LN), trachea, kidney, and lung. **(A)** SARS-CoV-2 RNA copies were detected in all tissues collected from cats inoculated with SARS-CoV-2. No viral RNA was detected in tissues from sham-inoculated cats. In SARS-CoV-2-infected cats, viral RNA copies were slightly increased in the TB LN between 4 to 8 dpi ($p=0.0567$) while viral RNA load in the lungs significantly decreased over the same period ($p=0.0007$). **(B)** fACE2 receptor RNA is significantly increased in the kidney of SARS-CoV-2 infected cats at 4 dpi compared to sham-inoculated controls ($p<0.0001$) SARS-CoV-3-infected cats at 8 dpi ($p<0.0001$). Data are expressed as means ± SEM. n=6 cats per group. Statistical comparisons made via two-way ANOVA. ***$p<0.001$; ****$p<0.0001$.