Clinical and epidemiologic features of SARS-CoV-2 in dogs and cats compiled through national surveillance in the United States

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Research Article

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Abstract

Objective

To characterize clinical and epidemiologic features of SARS-CoV-2 in companion animals detected through both passive and active surveillance in the U.S.

Animals

204 companion animals (109 cats, 95 dogs) across 33 states with confirmed SARS-CoV-2 infections between March 2020 and December 2021.

Procedures

Public health officials, animal health officials, and academic researchers investigating zoonotic SARS-CoV-2 transmission events reported clinical, laboratory and epidemiological information through a standardized One Health surveillance process developed by CDC and partners.

Results

Among dogs and cats identified through passive surveillance, 94% (n=87) had reported exposure to a person with COVID-19 before infection. Clinical signs of illness were present in 74% of pets identified through passive surveillance and 27% of pets identified through active surveillance. Duration of illness in pets averaged 15 days in cats and 12 days in dogs. The average time between human and pet onset of illness was 10 days. Viral nucleic acid was first detected at 3 days post exposure in both cats and dogs. Antibodies were detected starting 5 days post exposure and titers were highest at 9 days in cats and 14 days in dogs.

Conclusions and Clinical Relevance

Our data support that cats and dogs primarily become infected with SARS-CoV-2 following exposure to a person with COVID-19, most often their owners. Case investigation and surveillance that includes both people and animals is necessary to understand transmission dynamics and viral evolution of zoonotic diseases like SARS-CoV-2.

Introduction

Pet ownership provides many documented positive impacts, including improvements to mental health[1,2]. In the United States, a 2021–2022 survey reported that approximately 70% or 90.5 million households owned at least one pet[3], with around 23 million U.S. households acquiring a pet during the first year of the COVID-19 pandemic (March 2020–May 2021)[4]. Owners and their pets commonly have close relationships, often eating, sleeping, snuggling, and recreating together[5]. While these close interactions have many benefits, they also pose a risk for zoonotic disease transmission. However, the extent of surveillance efforts to detect zoonotic disease transmission in companion animals, including SARS-CoV-2, is limited at both the national and global level.

Similar to other coronaviruses, it is now evident that SARS-CoV-2 has a broad mammalian host range[6]. As of July 12, 2022, 35 countries have reported SARS-CoV-2 infections in species from 14 mammalian families to the World Organisation for Animal Health (WOAH)[7]. Susceptible animals can be categorized into four groups by the nature of their interaction with people: companion animals, farmed animals (including mink[8] and cervids[9]), free-ranging wildlife[10-12], and exotic animals (including big cats and non-human primates) in zoos, sanctuaries, and aquaria[13]. Companion animals are the second-most commonly reported animal group to be infected with SARS-CoV-2 after farmed mink[8], comprising 60% (n=399; cats: 205, dogs: 191, hamsters: 11, ferrets: 3) of all animals reported globally to WOAH between February 29, 2020 and December 31, 2021[14].

Here, we use the largest compilation of zoonotic SARS-CoV-2 surveillance data available globally to synthesize the epidemiological and clinical features of SARS-CoV-2 in companion animals, specifically dogs and cats, residing in the United States.

Materials And Methods

Identifying companion animals confirmed positive for SARS-CoV-2

In the United States, animal cases of SARS-CoV-2 are identified by passive or active surveillance. Through passive surveillance, case identification is typically initiated when owners bring animals to veterinary clinics or hospitals, and samples are submitted to a variety of veterinary diagnostic laboratories (governmental, university, and private) for SARS-CoV-2 testing. Through active surveillance, animals with a known SARS-CoV-2 exposure or clinical signs compatible with SARS-CoV-2 infection are actively sought out by health officials or researchers. These include collaborative One Health investigations of SARS-CoV-2 transmission among animals and people in households, animal shelters, animal rescues, animal rehabilitation centers, zoos, or veterinary clinics[15-17]. Regardless of whether animal cases are detected through passive or active surveillance, samples are first tested at governmental, university, or private veterinary diagnostic laboratories; many of which are members of the USDA's National Animal Health Laboratory Network (NAHLN). Test results from presumptive positive cases are shared with state and federal One Health partners, including public health and animal health officials[18], and under most circumstances, these samples are forwarded to the United States Department of Agriculture National Veterinary Services Laboratories (USDA-NVSL) to undergo confirmatory testing for SARS-CoV-2. Animals confirmed positive for SARS-CoV-2 are reported by USDA to WOAH[14].

According to the U.S. case definition[19], an animal is confirmed positive for SARS-CoV-2 at USDA NVSL if: a) SARS-CoV-2 sequence is generated either directly from suspect or presumptive positive animal samples or indirectly from a viral isolate recovered from that animal; or b) if serum from a suspect or presumptive positive animal demonstrates the presence of SARS-CoV-2 neutralizing antibody. Until March 2021, samples from every presumptive positive animal were requested to undergo confirmatory testing at USDA-NVSL. After March 2021, confirmatory testing expectations changed for dogs and cats to only the first dog and cat per state, territory, or tribal nation. In order to monitor viral changes, USDA-NVSL continues to request submission of any dog and cat samples that: a) are strong sequencing candidates with SARS-CoV-2 real-time reverse transcription PCR (hereafter RT-PCR) cycle threshold (Ct) values <30; b) are associated with unusual morbidity and mortality events; or c) are suspected or known to be infected with variants (e.g., Alpha, Delta, Omicron)[18].

Our dataset is comprised of companion animals that met the U.S. confirmed positive case definition from April 2020–December 2021; these animals are also reported on USDA's public dashboard[20].

Data reporting

Early in the pandemic, CDC experts developed a One Health toolkit and standardized data collection forms for public and animal health officials to jointly guide epidemiological investigations of animals suspected with SARS-CoV-2[21]. An electronic data reporting form was subsequently created in CDC's online secure COVID-19 surveillance database, HHS Protect[22], in which state health officials, including state public health veterinarians and state animal health officials, can provide standard information on animal cases of any species to CDC. The One Health Case Investigation Form for Animals with SARS-CoV-2[21] gathers information on animal signalment (species, age, sex), clinical signs, comorbidities, samples collected, and diagnostic results (including RT-PCR, sequencing, and virus neutralization (VN) or ELISA, and the results of respiratory panels, if available). This form is also used to gather information on the person likely associated with an animal's infection, including symptom onset dates, date of positive COVID-19 tests, and type and frequency of interactions with pets (e.g., feeding, walking, playing, sharing same bed, or administering medications).

Data analyses

Data for this project was shared with CDC by One Health partners and exported from HHS Protect case reports[22]. Data cleaning, visualization, and analytics occurred using R statistical programming[23] and Microsoft Excel[24].

Clinical Signs

We categorized clinical signs into 3 categories based on body systems affected: respiratory (cough, difficulty breathing or shortness of breath, sneeze, nasal discharge, ocular discharge), gastrointestinal (vomiting, diarrhea), and non-specific (lethargy, inappetence, fever). Clinical signs were described in 4 subsets: 1 – clinical vs subclinical among all confirmed positive companion animals; 2 – clinical vs subclinical based on surveillance detection method (active or passive surveillance); 3 – detailed clinical presentation among companion animals presenting with clinical signs; and 4 – detailed clinical presentation among companion animals presenting with clinical signs by species.

Multi-pet Households

In some instances, there was more than one companion animal known to live in a household. To assess the likelihood that another animal in the household would become infected following the first, we calculated conditional probability, subset to only animals detected through passive surveillance (where an index pet could be identified). Conditional probabilities were calculated based on whether the index pet was a cat, dog, or either, and whether the secondary animal was a cat, dog, or either.

Diagnostics

To understand timeline of infection and immune response of companion animals infected with SARS-CoV-2, we assessed Ct values (the number of cycles necessary for viral nucleic acid detection, with lower values indicating higher viral load) and VN titers (a measure of neutralizing antibody levels, indicating immune response) after exposure to a person with COVID-19 were assessed. Sampling days were calculated as the number of days between a person's symptom onset or date of positive SARS-CoV-2 test and the animal's sample collection date. In animals with clinical signs, the length of observable illness was defined as the number of days between onset and resolution of clinical signs. While extremely rare, a small number of animals died while positive for SARS-CoV-2, documented in Carpenter et al. 2021[25], and were therefore excluded from analyses. In analyses or visualizations that used Ct values, the lowest Ct value obtained from respiratory swabs (nasal & oral), collected on the same day was used. Non-respiratory samples such as fecal and rectal samples were excluded, since the viral load in these sample types is commonly low (i.e., higher average Ct values) compared to respiratory samples[26]. Conjunctival swabs were infrequently collected, but since their diagnostic efficacy has not been evaluated, were excluded. Fur swabs were also omitted from analyses, since they are used as indicators of environmental contamination and not infection.

SARS-CoV-2 RT-PCR results, measured by cycle threshold (Ct), and SARS-CoV-2 VN titers were compared to the presumed date of exposure, measured as the reported date of human symptom onset or positive

human test. The lowest Ct values among respiratory swabs (oral and nasal) and geometric mean titer were calculated in 2-day intervals with 95% confidence intervals. Average Ct values and log-transformed geometric mean virus neutralizing antibody titers were calculated for confirmed animals, by species. Analysis was conducted for all observations, as well as a stratified analysis by species. To account for the inherent rise and fall of viral nucleic acid and neutralizing antibody, a polynomial function was applied to detect trends in Ct values and VN titer over time since presumed exposure. As early sampling in the first several days after exposure was rarely conducted, fixed axis points were applied to the regression model to reflect a Ct of 40 (no viral nucleic acid present) and VN of 0 on the day of likely exposure (Day 0). Two animals with Ct values <38 on the day of presumed exposure (Day 0) were excluded from analysis, as it is not biologically plausible to have measurable infection or immunity this early after exposure. It is likely that the date of presumed exposure occurred earlier than what was reflected in the epidemiologic investigation for these two animals.

Variant analysis was conducted using whole-genome sequencing results from USDA-NVSL. In late 2020, SARS-CoV-2 variants were identified and classified by CDC based on their impacts to human health, diagnostics, therapeutics, and vaccines[27]. In this study, strains sequenced prior to the identification of the first variants were classified as early circulating strains.

Zoonotic Transmission

In analyses or visualizations that described the association between human SARS-CoV-2 infection and animal infection, a person's symptom onset date was assumed to represent most likely date of exposure in the animal. In instances where this date was not available, the date the person first tested positive for COVID-19 was used.

To assess whether population increases in COVID-19 in people might cause subsequent increases in companion animal cases, a time series analysis using a cross-correlation function was performed to determine if there was a relationship between national human COVID-19 case reporting data and SARS-CoV-2 cases in companion animals. Daily national human COVID-19 case counts were downloaded from CDC's COVID Data Tracker and aggregated into monthly counts from March 2020 to December 2021[28]. SARS-CoV-2 infections in cats and dogs were aggregated into monthly counts. Sample collection date, which was available for 161 of 204 (79%) animals, was used as a proxy for date of infection. The cross-correlation time series analysis was restricted to one year, March 2020 to March 2021, since all presumptive positive companion animal cases were forwarded to USDA-NVSL for confirmatory testing during this time.

Results

Overview

From March 2020 to December 2021, 345 animals from 33 states in the U.S. were confirmed positive for SARS-CoV-2 (Figure 1; Figure S1). Of these, 204 (59%), were companion animals including 109 cats and 95 dogs (Table 1; Table S1). SARS-CoV-2 was also detected by RT-PCR in one ferret; this animal was omitted from further analyses due to low sample size. In companion animal cases detected through passive surveillance, 94% were initially exposed to a person with COVID-19. In the remaining 6% of cases, the source of SARS-CoV-2 exposure was unknown (e.g., circumstances such as an animal tested positive upon arrival at a shelter, or owners declined investigation).

Clinical Signs

Overall, 48% (n = 97) of companion animals displayed clinical signs consistent with SARS-CoV-2 infection, while 52% (n = 107) had no reported clinical signs at the time of sampling. This varied significantly by surveillance method ($\chi^2(1) = 41.07$, $p < 0.0001$); 72% (n = 67) of animals identified through passive surveillance exhibited clinical signs, while only 27% (n = 30) of animals identified through active surveillance exhibited clinical signs.

Respiratory signs (n = 81, 84%) were most frequently reported among animals with clinical signs, followed by non-specific (n = 53, 55%) and gastrointestinal (n=16, 16%) signs. Clinical presentation also varied by species (Figure 2a, 2b); 50% (n = 55) of cats and 44% (n = 42) of dogs showed clinical signs, although this variation was not statistically significant ($\chi^2(1) = 3.42$, $p = 0.065$). Of the animals with clinical signs, sneezing (21%) and lethargy (16%) were the most common in cats, whereas lethargy (20%) and cough (16%) were most common in dogs (Figure 2a, 2b).

Multi-pet Households

36 households had more than one cat or dog. There was a 25% (Wilson CI 14–41) likelihood that if one cat or dog became infected in the household, a second cat or dog would also test positive for SARS-CoV-2 (data not shown). Probability was higher of a second cat or dog testing positive if the index pet was a cat (30%; Wilson CI 16–51), and lower if the index pet was a dog (15%; Wilson CI 4–42%).

Diagnostics

Of the 204 confirmed positive companion animals, 91 (45%) animals tested positive by VN only, 67 (33%) animals tested positive by RT-PCR only and 46 (23%) animals tested positive by both RT-PCR and VN

(Table S2).

The average Ct value from confirmatory RT-PCR was 28.6 for all confirmed positive companion animals with RT-PCR results (n = 69). VN titers (n= 107) ranged from 8 to 512, with a median titer of 64 (geometric mean titer of 1.8) for all confirmed positive companion animals. Titers from confirmed positive cats ranged from 32 to 512 with a median titer of 128 (geometric mean of 1.9), whereas results from dogs ranged from 8 to 128 with a median titer of 32 (geometric mean of 1.6). The highest titer of 512 was detected in a cat sampled 23 days after onset of symptoms in its owner.

Associations between SARS-CoV-2 nucleic acid detection and virus neutralizing antibodies differed by species and were analyzed separately. Molecular detection was as early as 3 days post-exposure for both cats and dogs (Figure 3b). Ct values for SARS-CoV-2 nucleic acid detection peaked at day 6 for cats (Ct = 27; Figure 3c) and day 5 for dogs at (Ct = 29; Figure 3d). Detection occurred, on average, up to day 23 after most likely exposure in cats (range: 15–33) and up to 13 days in dogs (range: 9–16). In cats, virus-specific antibodies were first detected 5 days after nucleic acid detection (5 days after presumed exposure) and peaked at a geometric titer of 2.1 on day 32 after exposure. For dogs, virus-specific antibodies were first measurable 3 days after nucleic acid detection (5 days after exposure) and peaked at a geometric titer of 1.7 at 18 days after exposure. Although sample size was limited at longer sampling periods, antibody titers gradually trended downwards, but appeared stable at a geometric titer of 1.5 through at least day 55 after exposure (Figure 3c-d).

Whole genome sequencing was successful on samples from 70 (34%) animals (n= 41 cats, n = 29 dogs). Early circulating strains (Table S3) and four variants were detected: Alpha (B.1.1.7)[29], Delta (B.1.617.2), Epsilon (B.1.429), and Iota (B.1.526). In animals with early circulating SARS-CoV-2 strains (n = 37), lethargy (48%) and shortness of breath (43%), were the most commonly reported in clinically affected animals (n=23, Table S4). There was a greater proportion of clinically ill cats (n=30, 73%) than dogs (n=18, 62%), but there was no significant difference in signs of illness between species ($\chi^2(1) = 0.94$, $p = 0.333$). Delta was the most common variant detected (n = 21); clinically affected animals with Delta (n=17) most frequently presented with cough (53%), lethargy (53%) and sneezing (41%).

Zoonotic Transmission

To estimate viral incubation period, the number of days between human symptom onset (or date of positive test) and onset of clinical signs in animals was calculated. Data for this analysis was restricted to animals with clinical signs only, and animals for which data were available to show that a person in the house had symptoms (n=32; Figure 4a). The median number of days between human symptom onset

and onset of clinical signs in a companion animal was 10 (9.5, range: 0–24) days in cats (n=23), and 6 (8, range: 1–24) in dogs (n=9). We also assessed the length of active infection using clinical sign onset and resolution dates (Figure 4b). According to data from confirmed RT-PCR-positive animals, excluding deceased animals, with both onset and resolution dates collected (n=24), the median length of clinical infection was 10 (7.25, range: 3–36) days in cats (n=16) and 16.5 (10.75, range: 1–31) in dogs (n=8).

The likelihood of detecting an active infection by RT-PCR is largely dependent on the length of time between the animal's most-likely exposure to SARS-CoV-2 and the sample collection date. The median delay from presumed exposure date to animal sampling for a positive RT-PCR result was 10 (9, range: 0–35) days in cats (n = 35) and 6 (5.5, range: 0–24) days in dogs (n = 15; Figure 4c).

We also investigated whether patterns in human case counts were predictive of companion animal case counts. Given the available data in the restricted timeframe, a time series analysis using a cross-correlation function determined that while there appeared to be an observable relationship between human and animal case counts, this relationship was not significant (Figure 5).

Discussion

This study is the first to summarize nationally compiled surveillance data on the epidemiological and clinical characteristics of natural SARS-CoV-2 infection in companion animals. While there are publications describing SARS-CoV-2 in companion animals in many countries including those in Europe[30-36] and Asia[37,38], studies are often led by academic institutions conducting independent research; surveillance is not sustainable or systematic. In the United States, data on SARS-CoV-2 positive animals is collected through systematic One Health investigations and is shared voluntarily through collaborations with local, state, and federal and academic public health and animal health officials[15-17,25]. This perhaps helps to explain why the majority (56%) of all companion animal cases reported globally are from the United States[14].

Overall, our data show that among companion animals detected through passive surveillance, 94% had known exposure to a person with COVID-19 prior to the animal's infection. This provides strong evidence that people, most often owners, are the source of infection for their pets. These results corroborate findings from a large-scale study in northern Italy that reported dogs living in households with COVID-19 positive people were more likely to have detectable antibodies than dogs living in households without[30]. Other case studies from countries in Europe, Asia and South America have identified similar patterns[39]. These results support guidance developed by federal One Health partners that was released in January 2020 and continues to be updated, including recommendations to avoid animals just like you would other

people when sick or have a suspected COVID-19 infection, and to wear a mask around both people and animals when ill with COVID-19[40].

While the evidence for human-to-pet transmission is robust, less data are available to determine the likelihood and frequency of pet-to-pet or pet-to-person transmission within households. Our analysis of 36 households containing more than one pet indicate that any cat or dog in the household has a 25% probability of becoming infected with SARS-CoV-2 if there is a positive index pet. This probability was higher when cats were the index pet (30%), than dogs (15%), in line with experimental and challenge studies that suggest cats are more susceptible[41,42] and may be more infectious based on lower overall Ct values than dogs. While these data suggest pet-to-pet transmission may occur in households, we cannot determine whether subsequent pets in a multi-pet household were infected from a person or another animal. More One Health research to examine transmission dynamics among animals and among animals and people living in household environments is warranted.

To-date, evidence of cats or dogs transmitting SARS-CoV-2 to people is limited, although detecting and accurately attributing transmission from an animal source is challenging against a background of significant human-to-human transmission. This is further complicated since, like people, animals may not be tested, especially if they are subclinical, but may still be capable of shedding virus and infecting other individuals. Attempts to attribute directionality of transmission requires both human and animal samples that can be successfully sequenced and compared, in addition to a robust epidemiologic One Health investigation. One recent case study suggests cat-to-human transmission as likely from an infected pet cat in Thailand[43]. Specifically, epidemiologic data indicated transmission may have occurred after the cat, who had been living with COVID-19 positive owners, sneezed on a veterinarian who subsequently became ill with COVID-19. Sequences from the veterinarian, COVID-19 positive owners, and the cat were all identical, although the veterinarian only had contact with the cat. Another investigation identified imported hamsters for sale as the likely source of infection on onward spread among people in Hong Kong[44]. In both the cat and hamster investigations, a strain of SARS-CoV-2 which was not previously circulating in the geographic area was detected, which aided in the identification of likely animal-to-person transmission. Taken together, this evidence suggests that pet-to-human transmission is possible, although likely uncommon.

With respect to clinical presentation in pets, 48% of all SARS-CoV-2 confirmed companion animal cases exhibited clinical signs. Respiratory signs, particularly sneezing and cough, were the most common among ill animals. The proportion of animals with clinical signs varied significantly by surveillance method. Active surveillance studies, which typically begin when a person with COVID-19 is identified, and where companion animal samples are sought irrespective of their health, are likely a more accurate

estimate of companion animal infection prevalence nationally. Overall, only 27% of actively infected (evidenced by detection of viral nucleic acid) companion animals sampled through active surveillance showed clinical signs, emphasizing that subclinical animals should not be discounted when evaluating the role of animals in SARS-CoV-2 transmission[45].

Our study also estimated thresholds of diagnostic detection in companion animals. Data from 142 companion animals (74 cats, 68 dogs) sampled after presumed exposure to a person with SARS-CoV-2 suggests that viral nucleic acid detection by RT-PCR occurs shortly after presumed exposure, typically less than 5 days. For cats, our data suggest the ideal sampling window to detect viral nucleic acid is 3–17 days after exposure, and 3–10 days for dogs (Figure 4). We also discovered that virus specific neutralizing antibody is rapidly produced. Rapid and sustained titers of neutralizing antibody after infection may have contributed to the mild nature of disease observed in the majority of animals in this study (see Carpenter et al.[25], Carvallo et al.[46], and Rotstein et al.[47] for descriptions of companion animal mortalities that occurred while pets were positive for SARS-CoV-2).

Finally, samples from 34% of companion animals included in our data were successfully characterized by whole genome sequencing. These sequences were used to identify variants and their corresponding clinical presentation (Table S4). Among this subset, early circulating strains and four variants were detected: each corresponded temporally with variants circulating in the human populations in the same geographic area at the time. Processes to continue to generate and analyze sequence information from animal populations are essential to ensure that novel mutations, strains and variants arising from animal populations, including companion animals, are detected expediently, ideally before detrimental impacts to public health can be recognized[48].

Some limitations exist with the nature of data collection and the analyses presented in this manuscript. First, no federal agency is currently mandated to oversee companion animal surveillance or response, including for emerging zoonotic diseases. Reporting for companion animal zoonoses to public or animal health officials may also be jurisdiction or disease specific. Given that surveillance varies by jurisdiction, the approach taken by One Health investigations and reporting are likely to have varied. Ongoing efforts to improve surveillance, including enhancing coordination and data sharing among One Health sectors and supporting data modernization initiatives, are underway[49].

Second, since there is no standardized diagnostic method or sample validation criteria for SARS-CoV-2 in animals in the U.S., we opted to include only companion animals that were confirmed positive at USDA-

NVSL to ensure consistency and comparability in diagnostic results. In doing so, however, we limited our sample size and perhaps skewed results toward animals that met standards of confirmation. Third, our analysis based on a human source of exposure does not account for households where multiple people may have been the source of pet infections, as symptom onset and positive test dates were recorded for only the first identified person with COVID-19 in each household. The date of animal exposure should therefore be considered an estimation. Finally, our results and interpretations are based on early circulating strains of SARS-CoV-2 and the four variants, including Delta, identified in companion animals before the end of 2021. This dataset does not extend into 2022 when Omicron became the most prevalent variant in the U.S.; conclusions about companion animal susceptibility, duration of infection, and transmissibility may be altered for animals infected with Omicron due to the virus's high number of mutations and are not addressed here. Future studies that implement a standardized approach to sample collection among all members of a household (both human and animal), and sample longitudinally through time may provide needed clarity to understand the role companion animals play in SARS-CoV-2 transmission at the human-companion animal interface.

Given that SARS-CoV-2 infections in animals are not currently nationally notifiable in the United States, it is possible that unreported animal cases were missed within the timeframe of the data included in this manuscript. This is corroborated by published research which also suggests that current surveillance may be vastly underestimating the true burden of SARS-CoV-2 in animals[15-17,36]. Without continued One Health collaboration across sectors to pursue more extensive surveillance (both active and passive), many SARS-CoV-2 infections in companion animals will remain undetected.

Conclusion

Despite the known susceptibility of companion animals to SARS-CoV-2, testing and disease reporting of pet cases of SARS-CoV-2 infection has been limited in the U.S. Lack of mandatory reporting of companion animal cases of SARS-CoV-2 infection has continued to be a challenge throughout the COVID-19 pandemic. Relying on voluntary reporting of a novel, emerging zoonotic disease with unknown transmissibility and disease in animals is a hurdle for understanding the clinical and epidemiological features of a rapidly spreading zoonosis. This is especially apparent with companion animals, whose oversight falls in a government jurisdictional void, and where structures and systems to detect, monitor, and respond to companion animal zoonoses are typically not a standard component of public health or animal health programs. This manuscript provides support that systematic surveillance in animal populations can be established, sustained, and beneficial in a global public health emergency. In the instance of SARS-CoV-2, strong collaborations between public health and animal health sectors at the local, state, and federal level were able to circumvent some of these issues. However, formalized One Health collaboration mechanisms that institutionalize joint investigation and coordinated surveillance are necessary to best protect human and animal health and to most efficiently respond to future emerging zoonotic disease threats.

Declarations

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Declarations

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Data and materials availability

All data are part of national surveillance and available on USDA's public-facing dashboard.

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Table

Table 1. Demographics of confirmed positive companion animals in the United States from March 2020 – December 2021.

	Cat	Dog
n	109	95
Sex n (%)		
Female	23 (21.1)	18 (18.9)
Male	38 (34.9)	26 (27.4)
Unknown	48 (44.0)	51 (53.7)
Age in Years (mean (SD))	6.64 (4.69)	6.89 (4.19)

Figures

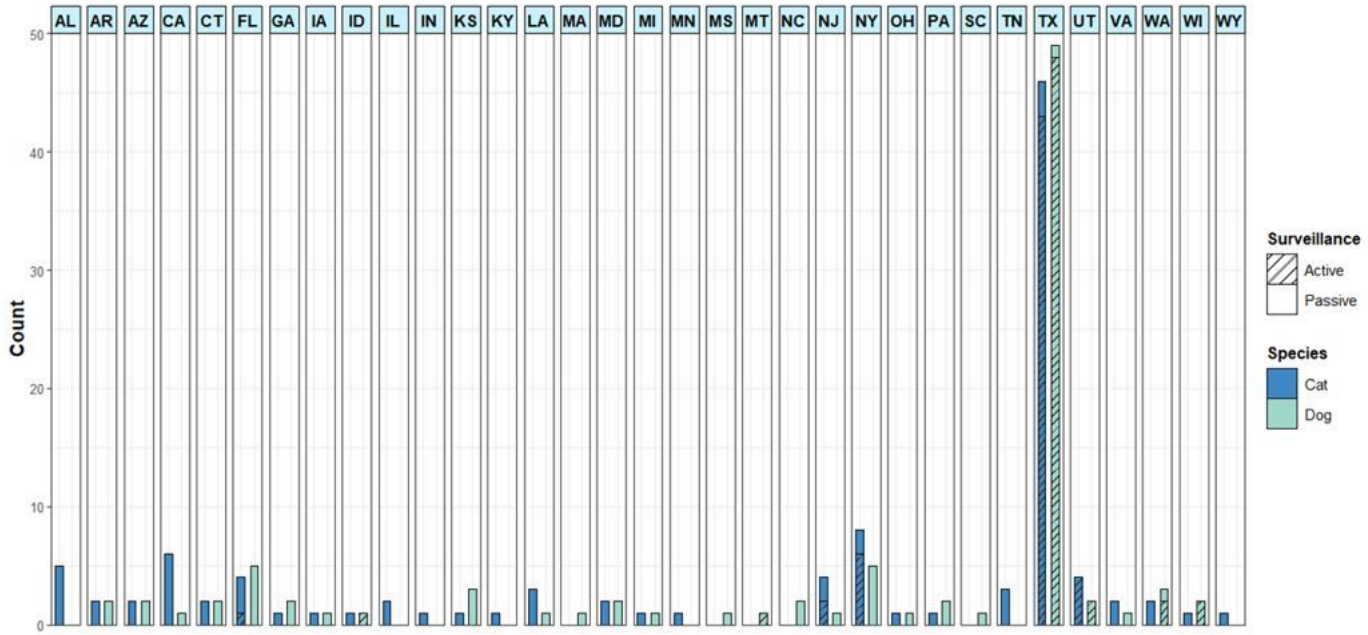

Figure 1

SARS-CoV-2 positive cats (n=109) and dogs (n=95) cases reported by state. Companion animals were identified through either passive or active surveillance.

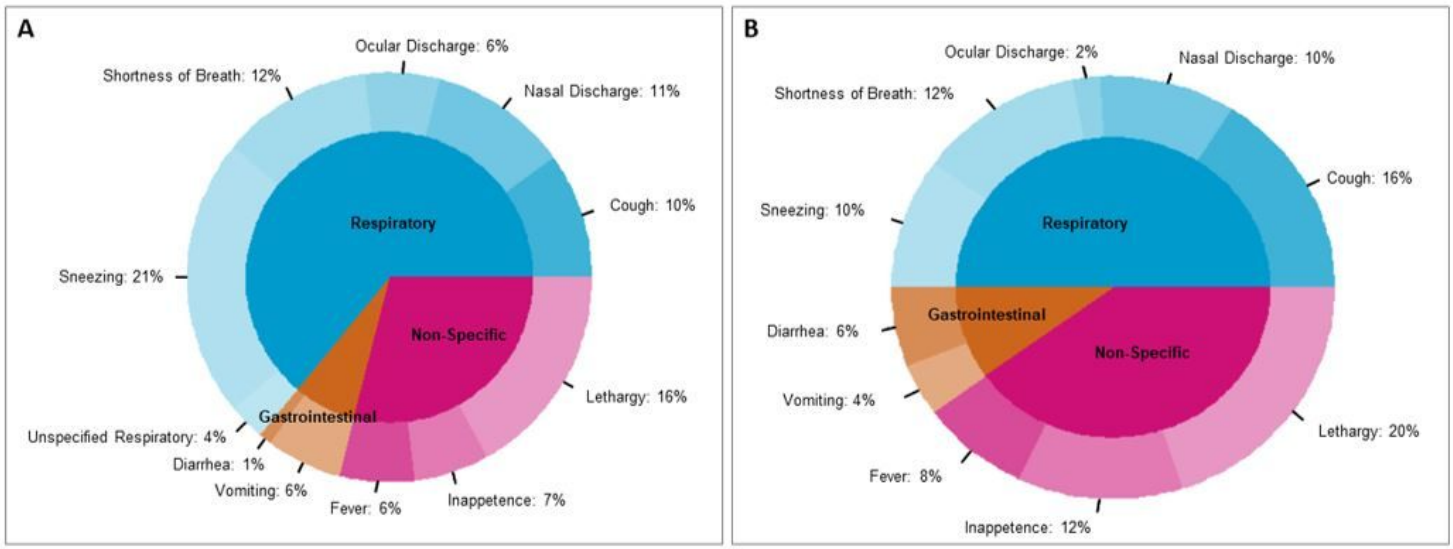

Figure 2

Clinical signs reported in cats (n=55; A) and dogs (n = 42; B). Of 97 animals with clinical signs, the proportion of each clinical sign being displayed are shown within each species. Since a given animal may display multiple clinical signs, percentages are calculated by number of signs displayed, not by individual animals.

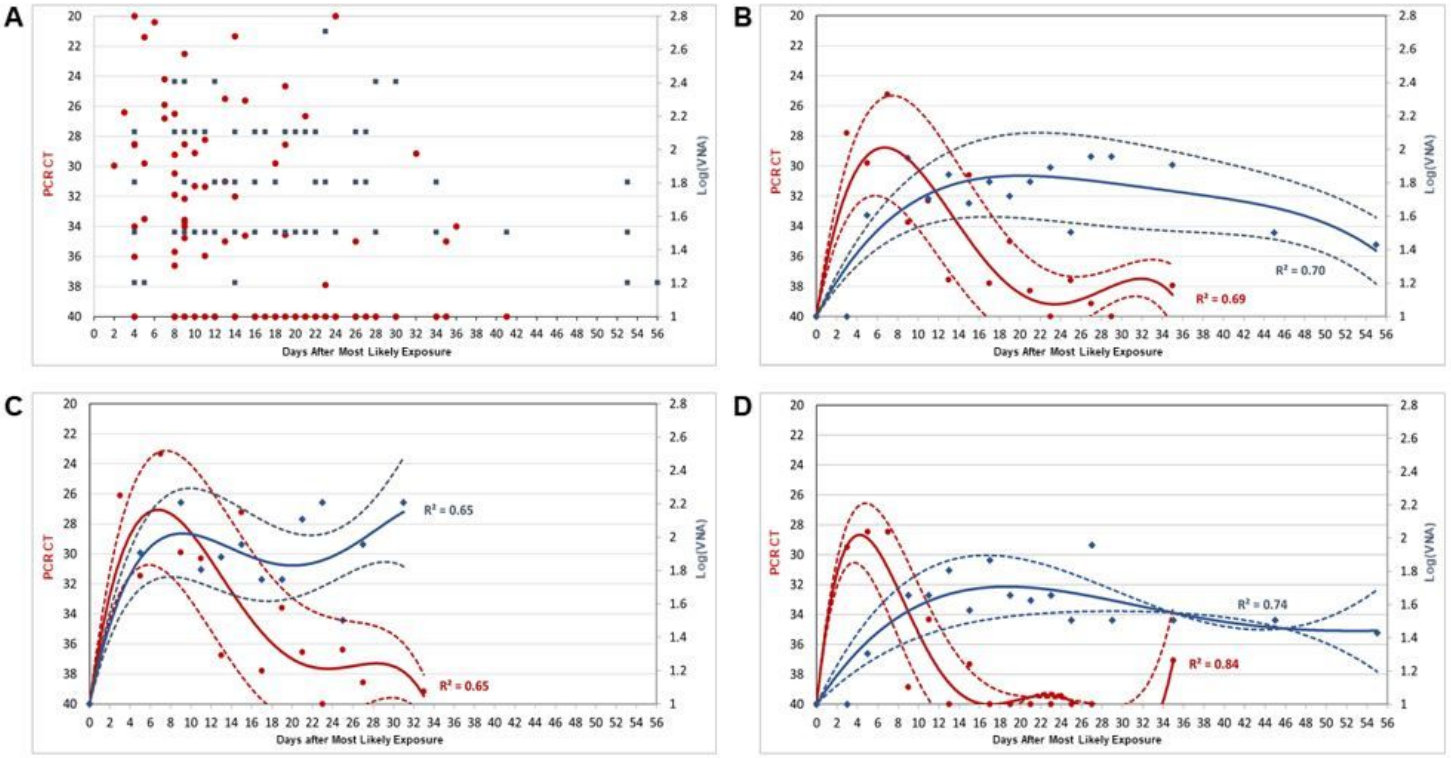

Figure 3

Trends in SARS-CoV-2 nucleic acid detection and virus neutralizing antibodies in dogs and cats with confirmed infection, 2019 – 2021. Red lines and red circles represent cycle threshold values from the SARS-CoV-2 real-time quantitative PCR assay. Blue lines and blue squares represent virus neutralizing antibody titers (VNA). (A) All dogs and cats registered as confirmed with SARS-CoV-2 infection during the study period / Individual values represented for each animal; (B) All dogs and cats / Average values represented over 2-day sampling frames with confidence intervals (dotted lines); (C) Only cats; (D) Only dogs.

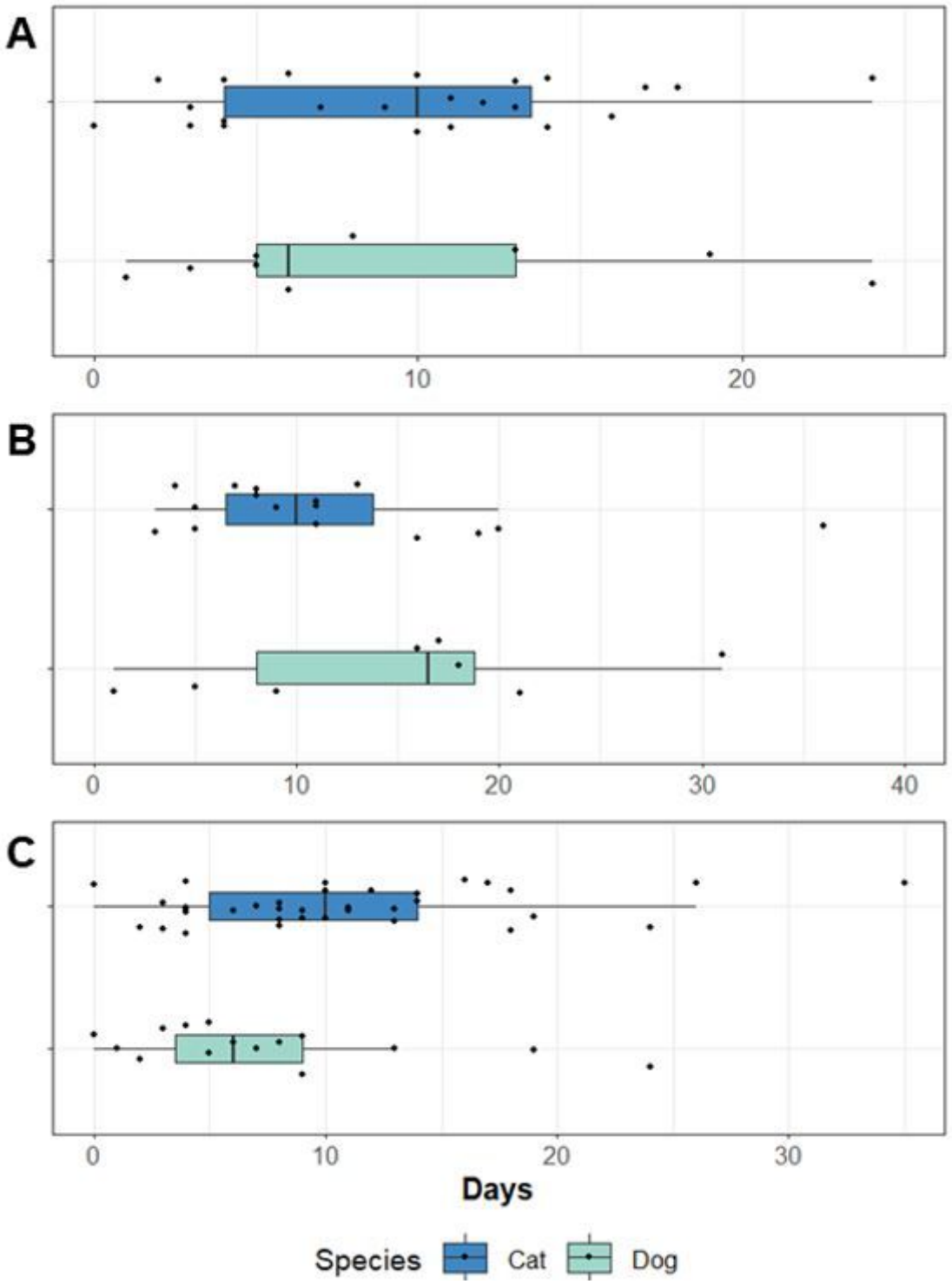

Figure 4

Timeline of days between human symptom onset and animal clinical sign onset. This analysis excludes subclinical animals. Jittering was used to better visualize distribution of the data and to prevent overlapping of values, with each point corresponding to an individual animal. (B) Days between clinical sign onset and resolution in animals. This serves to characterize the length of active infection in affected animals. Deceased animals were excluded from this analysis. (C) Days between human symptom onset

and positive animal test. The animal test date referenced is the collection date of the sample that yielded a positive RT-PCR result. This includes both clinically affected and subclinical animals.

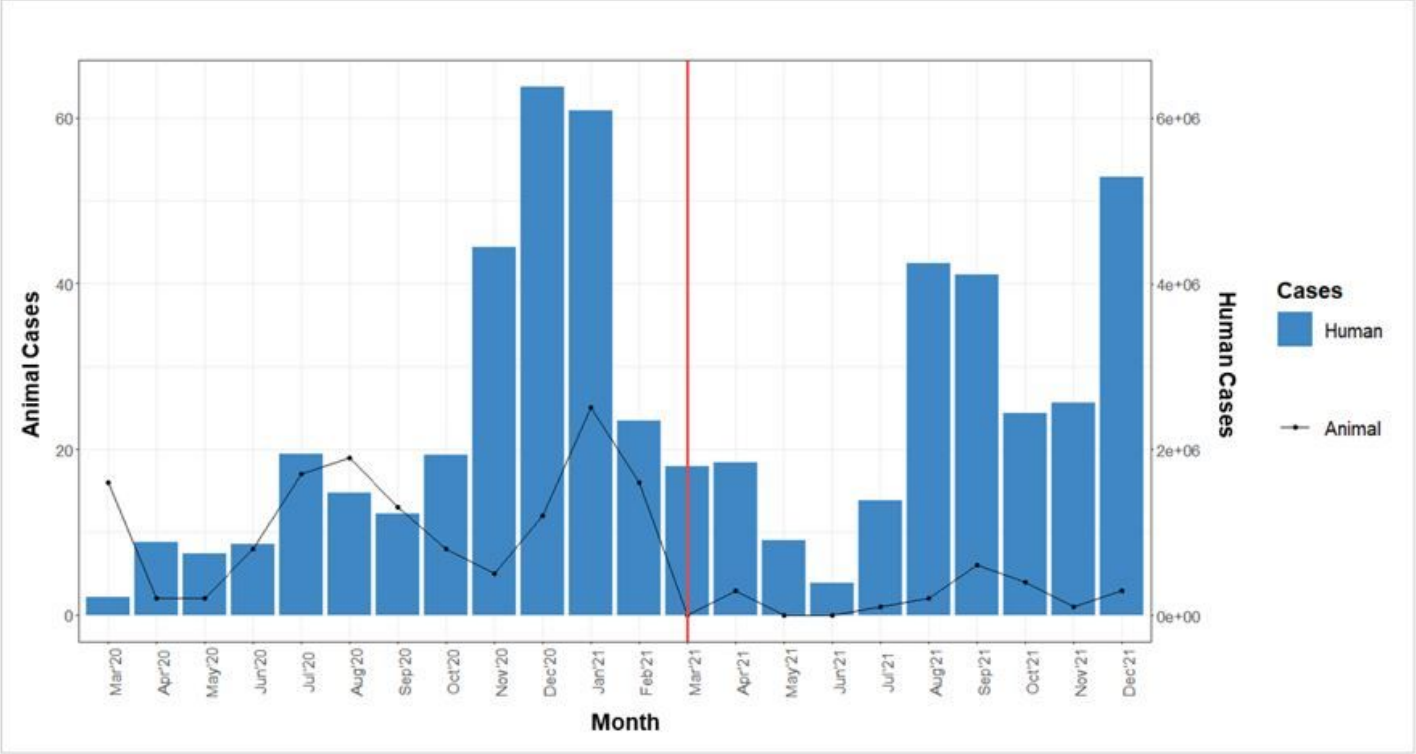

Figure 5

Time series of human COVID-19 monthly case count and animal infections of SARS-CoV-2. For animal cases, the date of sample collection was used. Effective March 2021, indicated by the red line, USDA expectations for confirmatory testing for companion animals were changed to include only the first domestic cat and dog in each state, territory, and tribal nation.

Supplementary Files

This is a list of supplementary files associated with this preprint. Click to download.

- CASupplementary.pdf