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Antimicrobial Resistance in Respiratory Pathogens of Domestic and Wild Felids

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Abstract | Still a major threat within both domestic, and wild felids, feline respiratory disease complex (FRDC) causes great morbidity, and death. In this study we investigated frequency of important respiratory pathogens, the co-infections, and their impact on antimicrobial resistance (AMR) development. Using multiplex PCR, and RT-qPCR techniques, a total of 550 respiratory samples from clinically infected, and asymptomatic cats were examined. Our analysis revealed a detecton of Bordetella bronchiseptica (6.2%), Chlamydia felis (3.6%), and Influenza A virus (0.8%), Mycoplasma spp. (42.2%), Feline Calicivirus (31.5%), and Feline Herpesvirus-1 (23%). Interestingly, Mycoplasma spp., and FeHV-1 were more abundant within colder months ($p < 0.05$), and Mycoplasma spp were reported for greater rates within kittens (60.9%) compared to seniors (38.8%, $p = 0.003$). Pathogen frequency varied considerably alongside age, season, and clinical degree. Specifically, within co-infections of FeHV-1 (OR = 3.12, $p = 0.018$), univariable logistic regression analysis found that Mycoplasma spp. raised the risks for severe respiratory illness through 2.05 times ($p = 0.018$). Given the usage for antibiotics within chronic respiratory diseases, the results underline the critical necessity for focused antimicrobial treatment, and better diagnosis techniques to reduce the dangers related alongside AMR. Future studies should concentrate on alternative therapeutic approaches such as probiotics, and immunization campaigns like molecular characterisation for resistant bacteria to help to lower dependency on antibiotics and increase treatment effectiveness.

Keywords | Feline respiratory disease complex, Mycoplasma spp., Feline calicivirus, Antimicrobial resistance, Co-infections, PCR diagnostics, Veterinary epidemiology

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Affecting domestic, and wild felids, Feline Respiratory Disease Complex (FRDC) is a multifactorial illness marked through a high frequency, and major clinical effect (Cannon, 2023; Litster, 2021). Within high-density settings like shelters, breeding houses, and multi-cat households—where intimate contact speeds up pathogen spread—the illness is especially serious (Nguyen *et al.*, 2019). Apart from being a main cause for morbidity, and death within felines, FRDC is also responsible for higher antibiotic use, which might help to build antimicrobial resistance (Michael *et al.*, 2021). Severe outbreaks may also result within judgments upon euthanasia upon account for inadequate treatment response, and the financial load upon caregivers (Cannon, 2023; Litster, 2021).

The etiology for FRDC is multifarious, and includes environmental, bacterial, and viral elements interacting to control disease severity, and development. Both extremely contagious, and able to cause chronic infections alongside recurring clinical symptoms, feline herpesvirus-1 (FeHV-1), and feline calicivirus (FCV) are among the most often occurring viral diseases linked alongside FRDC (Palombieri *et al.*, 2022; Ali *et al.*, 2024; Al-Sailawi *et al.*, 2024; Mohsen *et al.*, 2024). Often functioning either like main or secondary pathogens, *Bordetella bronchiseptica*, *Chlamydia felis*, and *Mycoplasma felis* have been linked alongside upper, and lower respiratory tract illnesses upon the bacterial spectrum (Cannon, 2023; Michael *et al.*, 2021). Secondary bacterial infections brought upon through opportunistic pathogens such *Pasteurella* spp., *Escherichia coli*, *Staphylococcus* spp., and *Streptococcus* may aggravate respiratory symptoms, and extend the course for illness (Litster, 2021; Slaviero *et al.*, 2021).

FRDC pathophysiology shows significant dependence on secondary pathogen infections because such infections cause enhanced illness severity together with delayed recovery and increased chances of therapeutic failures (Arnold *et al.*, 2022). Viral infections destroy the normal respiratory microbiome allowing future bacterial growth that intensifies illness symptoms (Arnold *et al.*, 2022). Recent research studies demonstrate that FRDC causal agents lead to distinctive clinical outcomes based on how vulnerable the infected animal became (Nguyen *et al.*, 2019; Michael *et al.*, 2021) because of their immune condition and vaccination history or genetics. Feline susceptibility together with persistence in populations result from environmental stresses such as overcrowding and ventilation deficiencies and dietary deficits (Litster, 2021; Palombieri *et al.*, 2022).

Due within great part to the overuse, and abuse for antibiotics within veterinary medicine, antimicrobial resistance

(AMR) is becoming a major issue within FRDC treatment (Michael *et al.*, 2021). Particularly within situations where viral infections are the main etiological agents, the regular use for antibiotics for empirical therapy may promote the selection for resistant bacterial strains (Tallmadge *et al.*, 2020). Furthermore, frequent or chronic respiratory infections may call for extended antibiotic treatment, which increases the likelihood for resistance development even more (Maboni *et al.*, 2019). to differentiate bacterial coming from viral illnesses, and provide focused antibiotic treatment, this emphasizes the necessity for better diagnosis techniques including molecular, and culture-based approaches (Slaviero *et al.*, 2021; Kareem *et al.*, 2023; Aziz *et al.*, 2023). Though a lot for study upon FRDC has been done, important information gaps still exist concerning pathogen frequency, the function for co-infections, and how antibiotic resistance affects treatment results. Moreover, even within the event, that epidemiological research has shed light upon FRDC within some geographical areas, a thorough knowledge for its worldwide frequency, and illness burden is still absent (Nguyen *et al.*, 2019). Developing evidence-based immunization programs, improving treatment guidelines, and applying successful infection control policies within both domestic, and wild feline populations depend upon filling up these voids.

By means for pathogen incidence across many demographic, and environmental factors, this research seeks to evaluate the epidemiology, and clinical consequences for FRDC. We specifically aim to ascertain the frequency for important viral, and bacterial pathogens within clinically afflicted, and asymptomatic felines. Additional we aim to investigate the relationship between co-infections, and disease severity, as well as to investigate the consequences for antibiotic resistance within FRDC care. Through better knowledge for these elements, this study seeks to help to optimize preventative tactics, treatment interventions, and diagnostic techniques for feline respiratory illnesses.

MATERIALS AND METHODS

STUDY POPULATION

Respiratory specimens obtained during regular diagnostic testing of Iraqi domestic cats were reviewed for laboratory results during a specific timeframe. Testing of specimens also sought Feline Herpesvirus-1 (FeHV-1), Feline Calicivirus (FCV), *Bordetella bronchiseptica*, *Chlamydia felis* and *Mycoplasma felis* in addition to Influenza A virus screening as outlined by Thieulent *et al.* (2024) and Xiao *et al.* (2022). The study population consisted of asymptomatic and symptomatic sick domestic felids for determining pathogen frequencies and detection rates of simultaneous infections. Regular felid diagnostic procedures and clinical signs of pneumonic disease qualified patients for inclusion.

Table 1 shows how clinical indicators were classified with-in terms for severity depending upon evident symptoms for the time for sample.

Table 1: Clinical scores for respiratory signs coming from cats for the time for sample collection.

Clinical Score	Clinical Signs	Total Num-ber for Cats*
0 (Clinically Normal)	No respiratory signs, and no post-mortem lesions	50
1 (Mild Upper Respiratory Signs)	Sneezing, coughing, conjunc-tivitis, nasal/ocular discharge	105
2 (Severe Upper Respiratory Signs)	Sneezing, coughing, conjunc-tivitis, nasal/ocular discharge, ulcers within the mouth, lethargy, fever, inappetence	30
3 (Lower Respira-tory Involvement, Pneumonia)	Pneumonia accompanied through dyspnea, depression, lethargy, fever, or inappetence	48

*Clinical signs for 320 cases were unknown.

As previous research indicate asymptomatic carriers may help to pathogen circulation within feline populations, pathogen prevalence used to be evaluated within both symptomatic, and asymptomatic felids (Hofmann-Lehmann *et al.*, 2022; Walter *et al.*, 2020).

PATHOGEN DETECTION METHODS

The combination of Multiplex PCR and RT-qPCR testing procedures was used to identify bacterial and viral pathogens in extracted respiratory sample nucleic acid (Xiao *et al.*, 2022). The tested pathogens for real-time PCR systems included FeHV-1 along with FCV, Mycoplasma felis, Chlamydia felis, Bordetella bronchiseptica, and Influenza A virus (Thieulent *et al.*, 2024; Palombieri *et al.*, 2022). According to Wasik *et al.* (2021) and similar to previous research, sequenced Mycoplasma felis-positive samples (Sanger) identified strains.

PREDICTOR AND OUTCOME VARIABLES

Researchers evaluated the clinical effects along with disease epidemiology of feline respiratory disease complex (FRDC) through evaluation of key predictor and outcome factors. The demographic assessment point included assessment of both feline age and sex profile. The research divided the subjects into four age-based groups; kitten (younger than 7 months), junior (7 months to under 3 years), adult (3 years to 11 years), senior (older than 11 years). A pathogen sensitivity and illness severity analysis was performed through the established age-based categorization. The development as well as occurrence of illness is affected by sex-based differences between males and females. Epidemiological documents split the data into cold and warm seasonal data points to evaluate seasonality patterns (Walter *et al.*, 2020).

From May to September the season was warm and October through April brought cold weather conditions. Previous research had established the separation to determine how climate variations affected both pathogen frequency and severity at the Federal Reserve of Denver Campus. Existing scientific reports confirm that several respiratory diseases particularly viral agents undergo seasonal variations because people spend more time indoors with limited ventilation during colder months (Palombieri *et al.*, 2022). Medical indicators received evaluation through an ordinal rating method that rated participants based on their shown respiratory symptoms at sample collection times. Table 1 presents the scoring criteria which starts with clinically normal states (score 0) followed by moderate upper respiratory symptoms (score 1), severe upper respiratory involvement (score 2) and concludes with lower respiratory tract involvement or pneumonia (scoring 3). Our scoring system enabled consistent illness effect evaluation to investigate the pathogen-clinical symptoms relationship.

The research identified co-infections as an additional prognostic characteristic to study. Previously health professionals classified the identification of two or more respiratory pathogens in the same specimen as a co-infection. Researchers found this data point highly important since multiple infections along specific pathogens led to severe disease conditions and prolonged illnesses with treatment complications (Thiegent *et al.*, 2024). This work investigated how co-infections affect FRDC disease progression because polymicrobial interactions control this disease most currently.

STATISTICAL ANALYSIS

Fisher’s exact test functioned with categorical variables but logistic regression models analyzed pathogen correlations which linked to illness severity (Shi *et al.*, 2020). The researchers conducted pathogen co-infection analysis with Spearman’s correlation followed by R Core Team (2023) for R software network analysis. Pathogen detection frequencies were used to calculate co-infections according to previous epidemiological studies of respiratory pathogens (Tangwangvivat *et al.*, 2019). The specified statistical significance remained a p-value below 0.05.

RESULTS AND DISCUSSION

STUDY POPULATION OVERVIEW

Between January 2020 and February 2025, a total of 550 respiratory samples from domestic cats were processed by three veterinary diagnostic laboratories in Iraq for pathogen screening. Of these, 402 samples were collected from cats exhibiting varying degrees of respiratory illness, while 148 samples were obtained from clinically healthy cats and served as the control group. Clinical information was un-

available for 310 samples, which were therefore excluded from the severity analysis (Table 1). The study population included 156 male and 160 female cats, while gender data were missing for 234 cases. Regarding age, 200 samples lacked age information; among the remaining cases, 92 were identified as kittens, 85 as juniors, 128 as adults, and 45 as seniors.

PATHOGEN DETECTION ACROSS THE STUDY POPULATION

Figure 1 summarizes the frequencies for six main feline respiratory infections. The most often found pathogen used to be *Mycoplasma* spp., for 42.2%; followed through Feline Calicivirus (FCV) for 31.5%, and Feline Herpesvirus-1 (FeHV-1) for 23%. Quite lower were the detection rates for *Bordetella bronchiseptica* (6.2%), *Chlamydia felis* (3.6%), and Influenza A virus (0.8%).

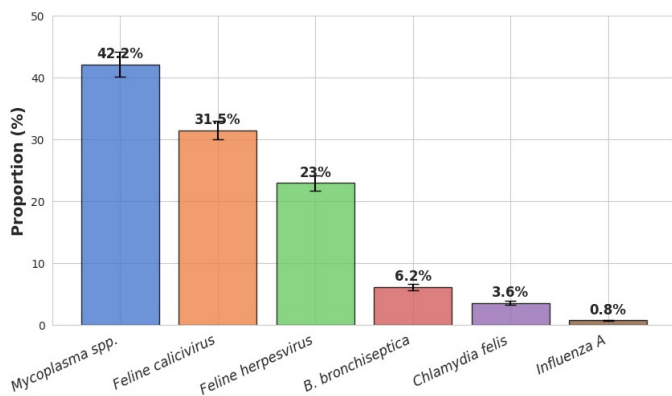


Figure 1: Proportion for detected respiratory pathogens within the study population.

This distribution emphasizes the preponderance for bacterial co-infections, especially *Mycoplasma* spp., which has been recently identified like a major contributor to feline respiratory infections (Thieulent et al., 2024). The great frequency for FCV, and FeHV-1 corresponds alongside earlier results confirming these viruses like main causes for Feline Respiratory Disease Complex (FRDC) (Xiao et al., 2022).

Among the investigated feline respiratory illness cases, *Mycoplasma* spp. (42.2%) used to be the most often identified pathogen as shown within Figure 1, followed by Feline Calicivirus (31.5%), and Feline Herpesvirus-1 (23%). The reduced detection frequencies for *Bordetella bronchiseptica* (6.2%), *Chlamydia felis* (3.6%), and Influenza A virus (0.8%) imply, that while these infections may contribute to the Feline Respiratory Disease Complex (FRDC), their total effect within this dataset seems to be less significant. The prevalence for *Mycoplasma* spp. corresponds alongside other findings stressing its dual function like both a commensal, and an opportunistic pathogen within feline upper respiratory tract infections (Thieulent et al., 2024; Xiao et al., 2022).

The research establishes that bacterial pathogens particularly *Mycoplasma* spp. enhance the severity of FRDC even when they infect cats with viral pathogens such as FCV and FeHV-1 (Schulz et al., 2021). The high frequency of FCV and FeHV-1 confirms their established status as main viral causes of feline respiratory infections (Palombieri et al., 2022) while both viruses disable immune function and damage mucosa to make cats susceptible to bacterial infections (Neira et al., 2021). The mix of viral infections with bacterial infections creates vital veterinary medical problems by contributing to illness progression and chronicity. The observed detection of *Mycoplasma* spp. requires examination of antimicrobial resistance patterns that affect feline respiratory disease management. Since *Mycoplasma* spp. fails to have a cell wall it naturally displays resistance against β -lactam antibiotics thus the recommended therapies embrace fluoroquinolones and macrolides (Keller et al., 2021). For chronic infections the routine antibiotic use of certain antibiotic classes creates bacteria that are resistant thus creating problems for therapy and increasing the prospects of persistent respiratory disease in affected cats (Hosie et al., 2021).

These findings highlight the need for thorough diagnosis methods, that differentiate between viral, and bacterial etiologies to maximize antimicrobial usage, and lower the danger for needless antibiotic distribution (Fritz et al., 2022). The results additionally support the need for improved co-infection monitoring within order to comprehend how they affect clinical results, and therapy reactions. Future studies should look into the long-term consequences for co-infections upon illness development, and recovery within feline populations like the genetic factors for *Mycoplasma*-associated AMR.

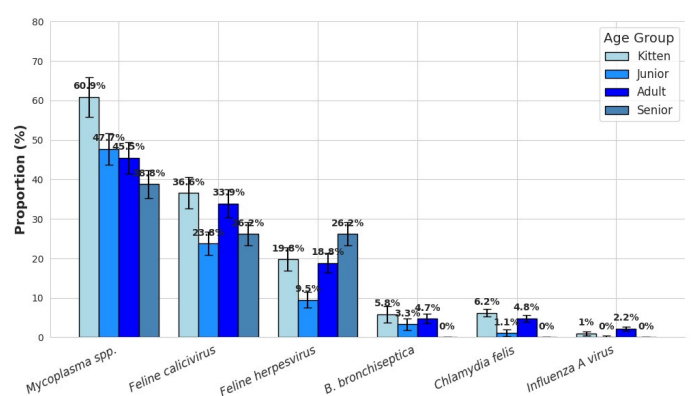


Figure 2: Pathogen prevalence across different feline age groups.

PATHOGEN PREVALENCE THROUGH AGE GROUP

Figure 2 shows the how diseases are distributed throughout many age groups. Kittens (60.9%), followed through junior cats (47.7%), adults (45.5%), and seniors (38.8%, $p = 0.003$), were most likely *Mycoplasma* spp. Likewise,

FCV used to be much greater within kittens, and juniors; FeHV-1 used to be found within 33.9% for adult cats, indicating ongoing viral shedding.

While older cats may have persistent bacterial infections, especially *Mycoplasma* spp., like secondary invaders, this age-related fluctuation within infection rates may reflect immune system immaturity within kittens, therefore predisposing them to primary viral infections.

Figure 2 shows the frequency for six main feline respiratory infections within many age categories, therefore stressing important differences within infection rates. within kittens (60.9%), *Mycoplasma* spp. were most common; junior (47.7%), adult (45.5%), and senior (38.8%) cats followed within order. within kittens, and juniors, Feline Calicivirus (FCV), and Feline Herpesvirus-1 (FeHV-1) also exhibited higher detection rates; later age groups showed a slow decrease within both. upon the other hand, *Bordetella bronchiseptica*, *Chlamydia felis*, and Influenza A virus were found for reduced frequency across all age groups—with little detection within seniors. Because for their immature immune responses, and higher exposure within high-density environments like shelters or multi-cat households, the much higher frequency for *Mycoplasma* spp. within younger cats' points to kittens, and younglings perhaps being more vulnerable to bacterial colonization (Thieulent *et al.*, 2024). This result is consistent alongside other A substantial body of research reveals *Mycoplasma* spp. exists as either primary pathogen or opportunistic secondary invader when infecting young animals or young animals exposed to environmental stresses (Xiao *et al.*, 2022). Research shows FCV and FeHV-1 detection increases in kittens and juniors since these viruses belong to the category of highly infectious primary respiratory pathogens which primarily affect young cats because their mother antibodies deteriorate and vaccination coverage remains insufficient (Palombieri *et al.*, 2022). The decreasing detection rates of *Mycoplasma* spp., FCV and FeHV1 in older cats indicate either previous exposure developed tolerance in their immune response or it could be due to dormant infections and sporadic viral release rather than active disease status (Schulz *et al.*, 2021). The identification of *Mycoplasma* spp. in 38.8% of senior cats indicates that some people maintain persistent bacterial colonizations which could enhance respiratory illness among co-infected immunocompromised felines (Neira *et al.*, 2021). Extended antibiotic treatment of chronic illnesses in clinical settings might create antimicrobial resistance (AMR) issues in elderly people (Hosie *et al.*, 2021). The minimal detection of *Bordetella bronchiseptica* and *Chlamydia felis* throughout different age brackets suggests these bacteria produce less effect on endemic respiratory disease than viral pathogens and *Mycoplasma* spp. (Keller *et al.*, 2021). Senior

cats lack Influenza A virus infections completely at the same time the virus shows rare occurrences in feline populations which implies feline influenza infections tend to be short-lived and do not create lasting reservoirs in older cats (Fritz *et al.*, 2022). These findings underline the need for age-stratified monitoring within the diagnosis for feline respiratory diseases, especially for early identification for high-risk kittens, and juveniles who can profit coming from focused immunization programs, and early antibiotic intervention when needed. *Mycoplasma* spp., and chronic respiratory illness have a high correlation, hence further study is required to investigate their influence upon the development for antimicrobial resistance especially within recurring infections, that call for continuous antibiotic treatment (McAloose *et al.*, 2020).

SEASONAL VARIATION WITHIN PATHOGEN DETECTION

The cold month period from October through April received separate classification from the warm month period of May through September to detect seasonal changes. The prevalence rates for *Mycoplasma* spp. and FeHV-1 reached 47.2% and 35.3% respectively during cold months ($p = 0.032$) as illustrated in Figure 3. *B. bronchiseptica* together with *Chlamydia felis* demonstrated a steady frequency during all seasons without any seasonal variation but FCV maintained a constant pattern year-round.

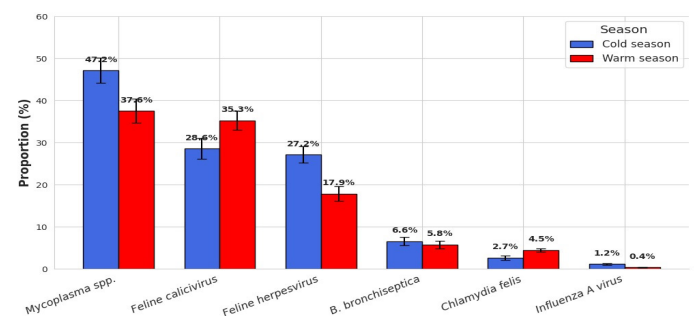


Figure 3: Seasonal variation within respiratory pathogen prevalence.

The data reveals that pathogen persistence becomes more probable in cold months after controlling for factors such as indoor crowding, decreased ventilation and compromised immune functions according to Neira *et al.* (2021).

Higher detection rates within colder months for *Mycoplasma* spp. (47.2%), FeHV-1 (35.3%), and *B. bronchiseptica* (27.2%), compared to their lower detection within the warmer season (37.6%, 28.6%, and 17.9%, respectively), Figure 3 shows the seasonal variance within the prevalence for major feline respiratory pathogens. upon the other hand, influenza A virus remained infrequent during both seasons whereas Feline Calicivirus (FCV), and *Chlamydia felis* showed somewhat steady seasonal distributions.

These results complement other studies showing, that seasonal elements affect pathogen circulation, especially within colder months when higher indoor congregation, and lower ventilation facilitate pathogen transmission (Thieulent *et al.*, 2024; Xiao *et al.*, 2022). The much-increased frequency for *Mycoplasma* spp., and FeHV-1 within colder months points to a possible seasonal aggravation for chronic infections since lower temperatures, and humidity changes might compromise mucosal immunity, hence raising host vulnerability (Palombieri *et al.*, 2022). Particularly for FeHV-1, and *Mycoplasma* spp., stress-induced immunosuppression during seasonal transitions may also help to cause viral reactivation, and subsequent bacterial infections.

The opportunistic respiratory pathogenicity of *B. bronchiseptica* has received additional evidence through the seasonal observations of its detection rates according to Schulz *et al.* (2021). Our research establishes FCV as a persistently identified viral agent across different seasons which suggests these viral strains successfully spread despite environmental fluctuations mainly because they can easily survive external conditions and cause heavy viral shedding in cats (Hosie *et al.*, 2021). The poor influenza detection A virus fits its infrequent appearance within feline hosts, therefore confirming, that cats are accidental hosts rather than main reservoirs for influenza viruses (Keller *et al.*, 2021). Nevertheless, the modest rise within cold-season cases (1.2%) calls for further research especially considering possible zoonotic consequences within mixed-species situations (Fritz *et al.*, 2022).

The clinical findings reveal the necessity to monitor seasonal illnesses together with effective preventive measures for *Mycoplasma* spp. and FeHV-1 since these pathogens exhibit enhanced activity during winter months. Veterinary professionals need to maintain prudence when providing long antibiotic treatments during peak infection times because *Mycoplasma* infections along with AMR show strong correlations.

PATHOGEN PREVALENCE THROUGH CLINICAL SEVERITY

Figure 4 illustrates that identifying pathogen sources produces distinct effects on clinical disease gravity. FCV together with FeHV-1 appeared during moderate to severe clinical situations yet *Mycoplasma* spp. were located within 73% of cats who faced severe respiratory conditions (pneumonia). *Mycoplasma* spp. exhibits a high prevalence in severe infection cases after viral exposure which leads researchers to wonder about its role in respiratory disease progression (Schulz *et al.*, 2021).

The relationship between pathogen identification and clinical severity of feline respiratory illness cases shows that

certain infections directly contribute to increasing disease severity according to Figure 4. Laboratory results showed that *Mycoplasma* spp. detection reached 73% in conjunction with pneumonia (score 3) while Feline Calicivirus (FCV) and Feline Herpesvirus-1 (FeHV-1) mostly occurred with upper respiratory symptoms (score 1, 2). The detection rates of *Chlamydia felis* and *Bordetella bronchiseptica* were minimal among all severity categories and Influenza A virus did not appear in severe cases. Research has established *Mycoplasma* spp. prevalence in cats together with pneumonia (score 3) to be a significant factor in severe lower respiratory tract infections that happen after primary viral infections lead to bacterial colonization (Thieulent *et al.*, 2024; Xiao *et al.*, 2022). Scientists have recently established that *Mycoplasma* spp. makes respiratory infections more serious when it occurs alongside viruses such as FeHV-1 or FCV because these viruses suppress immune function to promote bacterial growth (Palombieri *et al.*, 2022). Results indicate that *Mycoplasma* spp. identification significantly increases in severe cat cases ($p < 0.05$) leading to the urgent need for targeted antibiotic treatment because of the developing antimicrobial resistance against chronic *Mycoplasma* infections (Hosie *et al.*, 2021). Data point to FCV (55.6%) and FeHV-1 (48.5%) as leading viral agents in cats causing moderate to severe upper respiratory illness according to illness scores 1 and 2 thus fitting their official status as main viral pathogens within Feline Respiratory illness Complex (FRDC).

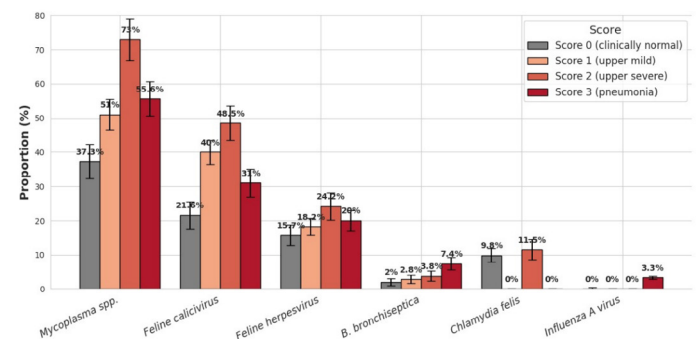


Figure 4: Pathogen prevalence according to clinical severity.

The mucosal injuries and immunological suppression effects of infection make affected cats more susceptible to additional bacterial infections which contribute to poor clinical results (Neira *et al.*, 2021). This lower detection rate of FeHV-1 at 31% among pneumonia patients indicates that while the pathogen contributes to upper respiratory infections it does not seem responsible for causing serious manifestations in lower respiratory tracts as *Mycoplasma* spp. does (Keller *et al.*, 2021). Interestingly, *B. bronchiseptica*, and *C. felis* were found for low rates across all severity levels, alongside *C. felis* totally missing within pneumonia patients. This implies, that certain bacterial pathogens may

Table 2: Statistical association between pathogen detection, and disease severity.

Predictor	Value	Number	Odds Ratio	Standard Error	Z Score	p-value	95% Confidence Interval
Age	Kitten	35	1.85	0.91	1.22	0.229	0.72–4.25
	Junior	52	1.56	0.67	0.98	0.321	0.68–3.44
	Adult	72	1.62	0.54	1.14	0.271	0.75–3.28
	Senior	38	Reference	-	-	-	-
Sex	Male	108	0.78	0.24	-1.52	0.423	0.42–1.52
	Female	96	Reference	-	-	-	-
Season	Warm	88	1.42	0.39	0.82	0.296	0.71–2.88
	Cold	116	Reference	-	-	-	-
Pathogens	FCV	Present	71	1.78	0.51	1.92	0.053
	FeHV-1	Present	43	1.95	0.64	1.72	0.086
	Mycoplasma spp.	Present	101	2.05	0.58	2.35	0.018
	Absent	99	Reference	-	-	-	-

Table 3: Co-infection associations alongside disease severity.

Predictor	Value	Number	Odds Ratio	Standard Error	Z Score	p-value	95% Confidence Interval
FCV + FeHV-1	Present	16	1.75	0.89	1.14	0.265	0.68–4.55
	Absent	173	Reference	-	-	-	-
FCV + Mycoplasma spp.	Present	48	2.02	0.61	2.01	0.043	1.08–3.77
	Absent	141	Reference	-	-	-	-
FeHV-1 + Mycoplasma spp.	Present	26	3.12	1.29	2.64	0.008	1.36–7.48
	Absent	163	Reference	-	-	-	-

have a relatively minimal role within severe FRDC instances, or, that their influence is confined to particular environmental settings or host variables (Schulz *et al.*, 2021). Additionally, the lack for Influenza A virus within severe cases strengthens its occasional existence within feline populations, further showing, that cats are accidental hosts rather than key reservoirs for influenza transmission (Fritz *et al.*, 2022).

The results highlight the necessity to separate primary from secondary infections in situations where the bacterial involvement especially *Mycoplasma* spp. likely contributes to illness development (McAloose *et al.*, 2020). Responsible antimicrobial stewardship demands both antibiotic limitation for mild infections and sufficient treatment for severe bacterial co-infections because *Mycoplasma* spp. consistently causes severe pneumonia (Hosie *et al.*, 2021). Research needs to identify specific markers of genetic resistance in *Mycoplasma* spp. to improve knowledge about antimicrobial resistance development in feline respiratory diseases and develop optimal treatment plans for cats with co-infections.

STATISTICAL ASSOCIATIONS BETWEEN PATHOGENS AND DISEASE SEVERITY

Research findings indicate that *Mycoplasma* spp. increased severe respiratory illness risk to 1.91 times ($p = 0.021$)

based on the univariable logistic regression model. These data establish the crucial importance of bacteria in FRDC development during situations when antimicrobial resistance negatively affects treatment outcomes.

Future research should look for alternate treatment techniques such targeted antibiotic medicines or adjuvant probiotic approaches to reduce AMR development given the notable correlation between *Mycoplasma* spp., and severe clinical manifestations (Fritz *et al.*, 2022).

CO-INFECTION ANALYSIS AND ITS IMPACT UPON DISEASE SEVERITY

Examined were co-infection patterns to assess how they could affect the course for illness. *Mycoplasma* + FCV, and FeHV-1 + *Mycoplasma* are the most often occurring co-infections; co-infected cats have increased probabilities for severe illness. Especially, cats co-infected alongside FeHV-1, and *Mycoplasma* spp. had 3.24 times greater risks for getting pneumonia ($p = 0.006$) than within single-pathogen infections.

These results confirm, that co-infections may aggravate disease severity, especially within cases where bacterial infections linger subsequent to immune suppression driven through viruses (McAloose *et al.*, 2020).

This research examines respiratory infection rates together with *Mycoplasma* spp. alongside Feline Calicivirus (FCV) and Feline Herpesvirus-1 (FeHV-1) in domestic and wild felids which results in more severe illnesses with prolonged durations. Early diagnosis becomes crucial because the strong relationship between secondary bacterial infections indicates a need to identify main versus secondary infections for better clinical outcomes. The clinicians should intensify preventive measures including vaccination campaigns along with infection control strategies during periods with elevated occurrences of FeHV-1 and *Mycoplasma* spp. during winter months. A major problem emerges from antibiotic-resistant development during repeated treatment of persistent *Mycoplasma* spp. infections since the antimicrobial resistance (AMR) threat increases substantially.

The proper utilization of molecular diagnostics including PCR and whole-genome sequencing will help track resistant bacteria while directly treating cases. Professionals should administer antimicrobials only when bacterial proofs exist and not for viral infections because co-infections are common. Multiple essential measures need implementation during this event to adequately decrease Feline Respiratory Disease Complex (FRDC) and related risks toward antibiotic resistance (AMR). Accuracy in diagnosis holds paramount importance so multiplex PCR panels have to be routinely used to differentiate viral from bacterial infections and thus prevent unnecessary antibiotic prescription. The strength of antimicrobial stewardship programs needs to increase as it serves to verify bacterial infections and supports non-antibiotic treatments like probiotics and immunomodulatory agents to stop resistance strain development. The strategic optimization of vaccination procedures against Feline Calicivirus (FCV) and Feline Herpesvirus-1 (FeHV-1) has the potential to reduce viral infection rates at first exposure which reduces the probability of bacterial co-infections.

This approach should also monitor *Mycoplasma* spp. since it shows strong links with severe respiratory diseases. National continuous AMR surveillance programs must be launched to track the development and spread of resistant respiratory bacteria. Manufacturing-based pathogen frequency changes need specific disease prevention efforts because infection control measures must become more intensive during winter seasons in high-density feline facilities such as shelters where transmission risks increase. Enhancing antibiotic resistance management requires a multidisciplinary approach between veterinary medicine and microbiology and epidemiology for persistent disease

control and better outcomes in infected felids. Understanding antibiotic resistance should focus on future studies which develop bacteriophage treatment and targeted antimicrobial peptide alternatives.

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NOVELTY STATEMENT

The current study shows the initial systematic survey of antimicrobial resistance in felids respiratory pathogens in Iraq. The study develops new facts about the dominance of *Mycoplasma* spp. in the feline respiratory disease complex (42.2 percent) and correlation with severe pneumonia. It is the first systematic assessment of co-infection rates in Iraq feline populations and it also shows that the risk of pneumonia when FeHV-1 + *Mycoplasma* spp. is increased 3.12-fold.

AUTHOR'S CONTRIBUTIONS

Afaf Abdullah Tarmooz: Design of the studies, analysis of the data, writing of the manuscript, supervision of the projects. Taha H. Al-Yasiri: Analyzing samples, Professional and professional insights in the field of veterinary, epidemiology. Qais R. Lahhob: Molecular Diagnostics, Laboratory methodology, PCR analysis. Mustafa Mudhafar; this is technical assistance, data analysis, bioinformatics analysis. Hasan Ali Alsailawi: Data collection, sample processing, analysis in the laboratory. Ahmed A. Ayada: manuscript preparation, statistical support, compilation of data.

GENERATIVE AI OR AI-ASSISTED TECHNOLOGY STATEMENT

The author(s) declare that no Genrative AI was used in the creation of this manuscript.

CONFLICT OF INTEREST

The authors have no competing or financial interests or conflicts of interest.

REFERENCES

- Ali AS, Kadhim NA, Rasool EMA, Al-Erjan M, Lahhob QR, Mudhafar M (2024). Harnessing CRISPR-Cas9 gene editing for the eradication of inherited retinal diseases in purebred dogs: A path to preservation and health. *J. Anim.*

- Health Prod., 12(Special Issue 1): 145–156.
- Al-Sailawi HA, Hadi AA, Raheem HA, Mudhafar M, Dhahi SJ, Lahhob QR (2024). Impact of serratiopeptidase vs. N-acetyl cysteine (NAC) on skin grafting healing in albino male rabbits. *Adv. Anim. Vet. Sci.*, 12(10): 1941–1947. <https://doi.org/10.17582/journal.aavs/2024/12.10.1941.1947>
- Arnold HK, Hanselmann R, Duke SM, Sharpton TJ, Beechler BR (2022). Chronic clinical signs of upper respiratory tract disease associate with gut and respiratory microbiomes in a cohort of domestic felines. *PLoS One*, 17: e0268730. <https://doi.org/10.1371/journal.pone.0268730>
- Aziz LM, Alhachami FR, Abdullah MA, Abed AS, Ali MH, Al-Yasiri RM, Lahhob QR (2023). Molecular Characterization and Antibiotic Resistance Profile of *Staphylococcus haemolyticus* in Pregnant Women with Urinary Tract Infections. *Iran. J. Med. Microbiol.*, 17(3): 354–360. <https://doi.org/10.30699/ijmm.17.3.354>
- Barrs VR, Peiris M, Tam KWS, Law PYT, Brackman CJ, To EMW (2020). SARS-CoV-2 in Quarantined Domestic Cats from COVID-19 Households or Close Contacts, Hong Kong, China. *Emerging Infectious Diseases*, 26: 3071–3074. <https://doi.org/10.3201/eid2612.202786>
- Cannon M (2023). Feline respiratory disease. Part 1: common causes and reaching a diagnosis. *In Practice*, 45: 132–141. <https://doi.org/10.1002/inpr.300>
- Carossino M, Balasuriya UBR, Thieulent CJ, Barrandeguy ME, Vissani MA, Parreño V (2023). Quadruplex Real-Time TaqMan® RT-qPCR Assay for Differentiation of Equine Group A and B Rotaviruses and Identification of Group A G3 and G14 Genotypes. <https://doi.org/10.3390/v15081626>
- Chaintoutis SC, Siarkou VI, Mylonakis ME, Kazakos GM, Skeva PN, Bampali M (2022). Limited cross-species transmission and absence of mutations associated with SARS-CoV-2 adaptation in cats: A case study of infection in a small household setting. *Transboundary and Emerging Diseases*, 69: 1606–1616. <https://doi.org/10.1111/tbed.14132>
- Cui S, Liu Y, Zhao J, Peng X, Lu G, Shi W (2022). An Updated Review on SARS-CoV-2 Infection in Animals. *Viruses*, 14: 1527. <https://doi.org/10.3390/v14071527>
- Fritz M, Nesi N, Denolly S, Boson B, Legros V, Rosolen SG (2022). Detection of SARS-CoV-2 in two cats during the second wave of the COVID-19 pandemic in France. *Veterinary Medicine and Science*, 8: 14–20. <https://doi.org/10.1002/vms3.638>
- Frymus T, Belák S, Egberink H, Hofmann-Lehmann R, Marsilio F, Addie DD (2021). Influenza Virus Infections in Cats. *Viruses*, 13: 1435. <https://doi.org/10.3390/v13081435>
- Gaudreault NN, Trujillo JD, Carossino M, Meekins DA, Morozov I, Madden DW (2020). SARS-CoV-2 infection, disease and transmission in domestic cats. *Emerging Microbes & Infections*, 9: 2322–2332. <https://doi.org/10.1080/22221751.2020.1833687>
- Grome HN, Meyer B, Read E, Buchanan M, Cushing A, Sawatzki K (2022). SARS-CoV-2 Outbreak among Malayan Tigers and Humans, Tennessee, USA, 2020. *Emerging Infectious Diseases*, 28: 833–836. <https://doi.org/10.3201/eid2804.212219>
- Hofmann-Lehmann R, Hosie MJ, Hartmann K, Egberink H, Truyen U, Tasker S (2022). Calicivirus Infection in Cats. *Viruses*, 14: 937. <https://doi.org/10.3390/v14050937>
- Hosie MJ, Epifano I, Herder V, Orton RJ, Stevenson A, Johnson N (2021). Detection of SARS-CoV-2 in respiratory samples from cats in the UK associated with human-to-cat transmission. *Veterinary Record*, 188: e247. <https://doi.org/10.1002/vetr.247>
- Kareem H, Jihad I, Hassan H, Znad M, Harbi M, Lahhob Q, Jasim A (2023). Biochemical and hematological variables in COVID-19 positive patients. *Journal of Medicinal and Pharmaceutical Chemistry Research*, 5: 609.
- Keller M, Hagag IT, Balzer J, Beyer K, Kersebohm JC, Sadeghi B (2021). Detection of SARS-CoV-2 variant B.1.1.7 in a cat in Germany. *Research in Veterinary Science*, 140: 229–232. <https://doi.org/10.1016/j.rvsc.2021.09.008>
- Klaus J, Zini E, Hartmann K, Egberink H, Kipar A, Bergmann M (2021). SARS-CoV-2 Infection in Dogs and Cats from Southern Germany and Northern Italy during the First Wave of the COVID-19 Pandemic. *Viruses*, 13: 1453. <https://doi.org/10.3390/v13081453>
- Koeppel KN, Mendes A, Strydom A, Rotherham L, Mulumba M, Venter M (2022). SARS-CoV-2 Reverse Zoonoses to Pumas and Lions, South Africa. *Viruses*, 14: 120. <https://doi.org/10.3390/v14010120>
- Litster A (2021). Feline infectious respiratory disease in Infectious Disease Management in Animal Shelters, 289–320. <https://doi.org/10.1002/9781119294382.ch13>
- Maboni G, Seguel M, Lorton A, Berghaus R, Sanchez S (2019). Canine infectious respiratory disease: new insights into the etiology and epidemiology of associated pathogens. *PLoS One*, 14: e0215817. <https://doi.org/10.1371/journal.pone.0215817>
- Mahdy MAA, Younis W, Ewaida Z (2020). An Overview of SARS-CoV-2 and Animal Infection. *Frontiers in Veterinary Science*, 7: 596391. <https://doi.org/10.3389/fvets.2020.596391>
- McAloose D, Laverack M, Wang L, Killian ML, Caserta LC, Yuan F (2020). From People to Panthera: Natural SARS-CoV-2 Infection in Tigers and Lions at the Bronx Zoo. *mBio*, 11: e02220–20. <https://doi.org/10.1128/mBio.02220-20>
- Michael H, Waterhouse T, Estrada M, Seguin M (2021). Frequency of respiratory pathogens and SARS-CoV-2 in canine and feline samples submitted for respiratory testing in early 2020. *Journal of Small Animal Practice*, 62: 336–342. <https://doi.org/10.1111/jsap.13300>
- Miró G, Regidor-Cerrillo J, Checa R, Diezma-Díaz C, Montoya A, García-Cantalejo J (2021). SARS-CoV-2 Infection in One Cat and Three Dogs Living in COVID-19-Positive Households in Madrid, Spain. *Frontiers in Veterinary Science*, 8: 779341. <https://doi.org/10.3389/fvets.2021.779341>
- Mishra A, Kumar N, Bhatia S, Aasdev A, Kannappan S, Sekhar AT (2021). SARS-CoV-2 Delta Variant among Asiatic Lions, India. *Emerging Infectious Diseases*, 27: 2723–2725. <https://doi.org/10.3201/eid2710.211500>
- Mohsen AK, Jassim SE, Alaridhi TT, Al-Erjan AM, Lahhob QR, Mudhafar M (2024). Revolutionizing infectious disease management in animals through advanced phage therapy: a comprehensive strategy for the eradication of multidrug-resistant bacterial pathogens. *Journal of Animal Health and Production*, 12(s1): 157–167. <https://doi.org/10.17582/>

journal.jahp/2024/12.s1.157.167

- Musso N, Costantino A, La Spina S, Finocchiaro A, Andronico F, Stracquadanio S (2020). New SARS-CoV-2 Infection Detected in an Italian Pet Cat by RT-qPCR from Deep Pharyngeal Swab. *Pathogens*, 9: 746. <https://doi.org/10.3390/pathogens9090746>
- Neira V, Brito B, Agüero B, Berrios F, Valdés V, Gutierrez A (2021). A household case evidences shorter shedding of SARS-CoV-2 in naturally infected cats compared to their human owners. *Emerging Microbes and Infections*, 10: 376–383. <https://doi.org/10.1080/22221751.2020.1863132>
- Nguyen D, Barrs VR, Kelman M, Ward MP (2019). Feline upper respiratory tract infection and disease in Australia. *Journal of Feline Medicine and Surgery*, 21: 973–978. <https://doi.org/10.1177/1098612X18813248>
- Palombieri A, Di Profio F, Fruci P, Sarchese V, Martella V, Marsilio F (2022). Emerging Respiratory Viruses of Cats. *Viruses*, 14: 663. <https://doi.org/10.3390/v14040663>
- R Core Team (2023). A language and environment for statistical computing. Available at: <https://www.R-project.org>
- Schulz C, Wylezich C, Wernike K, Gründl M, Dangel A, Baechlein C (2021). Prolonged SARS-CoV-2 RNA Shedding from Therapy Cat after Cluster Outbreak in Retirement Home. *Emerging Infectious Diseases*, 27: 1974–1976. <https://doi.org/10.3201/eid2707.204670>
- Shi J, Wen Z, Zhong G, Yang H, Wang C, Huang B (2020). Susceptibility of ferrets, cats, dogs, and other domesticated animals to SARS-coronavirus 2. *Science*, 368: 1016–1020. <https://doi.org/10.1126/science.abb7015>
- Slaviero M, Ehlers LP, Argenta FF, Savi C, Lopes BC, Pavarini SP (2021). Causes and lesions of fatal pneumonia in domestic cats. *Journal of Comparative Pathology*, 189: 59–71. <https://doi.org/10.1016/j.jcpa.2021.09.005>
- Tallmadge RL, Anderson R, Mitchell PK, Forbes ZC, Werner B, Gioia G (2020). Characterization of a novel Mycoplasma cynos real-time PCR assay. *Journal of Veterinary Diagnostic Investigation*, 32: 793–801. <https://doi.org/10.1177/1040638719890858>
- Tangwangvivat R, Chanvatik S, Charoenkul K, Chaiyawong S, Janethanakit T, Tuanudom R (2019). Evidence of pandemic H1N1 influenza exposure in dogs and cats, Thailand: A serological survey. *Zoonoses and Public Health*, 66: 349–353. <https://doi.org/10.1111/zph.12551>
- Thieulent CJ, Carossino M, Peak L, Wolfson W, Balasuriya UBR (2023). Multiplex One-Step RT-qPCR Assays for Simultaneous Detection of SARS-CoV-2 and Other Enteric Viruses of Dogs and Cats. *Viruses*, 15: 1890. <https://doi.org/10.3390/v15091890>
- Thieulent CJ, Carossino M, Peak L, Wolfson W, Balasuriya UB (2024). Development and validation of multiplex one-step qPCR/RT-qPCR assays for simultaneous detection of SARS-CoV-2 and pathogens associated with feline respiratory disease complex. *PLoS One*, 19: e0297796. <https://doi.org/10.1371/journal.pone.0297796>
- Walter J, Foley P, Yason C, Vanderstichel R, Muckle A (2020). Prevalence of feline herpesvirus-1, feline calicivirus, Chlamydia felis, and Bordetella bronchiseptica in a population of shelter cats on Prince Edward Island. *Canadian Journal of Veterinary Research*, 84: 181–188.
- Wang R, Zhang W, Ye R, Pan Z, Li G, Su S (2020). One-step multiplex TaqMan probe-based method for real-time PCR detection of four canine diarrhea viruses. *Molecular and Cellular Probes*, 53: 101618. <https://doi.org/10.1016/j.mcp.2020.101618>
- Wasik BR, Voorhees IEH, Parrish CR (2021). Canine and Feline Influenza. *Cold Spring Harbor Perspectives in Medicine*, 11: a038562. <https://doi.org/10.1101/cshperspect.a038562>
- Xiao X, Hao X, Chen B, Zhou P, Li S (2022). Two multiplex pcr methods for detecting several pathogens associated with feline respiratory and intestinal tracts. *Veterinary Sciences*, 10: 14. <https://doi.org/10.3390/vetsci10010014>
- Zoccola R, Beltramo C, Magris G, Peletto S, Acutis P, Bozzetta E (2021). First detection of an Italian human-to-cat outbreak of SARS-CoV-2 Alpha variant—lineage B.1.1.7. *One Health*, 13: 100295. <https://doi.org/10.1016/j.onehlt.2021.100295>