

Source Tracing of a Community Psittacosis Outbreak by Epidemiological and Environmental Investigation

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Case Report

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Abstract

Objective

Psittacosis is a zoonotic infectious disease caused by *Chlamydia psittaci*, with an increasing number of documented clustered outbreaks associated with pet bird exposure. Nevertheless, high-resolution epidemiological data and evidence from laboratory traceability for community clusters of psittacosis remain insufficient in existing research.

Methods

In January 2026, a cluster of febrile illnesses involving three individuals occurred in Zhoushan City, Zhejiang Province, China. A field epidemiological investigation was conducted, including interviews with cases and close contacts. Clinical and environmental specimens were collected and tested for *C. psittaci* by reverse transcription quantitative polymerase chain reaction (RT-qPCR) and metagenomic third-generation high-throughput sequencing (TGS). Phylogenetic analysis was performed by comparing nucleotide sequences from clinical and environmental isolates.

Results

The cluster comprised one laboratory-confirmed case (Patient 1, a 73-year-old male) and two suspected cases (Patients 2 and 3, a married couple aged 78 and 75 years). All three shared a common exposure: Patients 2 and 3 kept parrots at their residence, which also housed a mahjong parlour where Patient 1 spent 3–4 hours daily before symptom onset. Environmental testing revealed *C. psittaci* nucleic acid positivity rates of 100% (10/10) in samples from the birdcage and master bedroom, and 37.5% (3/8) in samples from the mahjong table area. Traceability investigation of a supplier bird shop showed a positivity rate of 73.3% (11/15). The strain sequence from Patient 1's respiratory specimen differed by 1–2 nucleotides from environmental strains recovered from patients 2 and 3's residence.

Conclusion

This cluster was primarily driven by infected parrots as the reservoir, with transmission likely occurring through contact with pathogen-carrying birds or inhalation of contaminated aerosols in a shared indoor environment. Human-to-human transmission cannot be ruled out. Strengthened regulation of live bird markets, health education, and improved clinical recognition of psittacosis are recommended.

Introduction

Psittacosis, a zoonotic disease caused by the obligate intracellular bacterium *Chlamydia psittaci* (*C. psittaci*), poses a major global public health concern [1]. Human infection typically results from the

inhalation of dust containing dried secretions, excretions, or dander from infected birds or poultry. Clinical manifestations are highly variable, ranging from asymptomatic infection to influenza-like symptoms and severe atypical pneumonia, which can be misdiagnosed as community-acquired pneumonia (CAP) [2, 3]. The reported mortality rate for psittacosis is approximately 1.8%[4] .

In recent years, the increasing popularity of pet bird ownership has been associated with an increase in sporadic and clustered outbreaks of psittacosis [5–8]. In China, several family clusters and small outbreaks have been reported[5, 9, 10], yet detailed traceability data linking environmental sources to human cases remain scarce. In January 2026, a cluster of febrile illnesses involving three individuals occurred in Zhoushan City, Zhejiang Province. Subsequent epidemiological and laboratory investigations confirmed these findings as *C. psittaci* infections. This study describes the results of the field investigation and laboratory traceability analysis, with the aim of elucidating the transmission chain, identifying risk factors, and providing evidence-based recommendations for the prevention and control of similar outbreaks.

Methods

Outbreak recognition and initial response

On January 18, 2026, Zhoushan Hospital reported a severe pneumonia case in which metagenomic next-generation sequencing (mNGS) analysis of lower respiratory tract samples revealed *C. psittaci* infection. During the same period, two additional patients (a married couple) with unexplained fever were admitted to the Department of Infectious Diseases. Epidemiological linkage analysis suggested a possible clustered outbreak, prompting the Zhoushan Center for Disease Control and Prevention (CDC) to initiate an on-site investigation. Preliminary investigations revealed that the couple (patients 2 and 3) kept parrots at their residence, which also operated as a venue for mahjong gatherings. Patient 1 had participated in mahjong activities at this location prior to symptom onset.

Epidemiological investigations

Case definitions were established as follows: (1) Suspected Case: An individual who presents with febrile, respiratory, or gastrointestinal illness and who has a history of exposure (e.g., playing mahjong or having contact with parrots) within the residence of patients 2 and 3 between December 14, 2025, and February 1, 2026, in Dinghai District, Zhoushan City. (2) Confirmed Case: The suspected patient with laboratory confirmation of *C. psittaci* infection through RT–qPCR or mNGS in appropriate clinical samples.

Environmental investigation

Epidemiological investigations were conducted at the residence of patient 2 and patient 3, focusing on the areas where the captive parrots were housed. Additionally, onsite inspections were performed at the pet bird market where the infected parrots were purchased.

Sample Collection and Laboratory Testing

Throat swabs, sputum, bronchoalveolar lavage fluid (BALF), and blood specimens were collected from all three patients during hospitalization. Environmental samples—including parrot faeces, drinking water, food, birdcage swabs, and surface swabs from the master bedroom and mahjong table area at the residence of patients 2 and 3—were collected. Additionally, faeces and environmental swabs were obtained from three supplier flower-and-bird shops.

All specimens were transported to the Zhoushan CDC laboratory. Deoxyribonucleic acid (DNA) was extracted using a commercial kit (ABT, China) according to the manufacturer's instructions. *C. psittaci* nucleic acid was detected by RT-qPCR targeting the 16S rRNA gene. Serum samples were tested for *C. psittaci* IgM antibodies using commercially available enzyme-linked immunosorbent assay kits (GOYBIO, China; Shenzhen Henghao Biotechnology, China).

Phylogenetic Analysis

Specimens meeting sequencing criteria underwent metagenomic third-generation high-throughput sequencing (TGS) on the DPU-Third Generation Sequencer platform (DIPINORE, China). Sequence assembly, alignment, and traceability analysis were performed using the BiYi Bioinformatics Analysis System.

Results

Case descriptions

Patient 1 (Confirmed): A 73-year-old male developed lumbar and scapular pain on January 9, 2026. On January 13, he received cupping therapy. On January 15, he presented to Zhoushan Hospital with persistent pain, dysuria, fever (39.3°C), and a C-reactive protein (CRP) level of 189.5 mg/L (Table 1). Chest computed tomography (CT) revealed inflammatory lesions in the left upper lung lobe. On January 17, he was transferred to the intensive care unit (ICU) due to chest tightness, hypoxia (oxygen saturation 94% on face mask), and fatigue, and subsequently underwent endotracheal intubation. On January 18, mNGS of BALF and peripheral blood confirmed *C. psittaci* infection. He was treated sequentially with piperacillin sodium, moxifloxacin, and doxycycline, transferred to a general ward on January 29, and discharged on February 9 after full recovery.

Patient 2 (Suspected)

A 78-year-old male (spouse of patient 3) developed chills, fever (39.9°C), cough, nausea, and vomiting on January 9. He initially presented to a community health centre, then was transferred to Zhoushan Hospital with a CRP level of 75.6 mg/L and bilateral lower lobe pneumonia on chest CT (Table 1). Initial diagnoses included sepsis, CAP, systemic inflammatory response syndrome (SIRS), and gastroenteritis. Testing for COVID-19, influenza, and *Mycoplasma pneumoniae* was negative. He received piperacillin-tazobactam combined with enrofloxacin and was discharged on January 22 after 9 days of hospitalization.

Patient 3 (Suspected)

A 75-year-old female (spouse of Patient 2) developed fever (axillary temperature 38.1°C) and dry cough on January 3. Symptoms persisted despite self-medication. On January 7, she presented to the hospital with a temperature of 40.0°C, CRP 178.3 mg/L, left lung pneumonia with left pleural effusion on CT (Table 1), and negative influenza testing. She received the same anti-infective regimen as patient 2 and was discharged on January 16 after 10 days of hospitalization.

Table 1
Basic information and clinical characteristics of the three patients in the psittacosis cluster.

Gender	Patient 1	Patient 2	Patient 3	Median
	Male	Male	Female	
Age	73	78	75	75
Fever(°C)	39.3	39.9	40	39.9
Chill	No	Yes	Yes	
Fatigue	Yes	Yes	Yes	
Headache	No	Yes	Yes	
Cough	No	Yes	Yes	
Myalgia	Yes	No	No	
Vomit	No	Yes	Yes	
Dyspnoea	Yes	No	No	
WBC count (3.5–9.5*10 ⁹ /L)	5.9	5.2	7.8	5.9
Neutrophil count (1.8–6.3*10 ⁹ /L)	5.3	4.1	7.0	5.3
Percentage of neutrophils (40–75%)	89.8	77.9	89.1	89.1
Lymphocyte count (1.1–3.2*10 ⁹ /L)	0.2	0.7	0.5	0.5
CRP level (0–10 mg/L)	189.5	75.6	178.3	178.3
Pneumonia	LUL	BLL	L	
Pleural effusion	L	No	L	
ICU	Yes	No	No	
Length of stay (days)	25	9	10	10

WBC: White blood cell. CRP: C-reactive protein. LUL: Left upper lobe. BLL: Bilateral lower lobes. L: Left. ICU: Intensive care unit.

Exposure Investigation

To clarify the potential epidemiological correlation among the three cases and identify the infection source of *C. psittaci*, an epidemiological history investigation for all three patients was conducted .

Patients 2 and 3 resided in Unit 16–503, and patient 1 resided in Unit 16-1102, both in the same building of a residential complex in Zhoushan. Patient 2 had purchased five small parrots from a Flower and Bird Market in approximately September 2025 (Fig. 1). The parrots were kept in cages on the balcony of the master bedroom, with the sliding door to the bedroom frequently left open. Patient 2 performed daily feeding but cleaned and disinfected the cages infrequently (Fig. 2). All parrots escaped through open windows around early January 2026. No household members reported respiratory symptoms before the escape event.

The master bedroom was adjacent to the living room, which contained three automatic mahjong tables. Mahjong gatherings with approximately four participants per session were held frequently at this location. Patient 1 visited the residence almost every afternoon before January 9, with each visit lasting 3–4 hours. In summary, patients 2 and 3 had direct exposure to a parrot-rearing environment, while patient 1's exposure to *C. psittaci* occurred during prolonged mahjong activities at their residence (Fig. 1).

Epidemiological investigation of flower and bird shops

The Hongqiao Flower and Bird Shop, the identified source of the parrots, covered approximately 20 m² with a 3 m² bird display area and natural ventilation. It housed 47 birds of four small parrot species. No abnormal symptoms or mortality had been observed. The average number of daily visitors was 1–3 people, which increased to 3–5 people during the holidays. Bird faeces were collected irregularly and sometimes repurposed as fish feed. Two additional bird shops in the area were also investigated but showed no direct link to the cases.

Laboratory Testing Results

Human specimens: Patient 1 tested positive for *C. psittaci* by mNGS of BALF and by RT-qPCR of sputum, but negative on throat swab PCR. All specimens from patients 2 and 3 were PCR-negative. Serum samples from all three patients collected during both the early and recovery phases were negative for *C. psittaci* IgM and IgG. The throat swab and serum from the bird shop owner were also negative (Table 2).

Environmental specimens: As detailed in Table 3, all 12 specimens from the birdcage and master bedroom (parrot faeces, drinking water, food, and surface swabs) tested positive (100%). Among eight mahjong table surface swabs, three were positive (37.5%). At the supplier bird shop, 11 of 15 environmental samples (faeces and swabs) were positive (73.3%). Overall, 26 of 35 environmental specimens across all locations tested positive (74.3%).

Phylogenetic comparison: Genomic sequencing and sequence alignment were conducted on seven specimens that met the criteria for gene sequencing. The results confirmed *C. psittaci* serotype A (genotype 04DC42) as the causative pathogen of this outbreak. The *C. psittaci* strain sequence derived from patient 1's respiratory specimen differed by 1–2 nucleotides from the sequences obtained from

environmental swab samples collected at the residences of patients 2 and 3, indicating a close genetic relationship (Fig. 3).

Table 2
Summary of the laboratory test results for human samples from the psittacosis cluster.

Cases	Onset day	Sample type	Sampling date	Test method	Result
Patient 1	9 Jan	BALF	17 Jan	mNGS	Positive
		sputum	19 Jan/21 Jan	RT-qPCR	Positive
		throat swab	20 Jan	RT-qPCR	Negative
		serum	14 Jan/18 Jan/20 Jan	IgM	Negative
Patient 2	9 Jan	throat swab	19 Jan	RT-qPCR	Negative
		serum	14 Jan/18 Jan	IgM	Negative
Patient 3	3 Jan	throat swab	20 Jan	RT-qPCR	Negative
		serum	14 Jan/16 Jan	IgM	Negative
The owner of the flower and bird shop		throat swab	20 Jan	RT-qPCR	Negative
		serum	20 Jan	IgM	Negative

Table 3
Environmental specimen testing results for *C. psittaci* nucleic acid.

Location	Sample type	Number of samples	Number of positive samples	Positivity rate (%)
Residence - birdcage/bedroom	Faeces, water, food, swabs	12	12	100
Residence – mahjong area	Table surface swabs	8	3	37.5
Supplier bird shop	Faeces, environmental swabs	15	11	73.3
Total	-	35	26	74.3

Discussion

This investigation documents a cluster of *C. psittaci* infections in Zhoushan City, highlighting the public health threat posed by this zoonotic pathogen in settings where pet birds and close human–animal contact coexist. Although only patient 1 was laboratory-confirmed by RT-qPCR/mNGS, the high positivity of environmental samples at the residences of patients 2 and 3, combined with their compatible clinical presentations, strongly supports that all three patients were part of the same *C. psittaci* outbreak.

The most likely transmission scenario is that patients 2 and 3 acquired infection through direct contact with infected parrots or inhalation of aerosolized particles from bird faeces and secretions in their home. Patient 1, who had no direct contact with the birds, likely became infected by inhaling contaminated aerosols while spending prolonged periods in the mahjong parlour adjacent to the contaminated master bedroom. Notably, the parrots appeared asymptomatic before the onset of human illness, yet *C. psittaci* nucleic acid was detectable in environmental samples more than two weeks after the birds escaped. This underscores that avian hosts can act as asymptomatic carriers[11–13] and that environmental contamination can persist after the animals are no longer present [14].

The high positivity rate (73.33%) at the supplier bird shop suggests that the live bird market was the primary source of infection. These findings align with those of numerous studies demonstrating the widespread prevalence of *C. psittaci* in various avian populations, including wild birds [12, 15, 16], poultry [17–19], and companion birds [20]. In this study, the dispersal of *C. psittaci*-carrying parrots may result in the transmission of *C. psittaci* to local wild bird populations [21]. The increasing trend of pet bird ownership—including online purchases—amplifies the risk of human and wild bird exposure and calls for stricter market surveillance and quarantine measures [22].

From a clinical perspective, this outbreak reinforces that psittacosis should be considered in the differential diagnosis of CAP, particularly when epidemiological links to birds or bird-exposure environments exist. Incorporating *C. psittaci* nucleic acid testing into routine diagnostic workups for CAP can facilitate early detection and appropriate antimicrobial therapy (e.g. doxycycline), and reduced severity [14, 23]. A multidimensional prevention strategy integrating animal health management, clinical vigilance, and public health education is essential.

Limitations

Patients 2 and 3 lacked laboratory confirmation, likely due to the timing of specimen collection after antibiotic initiation. The escaped parrots could not be tested. All serological results were negative, possibly reflecting the timing of sampling relative to the antibody response window or the insufficient sensitivity of commercially available *C. psittaci* antibody detection kits. Despite these limitations, the convergence of epidemiological, environmental, and phylogenetic evidence provides strong support for the inferred transmission chain.

In conclusion, this cluster demonstrates that infected pet birds can serve as a reservoir for *C. psittaci* transmission in community settings, with indoor shared spaces acting as amplification environments.

Strengthened regulation of live bird markets, routine inclusion of psittacosis in CAP diagnostic panels, and targeted health education for bird owners and the public are critical to preventing future outbreaks.

Abbreviations

mNGS:Metagenomic next-generation sequencing

CT:Chest computed tomography

CDC:Center for Disease Control and Prevention

DNA: Deoxyribonucleic acid

RNA: Ribonucleic acid

RT-qPCR:Reverse transcription quantitative polymerase chain reactionq

SIRS:Systemic inflammatory response syndrome

Declarations

Ethics approval and consent to participate

This epidemiological tracing study involved anonymized residual human blood and pharyngeal swab specimens from three psittacosis patients, as well as non-invasive environmental swab specimens collected from parrot-related exposure environments. Ethical approval for this retrospective outbreak investigation was waived by the Ethics Committee of Zhoushan CDC (Waiver No. ZSCDC-IRB-2026-001) due to minimal risk and de-identified data usage. All human-related procedures were performed in accordance with the principles of the Declaration of Helsinki.

Verbal informed consent was obtained from all patients and parrot owners before sampling. Written consent was exempted for this field public health investigation, and the verbal consent procedure was approved by the ethics committee. No live animal experimentation or invasive animal sampling was conducted in this study.

Consent for publication

Not applicable. No individual clinical images, identifiable personal data, or case-specific identifiable information are included in this manuscript.

Availability of data and materials

The sequencing datasets generated and analysed during the current study are available in the Natonal Microbiology Data Center (NMDC) repository under BioProject accession NMDC10021000. All other

relevant data generated or analysed in this study are included within this published article and its supplementary tables and figures.

Competing Interests

The authors declare no competing interests.

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Authors' contributions

D.Y. and W.B. contributed equally to this work. T.A. and Y.J. conceived and supervised the study. D.Y., W.W., H.Y., and L.S. conducted the field investigation .W.B., and H.F.conducted the laboratory testing. D.Y. and W.B. drafted the manuscript. T.A. and Y.J. revised the manuscript critically. All authors read and approved the final version.

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Figures

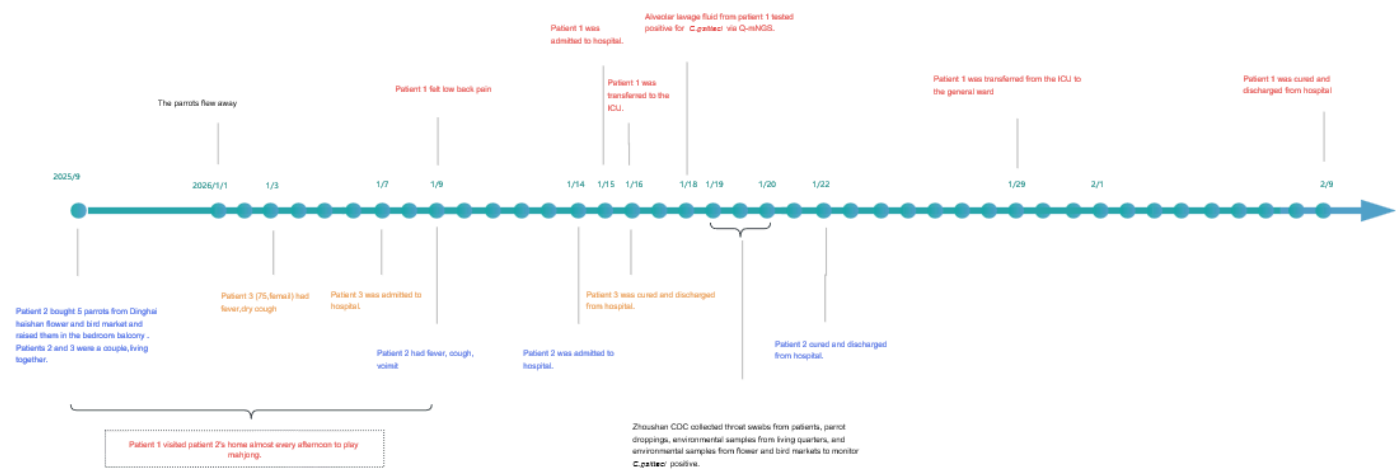


Figure 1

The exposure relationships and timeline of the outbreak. Red indicates the clinical course and relevant exposure history of Patient 1; The blue color represents the onset and treatment process for Patient 2. Orange represents the onset and treatment course of Patient 3.. Black denotes information related to parrots and the CDC investigation.

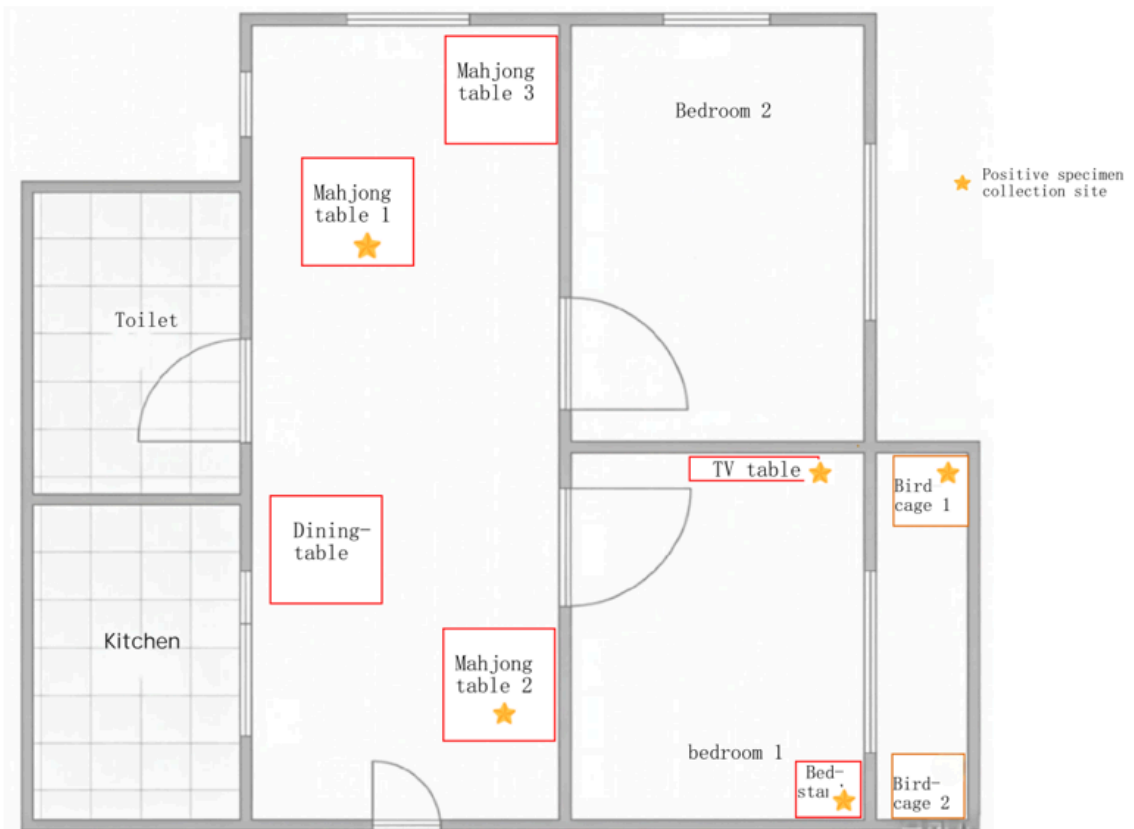


Fig. 2 Schematic diagram of the outbreak site; ★ Sampling sites where *Chlamydophila psittaci* nucleic acid testing has returned a positive result.

Figure 2

See image above for figure legend.

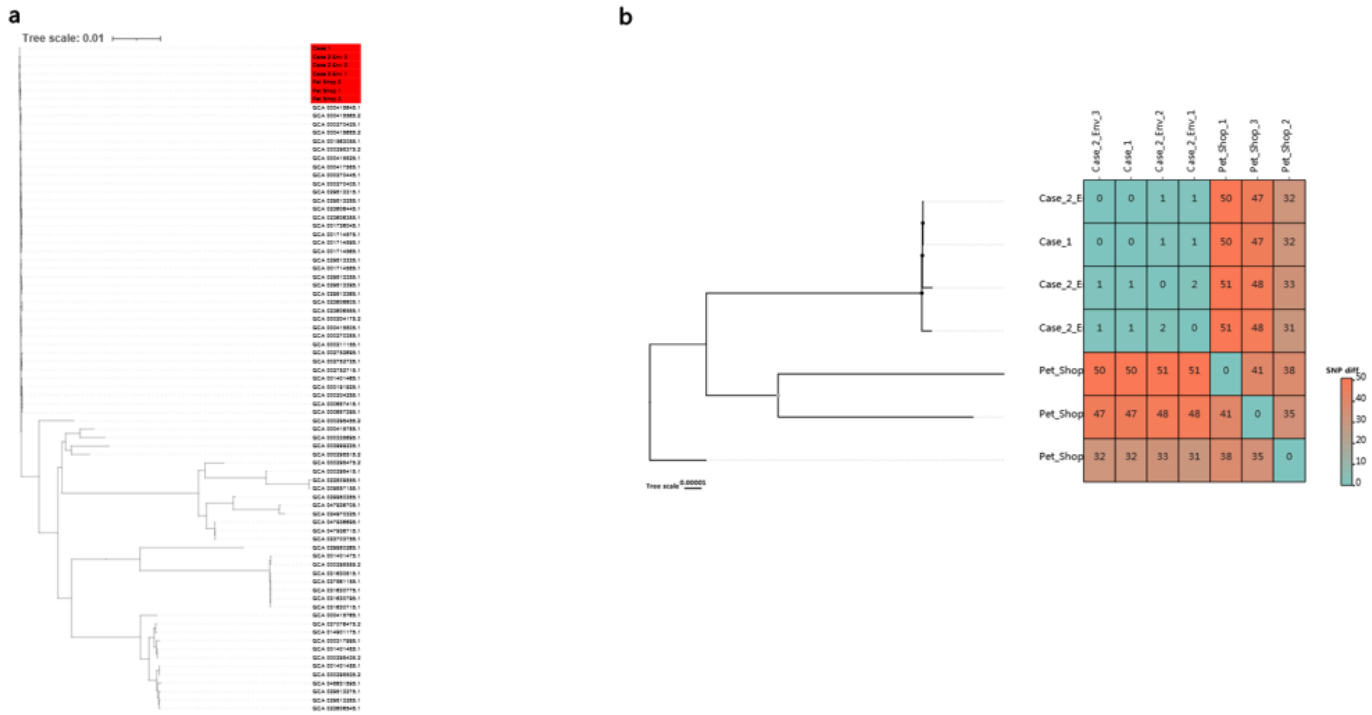


Figure 3

Phylogeny and mutation hotspots in the psittacosis cluster. a: The seven gene sequences obtained during this outbreak all belong to *C. psittacis* serotype A; b: The *C. psittaci* strain from patient 1's respiratory specimen differed by 1-2 nucleotides from sequences from patients 2 and 3 residence environmental swabs, indicating close genetic relationship