Outbreak Reports

# First Human Infection with Influenza A(H1N2)v Virus — Yunnan Province, China, 2026

Lihua Chen[1,2]; Yaoyao Chen[3]; Xiaoyu Han[3]; Ruize Ni[3]; Ming Zeng[4]; Jie Deng[4]; Chunyuan Deng[5]; Guijing Chen[5]; Xiaoqing Fu[3]; Jibo He[1]; Chunrui Luo[3,#]

**Summary**

**What is already known about this topic?**

Human infections with influenza A(H1N2)v viruses of swine origin have been sporadically reported in several countries, usually following direct or indirect exposure to pigs or contaminated environments. However, sustained human-to-human transmission has not yet been documented.

**What is added by this report?**

This report describes the first laboratory-confirmed human infection with the influenza A(H1N2)v virus in China. Whole-genome sequencing showed that all eight gene segments were closely related to influenza viruses of swine origin circulating in China. No secondary human cases were identified among the close contacts, and no evidence of sustained human-to-human transmission was detected.

**What are the implications for public health practice?**

This highlights the importance of routine influenza-like illness surveillance, timely whole-genome sequencing, and systematic investigation of unusual influenza A infections. Strengthened surveillance at the human-animal interface and cross-sector collaboration under the One Health framework are essential for early detection and risk assessment of variant influenza viruses.

## ABSTRACT

**Introduction**: Human infections with swine-origin influenza A(H1N2)v viruses have been reported sporadically worldwide, usually following direct or indirect exposure to pigs or contaminated environments. This report describes the first laboratory-confirmed human infection with influenza A(H1N2)v virus in China.

**Methods**: Following detection of a human infection with influenza A(H1N2)v virus through influenza-like illness surveillance in Yunnan Province in January 2026, an epidemiological investigation, close-contact tracing, animal and environmental sampling, and laboratory testing were conducted. Throat swab specimens were collected for real-time RT-PCR and whole-genome sequencing. Representative influenza virus sequences from the GISAID database were used for sequence comparison and phylogenetic analysis.

**Results:** A 2-year-old boy presented with fever, cough, and rhinorrhea, and recovered after antiviral, antibacterial, and supportive treatments. Whole-genome sequencing revealed the full-length sequences of all eight gene segments. The virus shared the highest nucleotide homology with swine-origin influenza viruses circulating in China, with nucleotide identities ranging from 95.17% to 98.53%, suggesting a reassortant swine-origin influenza A(H1N2)v virus. Epidemiological investigations revealed no clear history of direct contact with pigs or poultry, although the pigs and poultry were raised near the patient's residence. A total of 47 environmental samples and 28 animal samples were collected during the field investigation. Low viral loads of influenza A virus were detected in some swine and environmental samples; however, full subtyping and sequencing could not be performed for some samples because of low viral loads. Thirty close contacts were traced, and none developed relevant symptoms. No secondary cases or evidence of sustained human-to-human transmission was identified.

**Conclusion:** This case suggests a sporadic zoonotic transmission event with limited public health risk.

Variant influenza viruses originating from swine represent an ongoing threat to global public health, owing to their genetic diversity and capacity for reassortment (*1*). When swine influenza viruses infect humans, they are designated with the suffix "v" according to World Health Organization (WHO)

nomenclature. According to WHO influenza nomenclature, the suffix "v" is placed outside the subtype parentheses; therefore, the virus described in this report is referred to as influenza A(H1N2)v virus, rather than influenza A(H1N2)v virus. Although most variant influenza infections result in mild illness and limited human-to-human transmission, sporadic zoonotic events underscore the importance of integrated surveillance under the One Health framework (*2*).

Influenza A(H1N2)v virus has been sporadically reported in several countries and is primarily associated with direct or indirect exposure to pigs. To date, sustained human-to-human transmission has not been documented. In China, swine influenza A(H1N2) viruses have been detected in pig populations, and previous genetic studies have shown that swine influenza viruses circulating in China are genetically diverse and may undergo reassortment among H1N1, H1N2, H3N2, and other swine-origin influenza virus lineages. These findings indicate that swine influenza A virus circulating in domestic pig populations may pose a zoonotic risk. Human infections with A(H1N2)v are rare, and no confirmed cases have been reported in China prior to this event (*3*). Here, we report the first laboratory-confirmed human infection with A(H1N2)v virus detected through influenza-like illness (ILI) sentinel surveillance in Yunnan Province and describe the comprehensive field investigation and response measures undertaken (*4*). This case has public health significance because it represents the first recognized human A(H1N2)v infection in China and highlights the value of routine influenza surveillance for detecting rare variant influenza virus infections.

## METHODS

### Case Detection

On January 30, 2026, the Provincial CDC identified influenza A(H1N2)v virus in a respiratory specimen collected from an ILI patient at a sentinel hospital. The specimen was collected on January 26, 2026, at a local children's hospital, and the clinical specimen used for case confirmation was a throat swab. Initial screening for influenza A virus and subtype confirmation were conducted by the local CDC.

### Case Definition

A suspected human infection with a variant influenza virus was defined as an acute respiratory illness with laboratory evidence of influenza A virus infection that could not be subtyped as currently circulating seasonal influenza viruses or that showed subtype characteristics suggestive of swine-origin influenza virus infection. A confirmed case was defined as a respiratory specimen positive for influenza A virus and laboratory evidence of swine-origin influenza A(H1N2)v infection by subtype-specific real-time RT-PCR and/or whole-genome sequencing (*5*).

### Field Investigation

Upon confirmation, the local CDC dispatched a multidisciplinary investigation team comprising epidemiologists, laboratory specialists, and emergency response personnel to conduct field investigations, including case interviews, contact tracing, environmental assessments, and animal sampling.

We collected information on the patient's clinical course, healthcare-seeking history, travel history, animal exposure history, household environment, and contact history during the 10 days prior to illness onset.

### Close Contact Definition and Management

Close contacts were defined as persons who had unprotected close contact with the patient from one day before illness onset to discharge, including household members, caregivers, healthcare workers, and other persons with close exposure in enclosed settings. All close contacts were placed under medical observation for seven days after their last exposure. Respiratory specimens were collected from close contacts during the investigation and tested using real-time RT-PCR. The investigators also asked whether close contacts developed an influenza-like illness before the onset of the patient's illness.

### Laboratory Testing

Respiratory specimens were tested using real-time RT-PCR for influenza A virus and subtyped for the H and N genes. Real-time RT-PCR was performed using a Rapid Typing Kit for Influenza A Virus HxNy. The primers and probes used for H and N gene subtyping are included in the kit. Testing was conducted according to the manufacturer's instructions. Whole-genome sequencing was performed using next-generation sequencing (NGS). In the present study,

sequencing was performed using the MiniSeq next-generation sequencing system. The sequencing data were analyzed using CLC Genomics Workbench (version 23.0; QIAGEN, Aarhus, Denmark). Sequence assembly and analysis revealed the full-length sequences of all eight gene segments. Alignment with the GISAID database indicated that all gene segments shared the highest sequence homology with swine-origin influenza viruses prevalent in China, identifying the virus as a swine-origin influenza A (H1N2)v virus.

Phylogenetic analysis was conducted by comparing the human viral sequences obtained with representative domestic and international influenza virus sequences available from Global Initiative on Sharing All Influenza Data (GISAID). Full-length sequences of all eight gene segments were obtained from human cases, and phylogenetic trees were constructed to clarify the genetic origin of each segment. However, full viral genome sequences could not be obtained from influenza A-positive animals and environmental samples because of low viral loads; therefore, accession numbers for these samples were not available. The nucleotide sequences generated from the human case were not submitted to GISAID or GenBank; therefore, no accession numbers were available, and virus isolation was unsuccessful because of low viral load and/or insufficient viable virus in the residual specimens.

## Animal and Environmental Sampling

A total of 47 environmental and 28 animal specimens were collected during the field investigation. Animal and environmental specimens included pig nasopharyngeal swabs, poultry oropharyngeal and cloacal swabs, fecal samples, feed and drinking water samples, environmental surface swabs, wastewater samples, and tissue or fluid specimens from a dead pig in a neighboring household. All specimens were screened for influenza A virus, and influenza A-positive specimens were further tested for the H5, H7, H9, and HxNy subtypes when the viral load was allowed.

## Ethical Considerations

All the investigations were conducted as part of a public health emergency. Personal identifiers were anonymized to protect patient privacy. This investigation was conducted during routine infectious disease surveillance and public health emergency response activities.

# RESULTS

## Case Description

The patient was a 2-year-old boy residing in Yunnan Province. He lived in a rural household with his grandparents and other family members. His parents were migrant workers living outside the county.

The patient developed a fever with a maximum temperature of 38.9 °C, cough, and rhinorrhea on January 20, 2026, following cold exposure. He initially sought care at a township health center and later at a private clinic, which was a different healthcare facility from the township health center. He was treated with antipyretics, antibiotics, and antiviral medications without significant improvement. Owing to persistent fever, he was transferred to Kunming on January 25 and admitted to a local Children's Hospital on January 26. On admission, a physical examination revealed pharyngeal congestion, tonsillar enlargement, and coarse breath sounds with sputum rales. Laboratory tests showed elevated C-reactive protein levels but normal white blood cell counts. Respiratory pathogen testing was positive for influenza A virus. Chest radiography indicated increased bilateral lung markings. *Haemophilus influenzae* coinfection was diagnosed based on nucleic acid testing of a throat swab collected from the patient and performed by the hospital laboratory.

The patient was diagnosed with pneumonia complicated by influenza A virus and Haemophilus influenzae infections. The patient was treated with oseltamivir, cefoperazone–sulbactam, nebulized budesonide, and supportive therapy, resulting in clinical improvement. The patient was discharged on January 31, 2026 (Figure 1).

On January 20, 2026, the patient developed influenza-like symptoms and sought medical care multiple times before hospital admission on January 26. Laboratory confirmation of influenza A(H1N2)v was obtained on January 30, and the patient recovered and was discharged on January 31, 2026.

## Epidemiological Investigation

The patient lived in a rural village, where pigs, chickens, and pigeons were raised. Family members denied direct contact between the patient and the livestock. The patient had no travel history or exposure to live poultry markets in the 10 days prior to

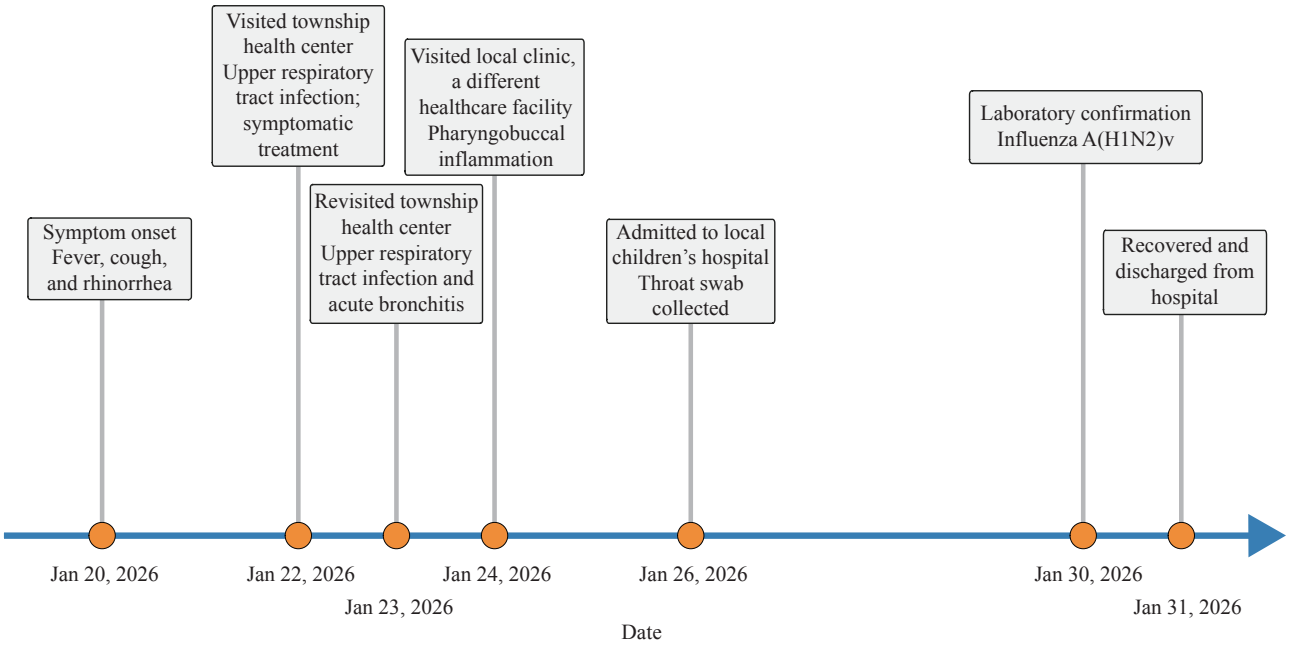


FIGURE 1. Timeline of symptom onset, healthcare visits, diagnosis, and recovery of the patient.

symptom onset. Although no direct animal contact was reported, the presence of pigs and poultry near the living area suggested the possibility of indirect environmental exposure.

A detailed activity history revealed that the patient remained primarily at home during the incubation period, with close contacts limited to household members who stayed mainly at home, used personal items such as a bed, feeding bottle, toys, and had contact mainly with grandparents, relatives, and occasional neighbors. No direct contact with poultry or livestock has been reported (Table 1).

Thirty close contacts including household members, healthcare workers, and caregivers were identified. All contacts were monitored for symptoms and tested using RT-PCR. No secondary cases were identified in this study.

## Environmental and Animal Investigation

The patient's residence comprised stone and brick structures with suboptimal sanitation. Pig and poultry enclosures were adjacent to the living areas. Environmental hygiene was poor, with visible poultry feces in courtyards (Figure 2).

Multiple rounds of animal sampling were conducted on pigs, chickens, geese, pigeons, and environmental surfaces. Most specimens tested negative for the

TABLE 1. Activity and exposure history of the case during the 10 days prior to illness onset.

| Date | Location | Items involved | Persons in contact | Contact with poultry or livestock |
|---|---|---|---|---|
| Jan-10-2026 | Home | Bed, feeding bottle, toys | Grandfather, grandmother, neighbor | No direct contact |
| Jan-11-2026 | Home | Bed, feeding bottle, toys | Grandmother, grandfather | No direct contact |
| Jan-12-2026 | Home | Bed, feeding bottle, toys | Grandmother, grandfather, great-uncle | No direct contact |
| Jan-13-2026 | Home | Bed, feeding bottle, toys | Grandmother, aunt, grandfather, uncle | No direct contact |
| Jan-14-2026 | Home | Bed, feeding bottle, toys | Grandmother, aunt, grandfather, uncle, great-uncle | No direct contact |
| Jan-15-2026 | Home | Bed, feeding bottle, toys | Grandmother, aunt, grandfather, uncle | No direct contact |
| Jan-16-2026 | Home | Bed, feeding bottle, toys | Grandmother, aunt, grandfather, uncle | No direct contact |
| Jan-17-2026 | Home | Bed, feeding bottle, toys | Grandmother, aunt, grandfather, uncle | No direct contact |
| Jan-18-2026 | Home | Bed, feeding bottle, toys | Grandmother, aunt, grandfather, uncle | No direct contact |
| Jan-19-2026 | Home | Bed, feeding bottle, toys | Grandmother, aunt, grandfather, uncle | No direct contact |

Abbreviation: Jan=January.

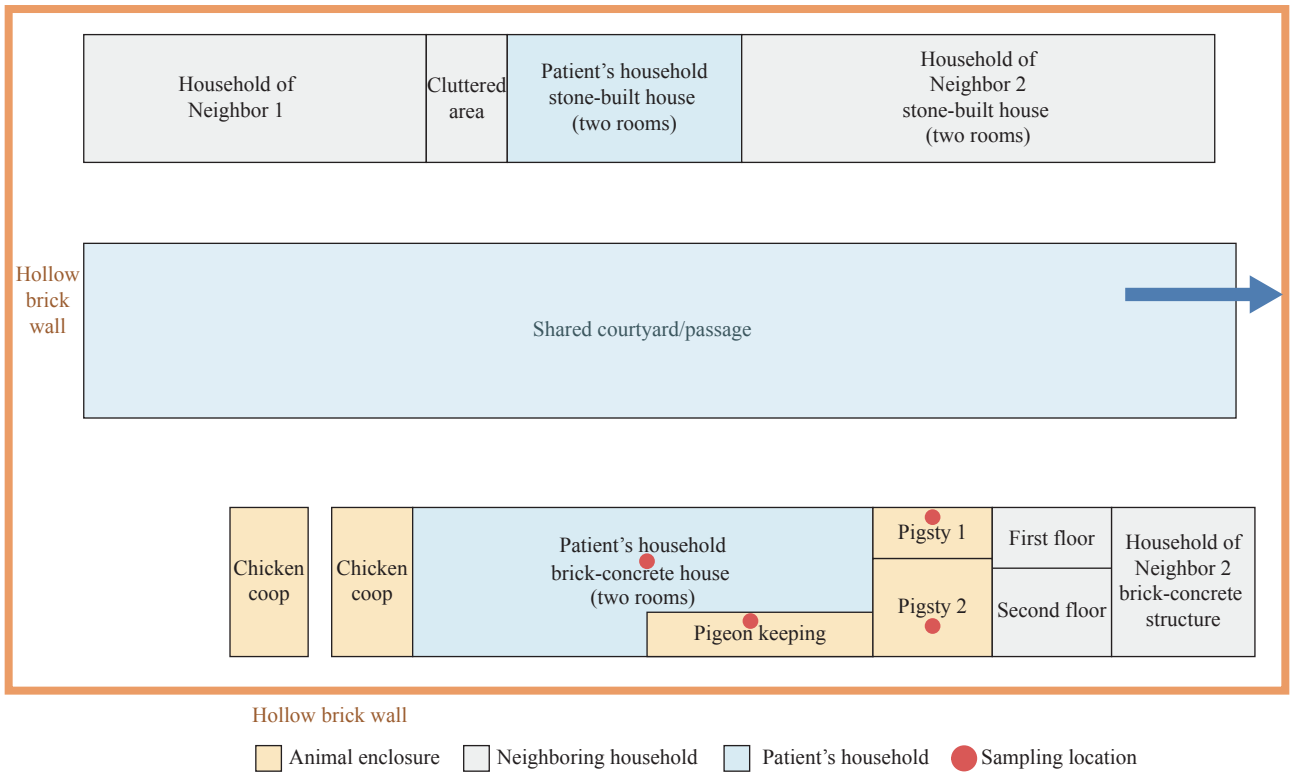


FIGURE 2. Layout of the patient's household and surrounding livestock facilities

influenza A virus. However, low loads of influenza A virus were detected in a small number of pig and environmental samples [cycle threshold (Ct) values >35] (Table 2).

## Laboratory Findings

The patient's throat swab tested positive for influenza A virus (Ct 31.10), H1 subtype (Ct 27.41), and N2 subtype (Ct 26.68), confirming infection with influenza A(H1N2)v.

Whole-genome sequencing demonstrated that all eight gene segments clustered with influenza viruses of swine origin circulating in China, with nucleotide homology ranging from 95.17% to 98.53%. Internal genes originated from reassortment among swine H1N1, H1N2, and H3N2 viruses, and sequence assembly and analysis revealed the full-length sequences of all eight gene segments. Alignment with the GISAID database indicated that the virus shared the highest sequence homology with influenza viruses of swine origin prevalent in China, which identified the virus as a swine-origin influenza A(H1N2)v virus. Further whole-genome sequencing and sequence analysis conducted by China CDC confirmed that the specimen was positive for swine-origin influenza A(H1N2)v virus. According to the World Health Organization nomenclature, because an H1N2 swine influenza virus infected a human, the suffix "v" (variant) was added, and the virus was therefore designated influenza A(H1N2)v. Amino acid analysis showed that no known critical mutations were detected. Similar to previously identified H1 swine influenza viruses in China, the HA receptor-binding site at amino acid position 222 was E, suggesting dual receptor-binding characteristics. The HA cleavage site did not contain multiple basic amino acids, indicating that the virus was of low pathogenicity. The PB2 protein carried SR at positions 590–591, suggesting mammalian adaptation, while positions 627 and 701 remained E and D, respectively, with no mutation detected. No mutations associated with resistance to neuraminidase inhibitors or polymerase inhibitors were identified, suggesting sensitivity to these antiviral drugs.

Further investigation identified an N2-positive sample from the lung tissue of a pig that had died in a neighboring household. However, because the viral load of the positive animal specimen was low, and full viral sequencing could not be obtained from animal or environmental samples, direct genomic evidence

TABLE 2. Detection of influenza A virus in animal and environmental samples during field investigation.

| Surveillance site | Sample ID / source | Specimen type | Collection date | Influenza A result | H5 | H7 | H9 | HxNy subtyping |
|---|---|---|---|---|---|---|---|---|
| Patient's household | Pig 1 | Nasopharyngeal swab | Jan-31-2026 | Negative | Negative | Negative | Negative | Negative |
| Patient's household | Pig 2 | Nasopharyngeal swab | Jan-31-2026 | Positive, Ct=36.58* | Negative | Negative | Negative | Not subtyped due to low viral load |
| Patient's household | Pig 3 | Nasopharyngeal swab | Jan-31-2026 | Positive, Ct=37.45* | Negative | Negative | Negative | Not subtyped due to low viral load |
| Patient's household | Pig feces | Fecal sample | Jan-31-2026 | Negative | Negative | Negative | Negative | Negative |
| Patient's household | Pig feed trough | Surface swab | Jan-31-2026 | Negative | Negative | Negative | Negative | Negative |
| Patient's household | Chicken feces | Fecal sample | Jan-31-2026 | Negative | Negative | Negative | Negative | Negative |
| Patient's household | Chicken feed | Feed sample | Jan-31-2026 | Negative | Negative | Negative | Negative | Negative |
| Patient's household | Chicken drinking water | Poultry drinking water | Jan-31-2026 | Negative | Negative | Negative | Negative | Negative |
| Patient's household | Chicken | Oropharyngeal and cloacal swab | Jan-31-2026 | Negative | Negative | Negative | Negative | Negative |
| Patient's household | Goose | Oropharyngeal and cloacal swab | Jan-31-2026 | Negative | Negative | Negative | Negative | Negative |
| Patient's household | Pigeon | Oropharyngeal swab | Jan-31-2026 | Negative | Negative | Negative | Negative | Negative |
| Patient's household | Bed frame in bedroom | Surface swab | Jan-31-2026 | Negative | Negative | Negative | Negative | Negative |
| Patient's household | Pillow in patient's bedroom | Surface swab | Jan-31-2026 | Positive, Ct=38.61* | Negative | Negative | Negative | Not subtyped due to low viral load |
| Patient's household | Medicine bowl | Surface swab | Jan-31-2026 | Negative | Negative | Negative | Negative | Negative |
| Patient's household | Quilt in patient's bedroom | Surface swab | Jan-31-2026 | Positive, Ct=36.31* | Negative | Negative | Negative | Not subtyped due to low viral load |
| Patient's household | Child's toy car | Surface swab | Jan-31-2026 | Positive, Ct=36.16* | Negative | Negative | Negative | Not subtyped due to low viral load |
| Patient's household | Pigeon cage | Surface swab | Jan-31-2026 | Negative | Negative | Negative | Negative | Negative |
| Neighbor1s household | Pig 4 | Nasopharyngeal swab | Jan-31-2026 | Positive, Ct=38.72* | Negative | Negative | Negative | Not subtyped due to low viral load |
| Neighbor1s household | Pig 5 | Nasopharyngeal swab | Jan-31-2026 | Negative | Negative | Negative | Negative | Negative |
| Neighbor1s household | Pig 6 | Nasopharyngeal swab | Jan-31-2026 | Negative | Negative | Negative | Negative | Negative |
| Neighbor1s household | Pig 4 feces | Fecal sample | Jan-31-2026 | Negative | Negative | Negative | Negative | Negative |
| Slaughterhouse | Chopping board | Surface swab | Jan-31-2026 | Negative | Negative | Negative | Negative | Negative |
| Slaughterhouse | Wastewater | Cleaning wastewater | Jan-31-2026 | Negative | Negative | Negative | Negative | Negative |
| Clinic | Heated table | Surface swab | Jan-31-2026 | Negative | Negative | Negative | Negative | Negative |
| Hospital | Bedside cabinet | Environmental swab | Jan-30-2026 | Negative | Negative | Negative | Negative | Negative |
| Hospital | Bed rail | Environmental swab | Jan-30-2026 | Negative | Negative | Negative | Negative | Negative |
| Hospital | Mobile phone | Environmental swab | Jan-30-2026 | Negative | Negative | Negative | Negative | Negative |
| Hospital | Bathroom door handle | Environmental swab | Jan-30-2026 | Negative | Negative | Negative | Negative | Negative |
| Hospital | Toilet flush button | Environmental swab | Jan-30-2026 | Negative | Negative | Negative | Negative | Negative |

Continued

| Surveillance site | Sample ID / source | Specimen type | Collection date | Influenza A result | H5 | H7 | H9 | HxNy subtyping |
|---|---|---|---|---|---|---|---|---|
| Hospital | Patient pillow | Environmental swab | Jan-30-2026 | Negative | Negative | Negative | Negative | Negative |
| Hospital | Nebulizer tubing | Environmental swab | Jan-30-2026 | Negative | Negative | Negative | Negative | Negative |
| Hospital | Consultation room | Environmental swab | Jan-30-2026 | Negative | Negative | Negative | Negative | Negative |
| Patient's household | Wastewater 1 | Water sample | Feb-3-2026 | Negative | Negative | Negative | Negative | Negative |
| Patient's household | Pig feeding trough | Surface swab | Feb-3-2026 | Negative | Negative | Negative | Negative | Negative |
| Neighbor's household | Wastewater 2 | Water sample | Feb-3-2026 | Negative | Negative | Negative | Negative | Negative |
| Neighbor's household | Pig feeding trough 3 | Surface swab | Feb-3-2026 | Negative | Negative | Negative | Negative | Negative |
| Neighbor1's household | Bronchoalveolar fluid | BAL fluid | Feb-1-2026 | Positive, Ct=37.16* | Negative | Negative | Negative | Not subtyped due to low viral load |
| Neighbor2's household | Pleural effusion 1 | Pleural fluid | Feb-1-2026 | Negative | Negative | Negative | Negative | Negative |
| Neighbor2's household | Pleural effusion 2 | Pleural fluid | Feb-1-2026 | Negative | Negative | Negative | Negative | Negative |
| Neighbor2's household | Lung tissue 1 | Lung tissue | Feb-1-2026 | Positive, Ct=35.43* | Negative | Negative | Negative | Hx not subtyped; N2 suspected, Ct=37.85* |
| Neighbor2's household | Trachea | Tracheal tissue | Feb-1-2026 | Negative | Negative | Negative | Negative | Negative |

Abbreviation: Ct=cycle threshold; BAL=bronchoalveolar lavage; Jan=January; Feb=February.
* All influenza A-positive samples were negative for H5, H7, and H9 subtypes. Samples with Ct values greater than 35 were considered low viral-load specimens, and full HxNy subtyping or sequencing was not possible for some of these samples because of insufficient viral nucleic acids.

linking human infection to a specific animal source was not available. Therefore, the available epidemiological and laboratory findings suggest a possible swine-associated zoonotic spillover event; however, the exact infection source and transmission route could not be definitively determined.

## DISCUSSION

This investigation documented the first confirmed human infection with the influenza A(H1N2)v virus in China. Similar to previous reports from the United States and Europe, human infections with A(H1N2)v have remained rare and have primarily been associated with influenza A viruses of swine origin that cross the species barrier (*6*). Most reported cases present with mild-to-moderate influenza-like illness, and sustained human-to-human transmission has not been documented (*7*). The clinical presentation in the present case was consistent with these observations, further supporting the characterization of A(H1N2)v as a sporadic zoonotic pathogen with limited transmissibility. The key finding of this investigation is that a swine-origin influenza A(H1N2)v virus was detected in a young child through routine ILI surveillance, with whole-genome sequencing supporting a swine-origin reassortant virus and no evidence of secondary human transmission.

Notably, unlike many previously reported A(H1N2)v cases in which direct exposure to swine was identified as a key risk factor (*8*), no direct contact with poultry or livestock was reported in this patient. This finding suggests that indirect or environmental exposure may play a role in the development of infection. Environmental contamination, shared living spaces, and short-distance exposure to animal housing have been proposed as alternative transmission pathways for various influenza viruses, particularly in rural settings where humans and animals coexist in close proximity (*9*). These findings underscore the complexity of exposure assessment in zoonotic influenza investigations. In the present case, pigs and poultry were raised near the residence, and influenza A virus was detected at low viral loads in several pig and environmental samples. These findings support the

possibility of indirect environmental exposure, but do not prove the exact source of infection.

The detection of this case through routine sentinel influenza-like illness (ILI) surveillance highlights the critical role of sensitive surveillance systems and rapid laboratory diagnostics in identifying rare and emerging influenza variants. Previous studies have emphasized that early identification of variant influenza viruses relies heavily on integrated virological surveillance and timely genetic characterization (*10*). In this context, the successful detection and confirmation of A(H1N2)v infection in this case reflect the effectiveness of China's existing influenza surveillance network. Compared with evidence based only on PCR subtyping, whole-genome sequencing provided stronger laboratory evidence for identifying this virus as a swine-origin influenza A(H1N2)v virus.

From a broader public health perspective, this event reinforces the importance of the One Health approach, which integrates the human, animal, and environmental health sectors. Swine populations are important mixing vessels for influenza A viruses, facilitating the reassortment and emergence of novel variants with zoonotic potential. Continuous surveillance in animal populations, particularly swine, combined with data sharing across sectors, is essential for early risk assessment and prevention of future spillover events. The genetic findings in this case were consistent with reassortment among swine influenza virus lineages circulating in China, further supporting the need for coordinated human and animal influenza surveillance.

This investigation has several limitations. First, several influenza A-positive animal and environmental samples had high Ct values, indicating low viral loads. Therefore, full subtyping or sequencing could not be performed on some specimens. Second, because complete viral sequences were not obtained from positive animals or environmental samples, the exact infection source and transmission route could not be confirmed. Third, follow-up respiratory specimens were not collected during treatment or after discharge; therefore, viral shedding was not monitored. Fourth, virus isolation was unsuccessful because of low viral load and/or insufficient viable virus in the residual specimen, limiting further phenotypic and antigenic characterization. Finally, this report described a single sporadic case; therefore, the findings should be interpreted with caution.

Human infection with the influenza A(H1N2)v virus described in this investigation represents a sporadic zoonotic event with no evidence of onward transmission and a limited public health impact. This case is comparable to previously reported A(H1N2)v infections globally, which are characterized by mild illness and the absence of sustained human-to-human spread.

Nevertheless, this finding highlights the ongoing risk posed by variant influenza viruses at the human–animal interface. Strengthened sentinel surveillance, timely epidemiological investigation, enhanced laboratory capacity, and cross-sector collaboration under the One Health framework remain critical for the early detection and mitigation of potential future outbreaks, confirming that human A(H1N2)v infection in China provides important evidence for national influenza surveillance and emphasizes the need to strengthen the genomic monitoring of swine-origin influenza viruses.

**Conflicts of interest:** No conflicts of interest.

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[#] Corresponding author: Chunrui Luo, yncdclcr@yncdc.cn.

[1] Epidemic Surveillance and Public Health Emergency Response Center, Yunnan Center for Disease Control and Prevention, Kunming City, Yunnan Province, China; [2] Department of Epidemiology, Faculty of Medicine, Prince of Songkla University, Songkhla, Thailand; [3] Institute for Acute Infectious Disease Control and Prevention, Yunnan Center for Disease Control and Prevention, Kunming City, Yunnan Province, China; [4] Surveillance, Early Warning and Emergency Response Center, Zhaotong Center for Disease Control and Prevention, Zhaotong City, Yunnan Province, China; [5] Zhenxiong County Center for Disease Control and Prevention, Zhaotong City, Yunnan Province, China.



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