



Article

Emerging Multi-Source Transmission of SFTS Virus on a Remote Japanese Island: A One-Health Perspective

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Abstract

Tick-borne viral infections, including severe fever with thrombocytopenia syndrome virus (SFTSV), are increasingly recognized as a significant threat to global public health owing to their rapid dissemination and high mortality rates. While isolated outbreaks within single species have been documented, reports of multi-host cluster cases remain scarce. This study describes a consecutive, cross-species outbreak of severe fever with thrombocytopenia syndrome disease between April and May 2024 on a remote island in Nagasaki Prefecture that involved four cats and four humans. An interdisciplinary investigation integrating molecular phylogenetic analysis of viral genomes—including previously identified Nagasaki strains of SFTSV—and haplotype network analysis provided insights into the infection dynamics. Despite the absence of confirmed direct contact between cats and humans, four animals and one patient succumbed to the infection. Genomic analyses demonstrated high similarity to circulating Nagasaki strains, whereas haplotype analysis indicated multiple viral introduction events and complex transmission pathways, reflecting diverse sources. These findings underscore the critical need for a One Health approach—integrating human, animal, and vector surveillance—to effectively monitor, understand, and control tick-borne viruses globally, in both endemic and emerging regions.

Keywords: cluster; severe fever with thrombocytopenia syndrome virus; human; cat; One Health



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1. Introduction

Tick-borne viruses are increasingly recognized as significant and growing global public health threats. These pathogens, primarily transmitted by ticks, can cause severe and often emerging infectious diseases, with notable examples including Crimean–Congo haemorrhagic fever virus, tick-borne encephalitis virus, and severe fever with thrombocytopenia syndrome virus (SFTSV), all of which are associated with high mortality rates [1–4]. The geographic distribution and incidence of tick-borne viral infections are expanding, driven by factors such as climate change, globalization, and land-use alterations that promote tick proliferation and increase human exposure to these pathogens. Additionally, the involvement of multiple hosts, including humans, livestock, and wildlife, and intricate ecological interactions complicate efforts to prevent and control these infections. This underscores the urgent need for enhanced surveillance, research, and international cooperation to effectively mitigate the global public health impact of tick-borne viruses.

Severe fever with thrombocytopenia syndrome (SFTS) is an emerging tick-borne viral disease of significant public health concern, attributed to the *Dabie bandavirus*, genus *Bandavirus*, family *Phenuiviridae*, and order *Bunyavirales* [5]. This virus is also known as SFTSV [5]. SFTSV possesses a tripartite, segmented, negative-strand RNA genome comprising the L, M, and S segments, each playing a critical role in viral infectivity and pathogenicity. The L segment encodes an RNA-dependent RNA polymerase essential for viral replication. The M segment encodes glycoproteins involved in host cell attachment and viral assembly, whereas the S segment encodes a nonstructural protein involved in immune evasion and the nucleocapsid protein (NP). NP encapsidates viral RNA, forming ribonucleoprotein complexes that shield viral genetic material from host immune responses and nuclease degradation [6]. A comprehensive understanding of the molecular biology of SFTSV is essential for the development of accurate diagnostics, effective vaccines, and targeted therapeutics to combat this high-mortality pathogen.

The first human SFTS case was reported in China in 2009 [5], followed by documented cases in Japan in 2013 [7]. Forty cases were reported in 2013, and the number has gradually increased, with 182 cases reported as of 31 October 2025 [8]. Although SFTSV is primarily transmitted by ticks of the genus *Haemaphysalis* sp., human-to-human transmission [9] and direct transmission from animals, such as cats, have also been documented [10]. These findings underscore the complex epidemiology of SFTSV and associated SFTS disease. Clusters of infection within households [9,11,12] or veterinary clinics suggest clear links between human and animal reservoirs [10]. Nevertheless, to date, there have been no reports of unlinked outbreaks involving multiple animals or humans confined to a specific area over a short period, raising concerns about undetected or emerging outbreaks of this disease. Understanding the transmission dynamics of SFTSV is crucial for implementing effective public health interventions and preventing its spread among humans and animals.

In Japan, laboratory diagnostics of suspected SFTS cases in companion animals have revealed that Nagasaki Prefecture has the highest number of feline cases [13]. However, epidemiological data from Nagasaki do not indicate clear geographic clustering of infected cats, and no cases among household members or nearby residents have been reported [14]. Between April and May 2024, four cats and four humans were diagnosed with SFTS within the same area of the Goto Islands in Nagasaki, raising concerns regarding the possible risk of local transmission of SFTSV. In response, we conducted a collaborative investigation with local hospitals and the Nagasaki Prefectural Institute of Environment and Public Health (NPIEPH) to better understand the outbreak. These findings highlighted the complexity of SFTSV transmission and reinforced the necessity of integrated surveillance of human and animal populations to prevent and control future outbreaks of SFTS.

2. Results

2.1. Clinical Information and Laboratory Data

The clinical courses of the eight SFTS cases are summarized in Figure 1, with day 0 designated as the first day of the outbreak timeline. Symptoms and laboratory data for all eight cases are presented in Table 1. The first case involved a cat (cat 1) that presented to a veterinary clinic on day 3 (mid-April) with fever, anorexia, and jaundice (Table 1). SFTSV RNA was detected in blood samples on day 3. A second cat (cat 2), examined on day 16 with similar symptoms, tested positive for SFTSV RNA. On the same day, a third cat (cat 3) succumbed to the infection, with SFTS confirmed via an oral swab. The fourth cat (cat 4) exhibited similar symptoms and was diagnosed with SFTS on day 37 (mid-May). Among the human cases, two individuals (humans 5 and 6) developed fever and malaise on day 24 (early May) and were diagnosed with SFTS. A third patient (human 7) experienced symptom onset shortly thereafter but died on day 30 (mid-May), with postmortem detection of SFTSV in the blood. The eighth case (human 8), presenting with fever and headache, was diagnosed on day 37 (mid-May). No direct contact was observed between the four cats and the four humans. The cats involved were domestic and allowed to roam freely. Notably, the patients were not the owners of these cats. Three patients (humans 5, 6, and 8) participated in outdoor activities, such as mowing grass and working in fields, which could have increased their exposure to ticks. Although human 7, who ultimately succumbed to the illness, had no known history of tick contact, he kept non-infected cats as pets.

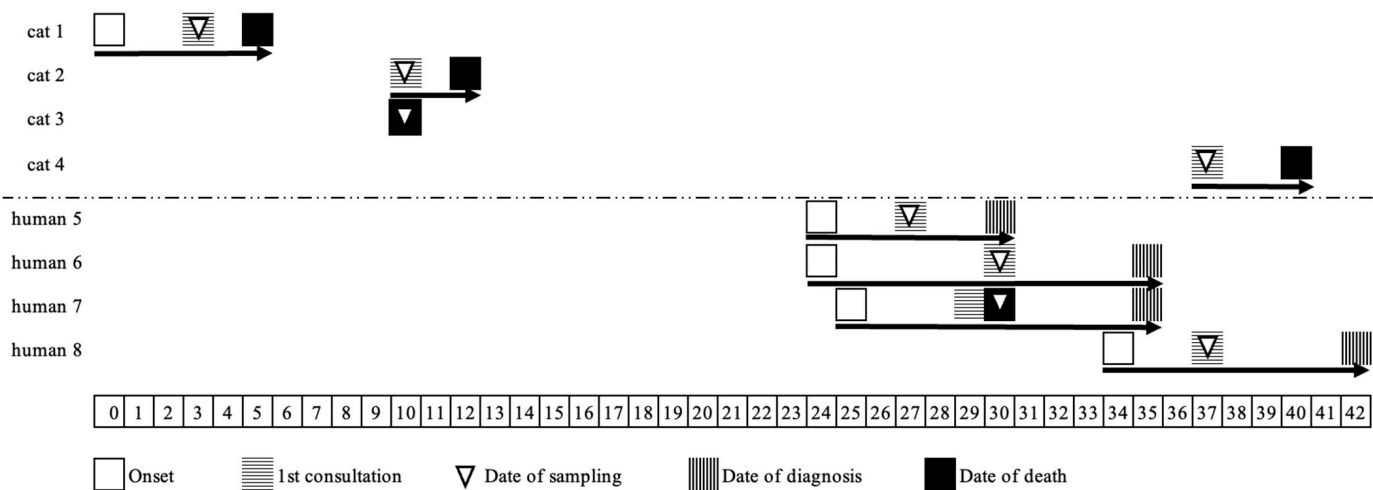


Figure 1. Timeline of the eight cases. Timeline of the eight cases (four cats and four humans) with severe fever with thrombocytopenia syndrome (SFTS). Day 0 represents the first day of the outbreak timeline. The onset days for cats 2, 3, and 4 were unknown. Cat 3 was found dead and diagnosed with SFTS based on an oral swab sample.

Table 1. Clinical symptoms and hematologic and diagnostic results for eight SFTS cases.

	Cat 1	Cat 2	Cat 3	Cat 4	Human 5	Human 6	Human 7	Human 8
Personal information								
Age	3–4	1	2	10	64	82	70	78
Sex	F	M	M	F	M	F	M	F
Outcome	Death	Death	Death	Death	Alive	Alive	Death	Alive
History of tick contact	NA	NA	NA	NA	No	No	No	No
History of keeping cat	NA	NA	NA	NA	No	No	Yes	No
Rearing environmental	Free to go out	Free to go out	Free to go out	Free to go out	NA	NA	NA	NA

Table 1. Cont.

	Cat 1	Cat 2	Cat 3	Cat 4	Human 5	Human 6	Human 7	Human 8
Clinical symptoms								
Fever	+	+	NA	+	+	+	+	+
Fatigue	+	+	NA	+	+	+	+	+
Headache	NA	NA	NA	NA	+	—	—	+
Nerve symptoms	—	—	NA	—	—	+	+	—
Coma	—	—	NA	—	—	—	+	+
Digestive symptoms	—	—	NA	—	+	—	+	—
Less of appetite	+	+	NA	+	+	+	+	+
Bleeding	—	—	NA	—	+	—	+	+
Jaundice	+	+	NA	+	—	—	—	—
Blood test								
RBC ($\times 10^4/\mu\text{L}$)	844	626	NA	645	NA	NA	NA	NA
WBC ($/\mu\text{L}$)	1380	5390	NA	3510	1550	850	2320	1040
Plt ($/\mu\text{L}$)	39,000	14,000	NA	134,000	49,000	62,000	33,000	28,000
AST (U/L)	320	201	NA	132	105	110	613	225
CRP (mg/dL)	NA	NA	NA	NA	0.01	0.03	0.11	0.19
Virological test								
Sample	Plasma	Serum	Oral swab	Serum	Plasma	Plasma	Plasma	Plasma
Ct value (L segment) *	17.6	31.7	27.0	29.3	29.6	26.0	25.0	27.1
Viral load (copies/mL) **	5.49×10^9	ND	1.49×10^7	1.35×10^4	2.40×10^6	3.60×10^7	2.74×10^7	9.26×10^6

NA: not applicable; ND: not detected; +: positive; —: negative; *: cut-off value was 40. **: cut-off value was 1.0×10^4 genome copies/mL.

At the NP/IEPH, cycle threshold (Ct) values were determined using reverse transcription quantitative polymerase chain reaction (RT-qPCR) targeting the L segment of the SFTSV. Viral loads were assessed at Nagasaki University using RT-qPCR targeting the NP gene in the S segment. No correlation was observed between viral load and clinical outcomes (Table 1).

2.2. Segment-Wise Phylogenetic Analysis

Whole-genome sequencing was performed using amplicon sequencing. Phylogenetic analysis of the eight SFTSV specimens and previously published sequences revealed that all strains of this virus belonged to genotype B2 (Figure 2), corresponding to strains previously reported in Nagasaki [14]. This finding suggested the presence of a localized viral population.

2.3. Nucleic Acid Variation and Amino Acid Analysis

Nucleic acid variation and sequence identity at the nucleotide level are shown in Supplementary Tables S1 and S2, respectively. Amino acid analyses across the genomes of the three segments of the SFTSV are shown in Table 2. Several characteristic amino acid mutations were identified among the eight cases. In the L segment, most samples harboured glutamine at position 58 and lysine at position 1705, whereas human 8 exhibited leucine and arginine at these sites. Furthermore, cat 4 had lysine at position 1189, in contrast to the arginine detected in other samples. In the M segment, most samples matched the consensus sequence, but only human 7 exhibited isoleucine, serine, proline, histidine, and threonine residues at positions 232, 341, 462, 467, and 468, respectively, all of which were minor variants. In the S segment, glycine was present in all registered strains except cat 1, which had valine at position 150.

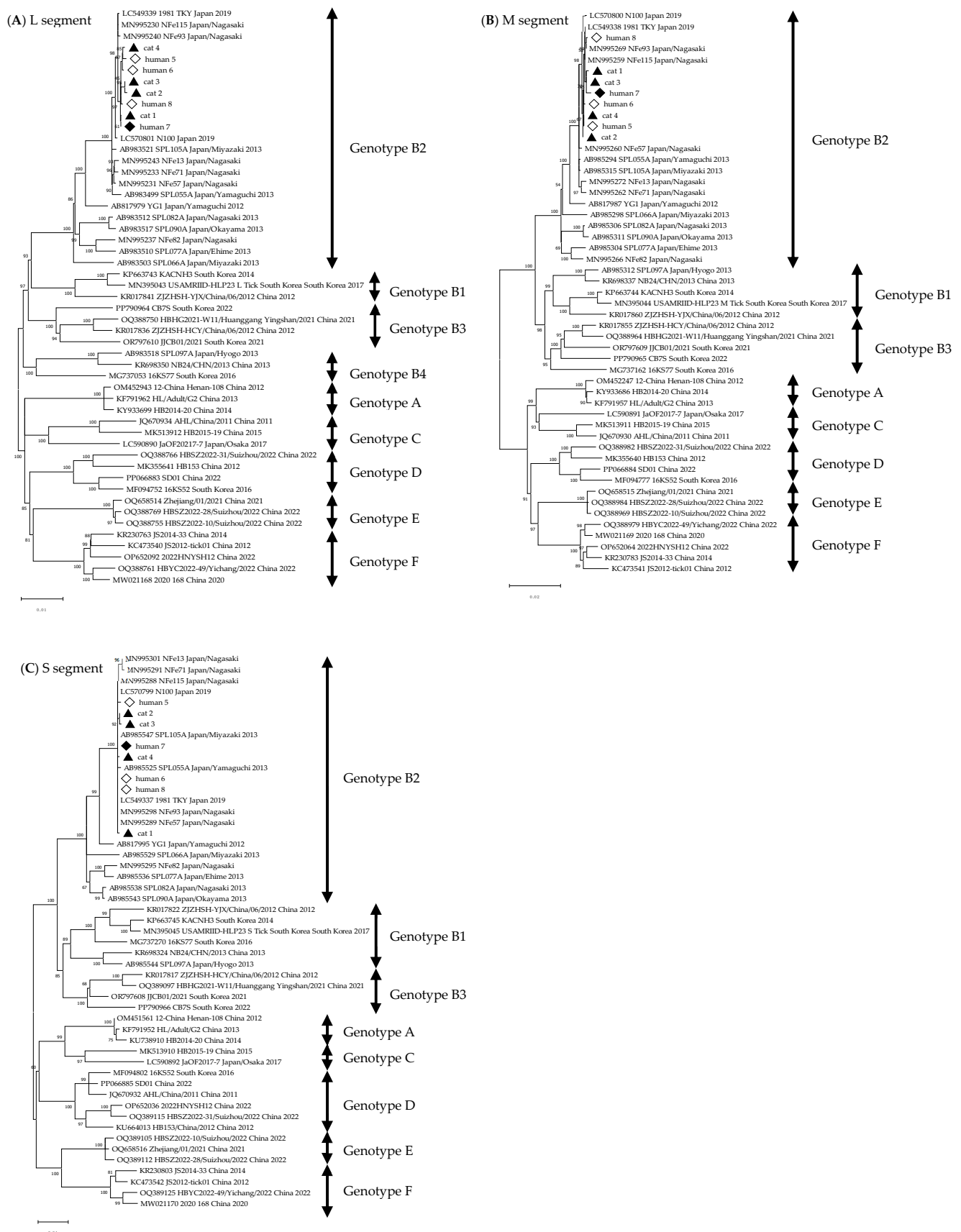


Figure 2. Phylogenetic analysis. Phylogenetic analysis of SFTSV strains obtained from the eight cases and previously reported sequences. The maximum-likelihood method with 1000 bootstrap replicates was used. (A) L segment, (B) M segment, and (C) S segment of the virus. Symbols indicate case outcomes: ▲, deceased cat; ◇, survived human; ◆, deceased human.

Table 2. Comparison of amino acid sequences of the genome segments across the eight SFTSV samples.

Segment	Position	Cat 1	Cat 2	Cat 3	Cat 4	Human 5	Human 6	Human 7	Human 8	Consensus *	% **
L	58	Q	Q	Q	Q	Q	Q	Q	L	Q L	99.91 0.09
	1189	R	R	R	K	R	R	R	R	R K	99.86 0.14
	1705	K	K	K	K	K	K	K	R	K -	100 -
M	232	V	V	V	V	V	V	I	V	V I	99.87 0.13
	341	P	P	P	P	P	P	S	P	Q P S/others	57.76 36.44 4.5/1.3
	462	L	L	L	L	L	L	P	L	L V/F/I/Q	99.643 0.134/0.134/ 0.045/0.045
	467	Y	Y	Y	Y	Y	Y	H	Y	L F/H	99.91 0.045/0.045
	468	M	M	M	M	M	M	T	M	M K	99.96 0.04
	150	V	G	G	G	G	G	G	G	G -	100 -
S	150	V	G	G	G	G	G	G	G	G -	100 -

The grey sections indicate regions in which mutations were observed in the strains isolated in this study. * The amino acid sequences of National Center for Biotechnology Information (NCBI)-registered strains were compared with the reference sequence, and shared amino acids were noted. ** The proportion of amino acids marked with an asterisk (*) is shown as a percentage.

2.4. Haplotype Network Analysis of SFTSV Identified in This Study

Haplotype network analysis is a powerful tool for elucidating the molecular epidemiology and phylogeographic relationships underlying infectious disease outbreaks in humans and animals. In this study, haplotype networks were constructed for eight SFTSV viral genomes obtained from our samples, together with six previously reported SFTSV strains from Nagasaki, to investigate potential transmission pathways (Figure 3). In the L segment, no distinct haplotypes were identified, although human 7 and cat 1 shared the most closely related sequences, differing by only one nucleotide. Cats 2 and 3 differed by four nucleotides, whereas cat 4 and human 6 differed by six nucleotides. Additionally, human 7 and strain NFe115 differed by six nucleotides. In the M segment, cat 4 and human 5 shared Haplotype I, which was closely connected to cat 2, differing by only one nucleotide. Haplotype I was further linked to human 6 and strain NFe115 by a two-nucleotide difference. In the S segment, cats 2 and 3 clustered within Haplotype II, whereas humans 6, 7, and 8, along with strains NFe57, NFe93, and NFe115, shared Haplotype III. Haplotype III was closely related, differing by only one nucleotide, to cats 1 and 4, as well as to Haplotype II. Human 5 was linked to Haplotype III by a two-nucleotide difference. Overall, these findings suggest possible transmission links among the hosts and strains examined, providing insights into viral dissemination dynamics.

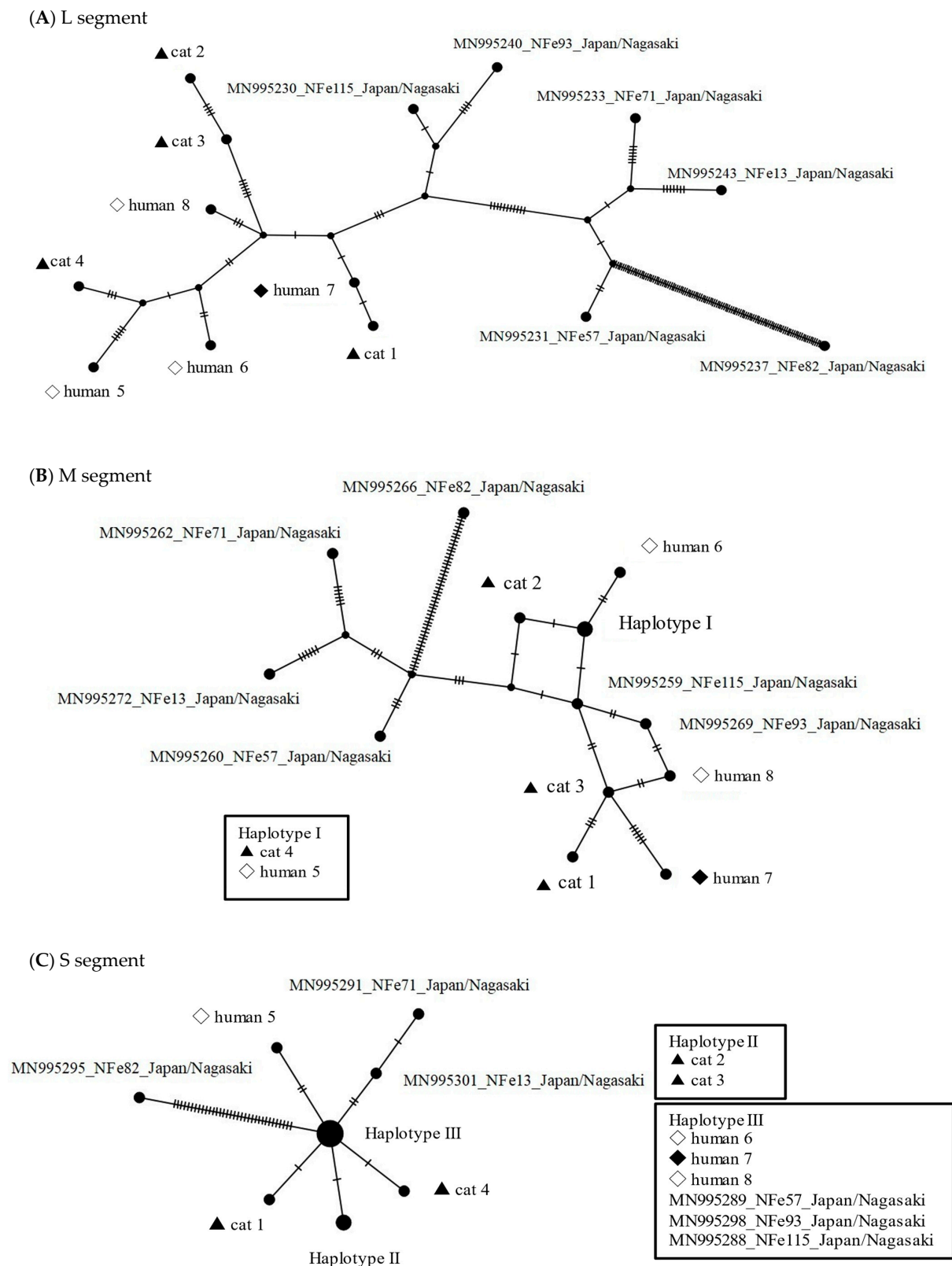


Figure 3. Haplotype network analysis. Haplotype network analysis using the median-joining algorithm for severe fever with thrombocytopenia syndrome virus (SFTSV) segments derived from the eight SFTS cases and six previously reported Nagasaki SFTSV strains. (A) L segment, (B) M segment, and (C) S segment. Branch marks between strains indicate the number of mutations. Strains enclosed within square frames share the same haplotype. Symbols indicate case outcomes: ▲, deceased cat; ◇, survived human; ◆, deceased human.

3. Discussion

A cluster outbreak of SFTS was confirmed on an island in Nagasaki Prefecture, with cases occurring predominantly within a 42-day period. The affected individuals included both cats and humans with no apparent contact history. Full-length viral genomes were obtained from all samples, and phylogenetic tree construction and haplotype network analyses were performed to investigate the outbreak dynamics.

This investigation was conducted in collaboration with local hospitals and the NPIEPH to determine the underlying causes of the SFTSV infection clusters. The clinical symptoms observed in cats were consistent with those reported in previous studies [15], including fever, lethargy, jaundice, and hemoptysis. The laboratory findings are summarized in Table 1. Human cases of SFTS exhibited hallmark symptoms, including fever, anorexia, malaise, neurological manifestations, and hemoptysis. The alarmingly high lethality associated with this disease is particularly concerning, as all infected cats succumbed to infection, underscoring its extreme pathogenicity. In comparison, the case fatality rate in humans was approximately 27% [16], whereas in cats it reaches approximately 62% [17]. Notably, human case 7, which harboured specific amino acid substitutions in the M segment, remains the only fatal case reported in this study. Importantly, no definitive correlation has been established between particular amino acid substitutions and virulence [18–26]. The future use of cloned viruses for functional validation holds promise for elucidating the mechanisms underlying virulence and pathogenesis.

Regarding the RT-qPCR results, it is noteworthy that our institute was unable to detect the virus from cat 2 in the S segment via RT-qPCR, likely owing to RNA degradation caused by delays in sample processing and repeated freeze–thaw cycles. However, by leveraging the high sensitivity of next-generation sequencing (NGS), we successfully obtained a complete viral genome sequence from the sample. This discrepancy in RT-qPCR findings between the two facilities highlights the significance of NGS as a complementary tool for comprehensive viral detection and characterization.

Although haplotype network analysis has been widely employed in studies of viruses such as SARS-CoV-2 [27,28], it has not previously been applied to SFTSV. In our analysis, humans 5, 6, and 7 developed symptoms within 48 h, as shown in Figure 1, suggesting the possibility of a common source of infection. However, these three samples did not share the same haplotype in the L, M, and S segments in Figure 3. Some SFTS cases demonstrated direct phylogenetic links, such as between cat 1 and human 7 in the L and S segments, whereas others involved indirect connections mediated through intermediate hosts or strains. No consistent haplotype correlation patterns were observed across the different genomic segments. These findings suggested complex transmission dynamics, likely involving vectors such as ticks or other animals that facilitate viral spread. The heterogeneity observed across segments underscores the possibility of multiple introduction events and intricate circulation patterns within the outbreak region.

The primary limitation of this study was the inability to collect tick samples from the field. The SFTSV genotype identified from the specimens was classified as genotype B2, which is the predominant strain in Nagasaki Prefecture. However, phylogenetic analyses revealed inconsistencies among different genome segments. Given that this period corresponded to the active tick season, it is plausible that infected ticks served as vectors. Unfortunately, timely tick collection was not possible because information on the eight SFTS cases became available only several months after the outbreak had occurred. Fortunately, no additional SFTS cases have been reported in the area, suggesting that this event may have been temporary. Another limitation was the restricted availability of data owing to privacy concerns among patients and pet owners, which may have affected the robustness

of our analyses. A larger dataset could improve the reliability and comprehensiveness of the results.

Based on this experience, we established a multidisciplinary One Health approach team, including regional government officials, virologists, tick ecology researchers, clinicians in both human and veterinary medicine, and statistical analysis experts, to prevent future cluster outbreaks of SFTS. We hypothesized that ticks temporarily accumulated in the area, leading to multiple infections in humans and cats. While an animal reservoir likely contributes to the SFTSV source, its exact origin remains uncertain. To address this, we initiated rapid tick surveys in and around the regions where SFTS cases were reported. Although the timing was suboptimal, as surveys were conducted late in the season and extended into winter, the team carried out a site visit 9 months after the outbreak and collected ticks from seven areas using the flagging method for 15 min per site. Despite collecting 54 ticks, none tested positive for SFTSV RNA. These findings underscore the challenges associated with detecting SFTSV-positive ticks. Previous studies have reported a wide range of SFTSV detection rates in ticks, from 0.0% to 19.5% [29–32], highlighting substantial variability influenced by regional and seasonal factors. Consequently, continued surveillance is essential to elucidate the spatial and temporal distribution of SFTSV-infected ticks. Because SFTSV infection rates in ticks vary by region and season [31], sustained surveys may provide insights into their distribution patterns. Furthermore, tick infection rates may be influenced by environmental variables such as location, seasonality, and climatic conditions, which warrant further investigation. Equally important is the identification of animal hosts that serve as blood sources and potentially transmit SFTSV to ticks. Understanding these ecological interactions is critical for developing comprehensive strategies to mitigate SFTS risk. Serum samples from wild animals and pets, provided by the Livestock Hygiene Center and the Nagasaki Prefecture Veterinary Medical Association, will be analyzed for SFTSV-reactive antibodies to identify key reservoir species in the region.

4. Materials and Methods

4.1. Data Source

In Japan, SFTS is designated as a Class 4 infectious disease under the Infectious Disease Control Act. Healthcare providers are mandated to promptly notify the nearest public health centre upon diagnosis. The NPIEPH and Nagasaki City Health and Environment Testing Laboratory compile reports from local hospitals and public health centres within Nagasaki Prefecture and submit these data to the Ministry of Health, Labour, and Welfare. Conversely, the reporting of zoonotic SFTS cases is not legally mandated in Japan. The data presented in this study were obtained through collaboration with the NPIEPH and local hospitals.

4.2. Specimens

Between April and May 2024, four feline cases (cats 1–4) and four human cases (humans 5–8) were identified in the Goto Islands. Feline blood and swab specimens were collected at Matsumoto Veterinary Clinic, and human specimens were collected at Goto Chuou Hospital using standard procedures. The collected samples were refrigerated and transported to NPIEPH via refrigerated courier. Subsequently, all samples were transferred to the Institute of Tropical Medicine, Nagasaki University, for comprehensive testing. To preserve sample integrity, all specimens were stored at -80°C with minimized freeze–thaw cycles. RNA was extracted from the samples using the QIAamp Viral RNA Kit (QIAGEN, Tokyo, Japan).

4.3. SFTS Reverse Transcription-Quantitative PCR

RT-qPCR was performed using the One Step PrimeScript™ RT-PCR Kit (Perfect Time; Takara Bio, Shiga, Japan) with the forward primer 5'-TGTCAGAGTGGTCCAGGATT-3', reverse primer 5'-ACCTTGICTCCTTCAGCTTCT-3, and probe FAM-TGGAGTTTGGTGAGCAGCAGCAGC-BHQ1. The reaction master mix included 5 µL of 2× One Step RT-PCR Buffer II, 0.2 µL of TaKaRa Ex Taq HS, 0.2 µL of PrimeScript RT Enzyme Mix II, 0.5 µL of SFTSV S-segment forward primer, 0.5 µL of SFTSV S-segment reverse primer, 0.2 µL of SFTSV S-segment probe, and 0.2 µL of ROX Reference Dye II. For each of the eight samples, 6.8 µL of the reaction master mix, 2.5 µL of sample, and 3.8 µL of ultrapure water were used. Thermal cycling conditions were 42 °C for 5 min, 95 °C for 10 min for one cycle, followed by 40 cycles of 95 °C for 5 s and 60 °C for 34 s.

4.4. Primer Design for Amplicon Sequencing

FASTA-format sequences corresponding to the L, M, and S segments of SFTSV were retrieved from the NCBI database to construct multiple sequence datasets. Duplicate sequences were eliminated using Cluster Database at High Identity with Tolerance (CD-HIT) (v.4.8.1; <https://github.com/weizhongli/cdhit/releases>; accessed on 20 July 2024) [33,34], and the remaining sequences were aligned using Multiple Alignment using Fast Fourier Transform (MAFFT) (v.7.490; <https://mafft.cbrc.jp/alignment/software/>; accessed on 20 July 2024) [35]. Aligned sequences were used to generate consensus sequences with Jalview (v.2.11.3.3; <https://www.jalview.org/>; accessed on 10 July 2024) [36]. Primers were initially designed to amplify approximately 400 bp fragments from the consensus sequences (Supplementary Table S3). Subsequently, primer sequences were refined based on initial sequencing data to improve specificity and efficiency (Supplementary Tables S3 and S4).

4.5. Next-Generation Sequencing and Analysis

Reverse transcription multiplex PCR was performed for amplicon sequencing. DNA libraries were prepared using the QIAseq FX DNA Library Kit (Qiagen, Hilden, Germany) according to the manufacturer's instructions. Following adapter ligation, library quality and concentration were assessed using a Qubit 2.0 Fluorometer (Invitrogen, Waltham, MA, USA) and a Bioanalyzer High-Sensitivity DNA Analysis system (Agilent Technologies, Santa Clara, CA, USA). Sequencing was performed on an Illumina MiSeq platform (Illumina, San Diego, CA, USA) with paired-end reads of 150 bp using the MiSeq Reagent Kit v2 for the initial run and the MiSeq Reagent Micro Kit v2 for subsequent runs. FASTQ files underwent quality control using FASTQC (v.0.11.9; <https://www.bioinformatics.babraham.ac.uk/index.html>; accessed on 7 September 2024) [37] and FASTP (v.0.23.4; <https://github.com/OpenGene/fastp>; accessed on 8 October 2024). High-quality reads were mapped to the reference sequence of the SFTSV strain YG1 (GenBank accession numbers AB817979, AB817987, and AB817995) using the Burrows–Wheeler Aligner (BWA) (v.0.7.17-r1188; <https://github.com/sghignone/bwa>; accessed on 16 September 2024) [38]. Consensus sequences were generated using SAMtools (v.1.20; <https://www.htslib.org/>; accessed on 24 September 2024) [39]. Sequence data were deposited in the DNA Data Bank of Japan (accession numbers LC864283–LC864306).

4.6. Phylogenetic Analysis

Consensus sequences derived from the eight samples were aligned with previously reported international sequences, including those from Nagasaki, using MAFFT (v.7.490) [35]. Phylogenetic analysis was conducted using IQ-TREE 2 (v.2.0.7; <https://github.com/iqtree/iqtree2>; accessed on 23 July 2024) [40] with the maximum likelihood method and 1000 bootstrap replicates to assess node support.

4.7. Haplotype Network Analysis

Haplotype network analysis is a powerful approach for elucidating the molecular epidemiology and phylogeographic relationships of infectious disease outbreaks in humans. We performed haplotype network analysis on eight viral genomes obtained from our samples, together with six previously reported SFTSV strains from Nagasaki, to investigate potential transmission pathways. Networks were constructed using Population Analysis with Reticulate Trees (PopART) (v.1.7; <https://popart.maths.otago.ac.nz/>; accessed on 17 November 2024) [41,42] with the median-joining algorithm.

5. Conclusions

A cluster outbreak of SFTS occurred in Nagasaki Prefecture, affecting both cats and humans. High lethality rates were observed, particularly among cats. Sequencing of the SFTSV genome revealed complex transmission dynamics, with no clear correlation between amino acid substitutions and virulence. Study limitations included the inability to collect tick samples promptly, which constrained vector analysis. To address future outbreaks, a multidisciplinary One Health approach was initiated, emphasizing continued tick surveillance and identification of wildlife reservoirs to improve understanding of SFTS dynamics and associated risks.

Supplementary Materials: The following supporting information can be downloaded at: <https://www.mdpi.com/article/10.3390/ijms27041702/s1>.

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Informed Consent Statement: Under Japan's Infectious Diseases Control Law, sample collection and reporting must be conducted in anonymized form. The National Institute of Infectious Diseases publicly releases the latest data on its website every three months. All pet samples have obtained informed consent from the owners, and the hospital has provided an informed consent certificate.

Data Availability Statement: The data presented in this study are openly available in NCBI (<https://www.ncbi.nlm.nih.gov/nucleotide/>, accessed on 27 January 2026).

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Abbreviations

The following abbreviations are used in this manuscript:

SFTS	Severe Fever with Thrombocytopenia Syndrome
SFTSV	Severe Fever with Thrombocytopenia Syndrome virus
RNA	Ribo Nucleic Acid
DNA	Deoxyribonucleic Acid
RT-qPCR	Reverse Transcription quantitative Polymerase Chain Reaction
NPIEPH	Nagasaki Prefectural Institute of Environment and Public Health
CD-HIT	Cluster Database at High Identity with Tolerance
MAFFT	Multiple Alignment using Fast Fourier Transform
BWA	Burrows-Wheeler Aligner
PopArt	Population Analysis with Reticulate Trees

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