



Research Article

The first discovery of severe fever with thrombocytopenia virus in the center of metropolitan Beijing, China

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ABSTRACT

Severe fever with thrombocytopenia virus (SFTSV), an emerging tick-borne bandavirus, poses a significant public health threat in rural China. Since 2021, an increase of local cases has been noted in the rural-urban fringe of Beijing. This study aimed to assess the formation of natural foci in urban areas by conducting a field survey of ticks and hedgehogs from the second to fifth ring roads of Beijing. Our survey revealed a diverse tick population in city parks, including the major SFTSV vector, *Haemaphysalis longicornis*. Parthenogenetic *H. longicornis*, known for its role in the rapid spread of SFTSV, was identified in key locations such as Beihai Park and Taoranting Park, near the Forbidden City. Notably, high SFTSV seroprevalence and RNA prevalence were found in hedgehogs and parasitic ticks in the center of Beijing. Phylogenetic analyses of SFTSV RNA and mitochondrial sequences of parthenogenetic *H. longicornis* ticks revealed the existence of diverse lineages of SFTSV and *H. longicornis* ticks within Beijing, suggesting multiple invasion events happened. These findings reveal the circulation of SFTSV in central Beijing, highlighting the need for urgent attention and enhanced surveillance measures.

1. Introduction

Severe fever with thrombocytopenia syndrome virus (SFTSV) emerged as a novel bandavirus in 2009, initially discovered in the Dabie Mountains at the convergence of Henan, Anhui, and Hubei provinces of China (Yu et al., 2011). Subsequently, it was reported in South Korea (Yun et al., 2014), Japan (Takahashi et al., 2014), Vietnam (Tran et al., 2019), Myanmar (Win et al., 2020), Pakistan (Zohaib et al., 2020), and Thailand (Rattanakomol et al., 2022). SFTSV infection elicits severe symptoms in patients, encompassing fever, gastrointestinal manifestations, thrombocytopenia, and leukopenia, with reported fatality rates ranging from 6% to 30% across various studies (Yu et al., 2011; Liu Q. et al., 2014; Liu S. et al., 2014).

As a tick-borne pathogen, SFTSV is primarily transmitted by the tick species *Haemaphysalis longicornis*, with *H. flava* identified as a potential vector (Fang et al., 2023). Recently, there has been a growing number of reports documenting human-to-human and animal-to-human transmission

via close contact (Gai et al., 2012; Kida et al., 2019; Yamanaka et al., 2020; Wu et al., 2022; Sun et al., 2024), a phenomenon corroborated by ferret animal models (Yu et al., 2019). *H. longicornis* is a unique tick species with both parthenogenetic and bisexual populations (Oliver, 1971). Karyotype analysis shows that parthenogenetic ticks are triploid, while bisexual ticks are diploid (Hoogstraal et al., 1968). Although the two populations are morphologically similar, parthenogenetic *H. longicornis* are slightly larger on average. Notably, parthenogenetic *H. longicornis* produce approximately twice as many offspring as their bisexual counterparts. In our previous study, we discovered that parthenogenetic ticks have a conserved deletion of a single base, T, at nucleotide position 8497 in the untranslated region of the mitochondrial genome, which allows us to easily distinguish between the two populations (Zhang et al., 2022; Zhao et al., 2024). Additionally, parthenogenetic *H. longicornis* exhibit similar susceptibility to SFTSV infection and comparable transmission capabilities to those of the bisexual population (Zhao et al., 2024). The parthenogenetic population spreads much faster and more widely than the bisexual population, and is strongly

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correlated with the geographic distribution of SFTSV-endemic areas, suggesting its important role in the rapid spread of SFTSV (Zhang et al., 2022). Meanwhile, bird migration significantly contributes to the long-distance dispersal of both *H. longicornis* and SFTSV (Yun et al., 2015; Shi et al., 2017; Zhang et al., 2022). High seroprevalence rates have been observed across diverse wild and domestic animal species, including sheep (69.5%), cattle (60.4%), dogs (37.9%), chickens (47.4%), as well as shrews, rodents, and hedgehogs (Chen et al., 2019). Among the investigated mammalian hosts, hedgehogs emerge as prominent wildlife amplifying hosts capable of sustaining SFTSV transmission via *H. longicornis* bites (Zhang et al., 2023).

Beijing, with a history spanning 3,000 years and having served as China's capital for 800 years since the Jin Dynasty in AD 1151, presents a distinctive urban landscape. The cityscape ranges from the iconic Forbidden City at its center to the surrounding periphery, which is encircled by a series of expressways, namely the 2nd, 3rd, 4th, 5th, and 6th ring roads. Within the 2nd ring road lies the historic core of the Ming and Qing dynasties, established in AD 1420. Urban Beijing comprises six districts, namely Dongcheng, Xicheng, Haidian, Chaoyang, Fengtai, and Shijingshan, with the majority situated within the 5th ring road. Part of areas between the 4th and 5th ring roads, and those between the 5th and 6th ring roads constitute the rural-urban fringe. Additionally, Beijing encompasses ten satellite cities including Shunyi, Mentougou, Pinggu, Tongzhou, Miyun, Huairou, Yanqing, Changping, Fangshan, and Daxing, predominantly located beyond the 5th ring road (Supplementary Fig. S1).

Urban Beijing, one of the most densely populated areas in the world, accommodates approximately 7,943 individuals per square kilometer, with densities exceeding 19,000 and 20,000 per square kilometer within the 2nd ring road and between the 2nd and 3rd ring roads, respectively (Beijing 2022 Year Book). Despite its predominantly flat terrain, urban Beijing is surrounded by mountainous regions to the west, north, and east, with elevations ranging from 1,000 to 1,500 m. Positioned along the migration route between East Asia and Australia, Beijing's avian biodiversity has flourished alongside the expansion of urban green spaces, with 508 bird species documented in 2023.

The first local human case of SFTS in Beijing was reported in October 2021, involving a 69-year-old resident in Longquanwu Village, Mentougou District (Sun et al., 2021; Yulan et al., 2023). Subsequent natural foci of SFTSV were identified in Longquanwu Village, Mentougou District, and Wanwanshu, Shunyi District in 2023 (Zhang et al., 2023). In light of recent observations suggesting the proliferation of hedgehogs and *H. longicornis* ticks in urban environments, including Beijing, due to rapid urbanization and ecological conservation efforts, we sought to investigate the potential establishment of SFTSV natural foci within metropolitan areas.

2. Methods and materials

2.1. Field survey

Hedgehogs were captured in parks and gardens throughout Beijing at night (7–9 p.m.), between July and August 2023. The density of hedgehogs was calculated by dividing number of captured animals by the area searched (no. of animals per km²). Following anesthesia, approximately 0.5 mL of blood was drawn from the heart of each hedgehog, after which ticks were collected using forceps. Additionally, ticks in grassy areas were also collected using flag-dragging method at several locations. All ticks were taxonomically identified under a dissecting microscope based on their morphological characteristics. Blood was separated into serum and blood cells and kept at –80 °C. The number of stray cats was obtained by interviewing the volunteers feeding the cats (Supplementary Table S1).

2.2. Phylogenetic analysis of ticks

One leg from each tick was removed for analysis. Parthenogenetic ticks were determined by the deletion of a single base T at nucleotide position 8497 in the untranslated region of the mitochondrial genome

(Zhang et al., 2022). Phylogenetic analysis was performed using the full-length mitochondrial genomes. Tick DNA was extracted using the MightyPrep reagent for DNA Kit (Takara, Japan) according to the manufacturer's instructions. The mitochondrial DNA was sequenced by next generation sequencing (Tsingke Biotech, China) and deposited in GenBank (Accession number: PP376089–PP376092 and PP386058). Mitochondrial genomes of *H. longicornis* ticks from SFTS endemic areas were included in Supplementary Table S2.

The maximum likelihood tree was constructed by using the maximum likelihood method (MEGA-X), with the bootstrap value set at 1000. For Bayesian-inference (BI) method, Best-fit models for BI method were selected by MrModeltest ver. 2.3; GTR + I + G model was chosen for all datasets according to the Akaike Information Criterion (AIC). The Markov chain Monte Carlo (MCMC) algorithm was run up to 1,000, 000 generations. Samples were taken every 1,000 generations, with a burn-in set to 25%. The average split frequencies between the runs were less than 1%. The two final trees were viewed and edited by FigTree ver. 1.4.3 and Photoshop CC 2018.

2.3. RNA extraction and amplification of SFTSV RNA by nested PCR

Total RNA was extracted from pooled tick homogenates and hedgehog blood cells utilizing either TRIzol reagent (Thermo Fisher Scientific, USA) or the RNeasy kit (Qiagen, Germany) in accordance with the respective manufacturer's protocols. The RNA samples were then reverse transcribed employing a One-Step SYBR PrimerScript reverse transcription (RT)-PCR kit (TaKaRa, Japan). Nested PCR conditions were as follows: initial denaturation at 95 °C for 3 min, followed by denaturation at 95 °C for 10 s, 40 cycles of amplification at 95 °C for 5 s, and annealing/extension at 60 °C for 30 s. Primer sequences utilized are detailed in Supplementary Table S3. The PCR products were sequenced by Sanger method and deposited in GenBase (Accession number C_AA059120.1–C_AA059155.1). The SFTSV RNA positive rate was calculated by dividing the number of positive PCR results by the total number of samples tested. SFTSV sequences retrieved from prior studies were acquired from GenBank (Yoshikawa et al., 2015; Shi et al., 2017) (Supplementary Table S4). Phylogenetic trees were constructed utilizing the maximum likelihood method within the MEGA program. The robustness of the resulting tree topologies was assessed via 1000 bootstrap replications to ascertain confidence levels.

2.4. Neutralizing assay

The neutralization titers of the sera samples obtained from hedgehogs and patients was evaluated using Focus Reduction Neutralization Test (FRNT). In brief, a fixed amount of rVSV-GFP-SFTSV AH12 strain (~1000 FFU) was mixed with heat-inactivated sera samples, which were serially diluted five-fold from 1:20 to 1:2500. After a 30-min incubation at room temperature, the virus-serum mixtures were added onto Vero cells in 96-well plates. The plates were then incubated at 37 °C for 2 h to allow virus entry and infection. Subsequently, the supernatants were replaced with fresh DMEM containing 2% FBS and 20 mM NH₄Cl, and the plates were further incubated at 28 °C for 24 h. The number of GFP-positive cells was counted and neutralization titers were calculated using the Reed-Muench method. The cut-off value of 30 was determined by naïve hedgehog samples.

3. Results

3.1. Case reports of three local SFTS patients

In 2023, six local cases of SFTS were reported in Beijing. Four of these cases were from Beishiqu, Houjiazhuang, and Donglujiao Villages in Pinggu District, one from Baixi Village in Fengtai District, and one from Gaoying Village in Tongzhou District (Chinese Center for Disease Control and Prevention) (Supplementary Fig. S1). Among these, three patients,

aged 50 to 61, from Beishiqu, Houjiazhuang, and Gaoying were admitted to Beijing Ditan Hospital. All three patients tested positive for SFTSV by real-time PCR, with two having a history of tick bites. Common symptoms included fever, altered consciousness, and slurred speech, accompanied by leukopenia and thrombocytopenia. Additionally, varying degrees of organ failure, including encephalitis, cardiac damage, liver injury, renal impairment, and elevated pancreatic enzymes, were observed. Treatment with favipiravir antiviral medication, dexamethasone, and supportive care for two weeks led to the recovery and subsequent discharge of all patients. Notably, a near-complete SFTSV genome was identified from the serum of the Gaoying patient, while only short segments were obtained from the sera of the other two patients.

3.2. Diversity of ticks in Beijing

All reported human SFTS cases thus far have been localized in the rural-urban fringe of Beijing (Supplementary Fig. S1). To assess the potential establishment of natural SFTSV foci in urban areas, a field survey

was conducted from July to August 2023. Host-seeking ticks were collected from vegetation at 6 sites, while parasitic ticks were collected from hedgehogs at 21 sites, covering patient residences as well as major parks and universities within the 5th ring road (Fig. 1, Table 1 and Supplementary Fig. S2). Analysis revealed that in the rural-urban fringe areas outside the 5th ring road, *H. longicornis* was the dominant tick species, followed by *H. flava*, *Rhipicephalus sanguineus*, and *Dermacentor* spp. Parthenogenetic *H. longicornis* were detected at Beijing Wildlife Rescue and Rehabilitation Center, Gaoying Village, and Beishiqu Village, with the latter two locations in close proximity to patient residences. Contrary to previous assumptions, urban areas, particularly within the 4th ring road, exhibited high diversity and abundance of ticks, predominantly *R. sanguineus*, followed by *H. flava*, with few *Dermacentor* spp. and *H. longicornis* (Fig. 1). The total tick infestation on hedgehogs reached as high as 130 per animal, with no significant difference observed from the 2nd ring to the 5th ring road (Table 1). In urban areas within 5th ring road, *H. longicornis* ticks were detected in Laoshan Park, Olympic Forest Park, Wanliu, Beihai Park, and Taoranting Park, with

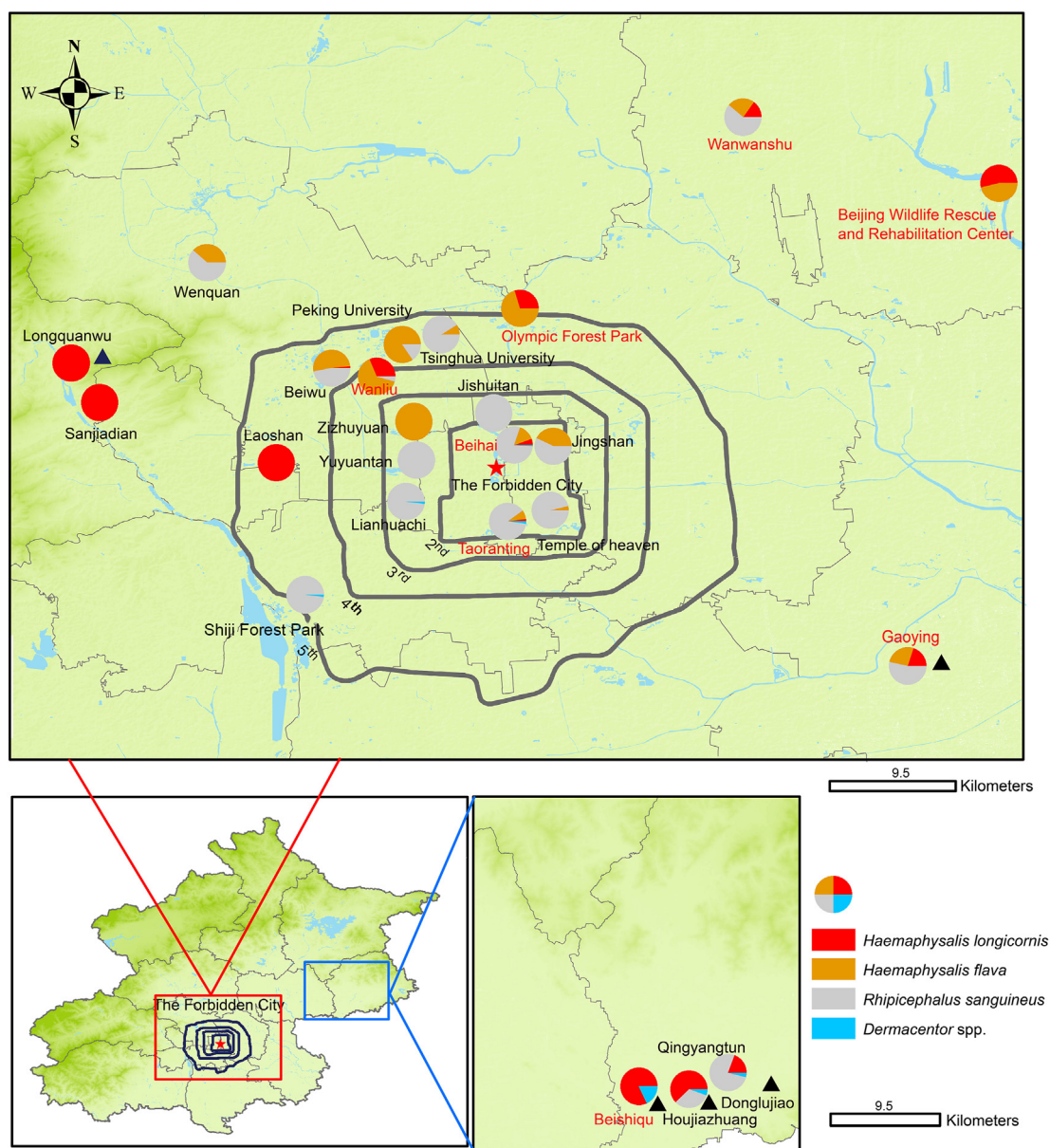


Fig. 1. Tick diversity in Beijing. The map was created by ArcMap 10.8 (ArcGIS Enterprise, ESRI, Redlands, CA, USA). The pie chart illustrates tick species distribution, with red font denoting sampling points containing parthenogenetic *H. longicornis*, and black triangles indicating locations of confirmed SFTS cases. Ring roads are delineated in grey.

Table 1
Epidemiological analysis of ticks and hedgehogs.

Location	Hedgehog SFTSV RNA Positive Rate	Hedgehog SFTSV antibody Positive Rate	Tick no. per hedgehog (average)	SFTSV RNA Positive Rate in hedgehog infested ticks ^a	SFTSV RNA in ticks on Vegetation ^b
< 2nd ring					
Jingshan	50% (1/2)	50% (1/2)	50	50% (1/2)	NA
Beihai	75% (3/4)	75% (3/4)	108	25% (1/4)	NA
Taoranting	NA	25% (1/4)	76	NA	NA
Temple of heaven	40% (2/5)	80% (4/5)	130	0 (0/5)	NA
2nd–3rd ring					
Zizhuyuan	100% (2/2)	40% (2/5)	40	50% (1/2)	NA
Jishuitan	100% (2/2)	50% (1/2)	43	NA	NA
Lianhuachi	50% (1/2)	0 (0/1)	102	NA	NA
Yuyuantan	0 (0/1)	0 (0/1)	20	0 (0/1)	NA
3rd–4th ring					
Wanliu	75% (3/4)	25% (1/4)	25	25% (1/4)	NA
4th–5th ring					
Laoshan	NA	NA	25	NA	–
Olympic Forest Park	0 (0/1)	100% (2/2)	105	0 (0/1)	–
Peking Univ.	0 (0/1)	NA	26	0 (0/1)	NA
Tsinghua Univ.	0 (0/2)	0 (0/1)	23	0 (0/2)	NA
Beiwu	0 (0/2)	0 (0/2)	32	50% (1/2)	+
Shiji Forest Park	50% (1/2)	100% (2/2)	112	NA	NA
> 5th ring					
Beishiqu	NA	100% (1/1)	63	NA	NA
Houjiazhuang	50% (2/4)	100% (2/2)	74	100% (4/4)	NA
Qingyangtun	0 (0/2)	50% (1/2)	66	50% (1/2)	NA
Wenquan	33% (1/3)	33% (1/3)	52	NA	NA
Gaoying	0 (0/2)	67% (2/3)	4	0 (0/2)	+
Longquanwu	20% (1/5)	80% (4/5)	60	20% (1/5)	NA
BWRRC	NA	NA	NA	NA	+

+ , positive; – , negative; NA, not available; No., number; Univ., university; BWRRC, Beijing Wildlife Rescue and Rehabilitation Center.

^a Hedgehog-parasitic ticks.

^b Host-seeking ticks.

numbers of 4, 18, 22, 10, and 2, respectively. Among them, parthenogenetic *H. longicornis* was identified in Olympic Forest Park, Wanliu, Beihai Park, and Taoranting Park, the latter two located inside the 2nd ring road adjacent to the Forbidden City (Fig. 1). Phylogenetic analysis of whole mitochondrial sequences of the parthenogenetic ticks revealed three distinct clusters, namely Beishiqu, Wanwanshu/Olympic Forest Park/Beijing Wildlife Rescue and Rehabilitation Center, and Gaoying/Beihai/Taoranting, indicating the invasion of at least three strains of parthenogenetic *H. longicornis* into Beijing (Fig. 2).

3.3. SFTSV prevalence in ticks and hedgehogs

A total of 50 hedgehogs from 18 locations spanning the 2nd to 5th ring road, as well as from patient residences, were assayed for SFTSV seroprevalence against the recombinant SFTSV AH12 strain. Of these, 28 hedgehogs from 15 locations tested positive for SFTSV-neutralizing antibodies, with the highest titer of about 1200 detected at Houjiazhuang Village in Pinggu District, adjacent to a patient's residence (Fig. 3). SFTSV-neutralizing antibodies were also detected in hedgehogs within the 5th ring road, with titers ranging from 30 to 250. Notably, positive hedgehogs were identified in all four locations within the 2nd ring road (Table 1 and Fig. 3).

Subsequently, the SFTSV genome was amplified from host-seeking ticks, hedgehog-parasitic ticks, and hedgehog blood samples using RT-PCR. Three out of five pools of host-seeking ticks tested SFTSV positive across the 2nd to 5th ring roads of urban Beijing. Among 37 pooled parasitic tick samples, 11 pools were positive for SFTSV RNA. Additionally, SFTSV RNA was amplified from 19 of the 46 hedgehog blood samples tested, with six positive hedgehogs identified from three locations within the 2nd ring road (Table 1).

All amplified SFTSV samples were sequenced using the Sanger method. Two nearly full-length genomes were obtained from parasitic

ticks in Houjiazhuang Village and Beishiqu Village in Pinggu District, near the patient residences. Phylogenetic analysis revealed that these two SFTSV isolates, along with the one from the Gaoying patient, belonged to the C2 lineage, based on the sequences of M and L segments (Fig. 4). Only partial sequences of S (~200bp), M and L segments (~800 bp) were obtained from samples collected within the 5th ring road. Alignment



Fig. 2. Phylogenetic analysis of the *H. longicornis* parthenogenetic population. Maximum likelihood tree was established with the mitochondrial genomes of *H. longicornis* collected in Beijing (red circle collected in 2023, red triangle collected in 2021) and from SFTS endemic areas. Constructed by MEGA-X with the bootstrap value set at 1000.

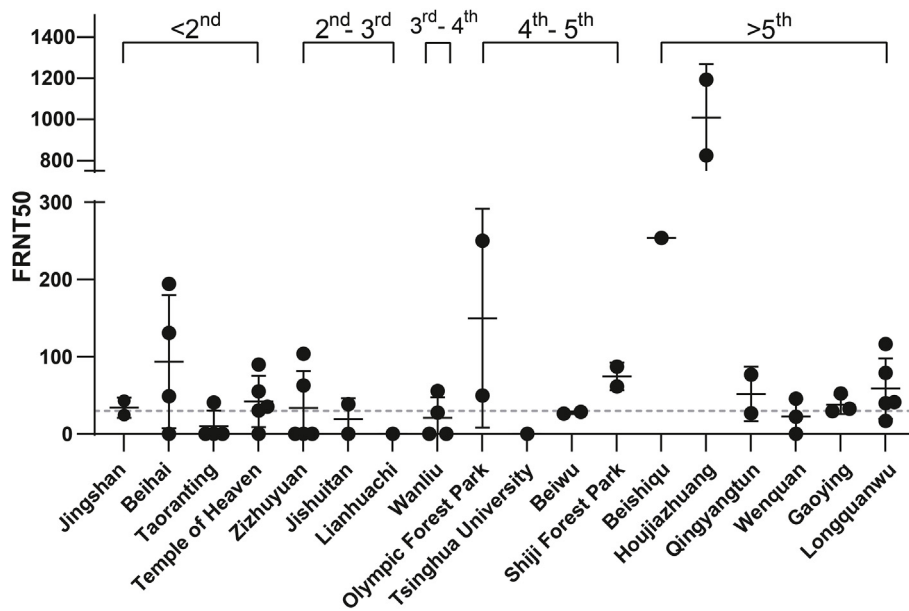


Fig. 3. Neutralizing antibody titers (FRNT50) in hedgehogs from various locations in Beijing. Neutralizing antibody titers against rVSV-GFP-SFTSV AH12 strain in hedgehogs captured at specified locations in Beijing are presented. The dashed line indicates the cutoff value set at 30.

with partial sequences of M or L segments indicated that all SFTSV isolated within the 5th ring road belonged to the C2 lineage (Fig. 4A and C). Surprisingly, the L segment sequence amplified from a hedgehog in Wenquan Village, Haidian District, located in the rural-urban fringe area, belonged to the C4 lineage (Fig. 1 and 4B). These findings suggest the existence of more than one SFTSV lineages in Beijing.

4. Discussion

Our previous research on the vectors and hosts of SFTSV led to two hypotheses. First, parthenogenetic *H. longicornis* ticks are strongly associated with SFTSV outbreaks and can serve as early indicators of SFTSV emergence in new areas (Zhang et al., 2022). Second, SFTSV

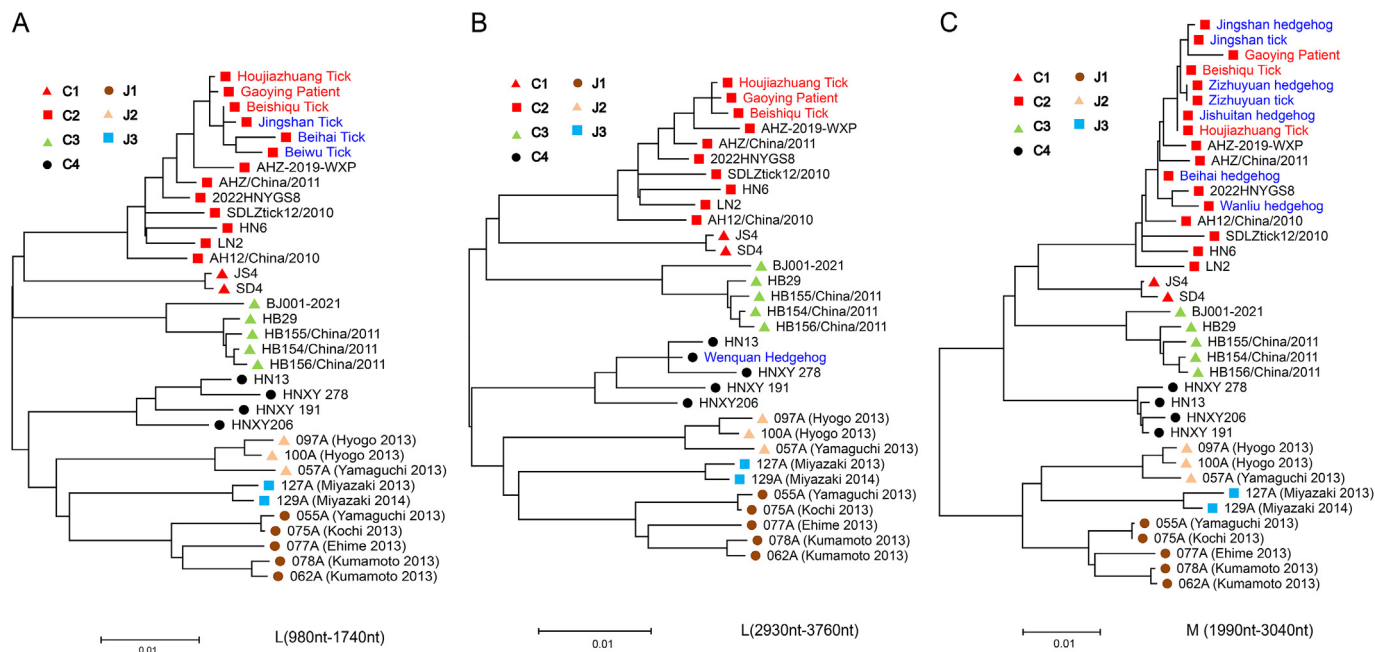


Fig. 4. Phylogenetic analysis of SFTSV isolates. Maximum likelihood trees were constructed based on L (980nt–1740nt, A), L (2930nt–3760nt, B) and M (1990nt–3040nt, C) segments of SFTSV isolates, respectively. SFTSV lineages are represented by colors and shapes. Red font signifies near-complete SFTSV genome sequences, while blue font indicates partial sequences of the SFTSV genome. The sequences of SFTSV isolates marked in black were acquired from GenBank, the accession numbers list in Supplementary Table S4.

transmission can be sustained between *H. longicornis* ticks and hedgehogs in urban areas across China (Zhao et al., 2022; Zhang et al., 2023).

Despite the rapid spread of SFTSV across China and Asia, no local cases were reported in Beijing following its initial discovery in central China in 2009. However, in 2019, parthenogenetic *H. longicornis* ticks were first identified in two rural-urban locations: Wanwanshu in Shunyi District and Olympic Forest Park in Chaoyang District (Zhang et al., 2022). Subsequently, SFTSV RNA was detected in *H. longicornis* collected from Wanwanshu in the spring of 2021. In the fall of 2021, the first SFTS patient was diagnosed in Longquanwu Village, Mentougou District, located 26 miles away from Wanwanshu (Zhang et al., 2023). In 2023, six human cases were reported: four in close proximity within three villages in Pinggu District, one in Gaoying Village, Tongzhou District, and one in Baixi Village, Fengtai District. Our field survey confirmed the presence of parthenogenetic *H. longicornis* ticks in Beshiqu and Gaoying Villages, further supporting their association with SFTSV transmission. Additionally, parthenogenetic ticks were detected within the 4th ring road in Wanliu, Beihai Park, and Taoranting Park, albeit in low abundance, suggesting that urban SFTSV circulation may still be in its early stages.

Beijing is highly urbanized, with population densities similar to Manhattan, particularly within the 4th ring road. However, strict ecological conservation efforts and increased greening rates have created an environment conducive to tick infestations. In addition to the common tick species *R. sanguineus*, *H. longicornis*, *H. flava*, and *Dermacentor* spp. are also widely distributed in Beijing. The most common mammals in the city are Amur hedgehogs and yellow weasels (*Mustela sibirica*). However, the tick-infestation rate and SFTSV seroprevalence in yellow weasels are low (Zhao et al., 2022). Stray cats are also present in parks and communities, albeit at lower densities compared to hedgehogs (Supplementary Table S1). Hedgehogs thus emerge as promising sentinel animals for SFTSV surveillance due to their high susceptibility to infection and their propensity to harbor ticks, including *H. longicornis* and *H. flava*. The average tick infestation rate on hedgehogs exceeded 100 ticks per animal in 33% of parks surveyed, indicating a high tick density in urban areas (Zhao et al., 2022). Our survey revealed a high prevalence of SFTSV RNA and seropositivity in hedgehogs, as well as SFTSV RNA prevalence in ticks infesting them, highlighting the potential role of hedgehogs in SFTSV maintenance. Moreover, the high density and diversity of birds in Beijing, including the spotted dove (*Spilopelia chinensis*), known for robust SFTSV viremia upon infection, may facilitate local SFTSV spread and tick dispersal (Li et al., 2019).

We propose that parthenogenetic *H. longicornis* and SFTSV were introduced into Beijing via migratory birds, given the city's location on the East Asian-Australasian Flyway and the presence of over 500 bird species (Zhang et al., 2023). Phylogenetic analysis of parthenogenetic tick mitochondrial genomes revealed close genetic relationships between ticks from Beijing Wildlife Rescue and Rehabilitation Center, Wanwanshu, and Olympic Forest Park, all detected in 2019 (Zhang et al., 2022). However, ticks collected from Beishiqu, Pinggu District and Gaoying, Tongzhou District, represent two new lineages. The proximity of the Beihai and Taoranting strains within the 2nd ring road to the Gaoying strain near the 6th ring road suggests potential tick spread from the city's periphery to its center. On the other hand, phylogenetic analysis of SFTSV sequences indicated the existence of both C2 and C4 lineages in Beijing, implying multiple SFTSV introduction events.

Notably, no SFTS cases have been reported within the 4th ring road thus far. This may be due to the low abundance of *H. longicornis* in the city and the fact that near-complete SFTSV genomes have been amplified from ticks near patients' residences in the rural-urban fringe, while only partial sequences have been obtained from urban areas. Additionally, the implementation of the "Keep off the grass" policy has significantly reduced tick exposure among city residents. However, ongoing monitoring of SFTSV seroprevalence among gardeners is still warranted. Our observations also revealed hedgehogs feeding on food provided for stray

cats, raising concerns regarding potential cat-to-human transmission of SFTSV, as reported in Japan and China (Yamanaka et al., 2020; Zhang et al., 2024). Therefore, caution is advised regarding contact with cats.

5. Conclusions

In conclusion, we are the first to discover the SFTSV in hedgehogs and ticks in central Beijing. The urban circulation of SFTSV is sustained between hedgehogs and *Haemaphysalis longicornis*, with multiple lineages present in the city's urban areas. Our findings highlight the establishment of urban SFTSV circulation in Beijing, emphasizing the need for urgent attention and comprehensive control measures.

Data availability

All the data generated during the current study are included in the manuscript and supplementary materials. The mitochondrial DNA sequences of ticks were deposited in GenBank (Accession number: PP376089–PP376092 and PP386058) and ScienceDB (DOI: 10.57760/sciencedb.16362). SFTSV sequences from tick samples were deposited in GenBase (Accession number C_AA059120.1–C_AA059155.1) and ScienceDB (DOI: 10.57760/sciencedb.16362).

Ethics statement

All animal studies were carried out in strict accordance with the recommendations in the Guide for the Care and Use of Laboratory Animals of the Ministry of Science and Technology of the People's Republic of China. The protocols for animal studies were approved by the Committee on the Ethics of Animal Experiments of the Institute of Zoology, Chinese Academy of Sciences (Approval number: IOZ20180058). Human serum samples from SFTS patients were obtained from Beijing Ditan Hospital, Capital Medical University, Beijing, China. A written consent form was obtained from the patients before they participated in this study.

Author contributions

Fei Yuan: formal analysis, investigation, validation, visualization, writing - original draft, writing - review&editing. Lianglong Zhu: formal analysis, investigation, visualization, writing - original draft. Di Tian: investigation, resources, visualization, writing - original draft. Mengyu Xia: formal analysis, investigation, resources, visualization. Ming-hao Zheng: investigation, resources. Qing Zhang: investigation, resources. Tingyu Zhang: investigation, resources. Xing Zhang: investigation, project administration, resources, validation. Aihua Zheng: conceptualization, funding acquisition, investigation, project administration, resources, supervision, writing - review&editing.

Conflict of interest

The authors declare that they have no known competing financial interests or personal relationships that could have appeared to influence the work reported in this paper.

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Appendix A. Supplementary data

Supplementary data to this article can be found online at <https://doi.org/10.1016/j.virs.2024.11.002>.

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