



COMMENTARY

Northeastern China, a Hotspot for Tick-Borne Viral Diseases

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Abstract

Northeastern China has a high incidence of tick-borne diseases. Emerging and re-emerging tick-borne viral diseases pose a considerable threat to public health. To date, ten tick-borne viruses have been identified to cause disease in humans or animals in northeastern China. The complex diversity of tick-borne viral diseases in the region poses substantial diagnosis and treatment challenges, but also offers valuable opportunities to study the genetic evolution and transmission dynamics of tick-borne viruses.

Key words: Xue-Cheng virus, ticks, tick-borne viruses, nairoviruses, tick-borne diseases, China

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Emerging tick-borne diseases pose a growing public health risk [1]. In China, tick-borne diseases are widespread, and incidence rates are particularly high in the northeastern region. In January 2025, in the *New England Journal of Medicine*, Zhang and colleagues reported Xue-Cheng virus (XCV), a novel orthonairovirus associated with human febrile illness [2]. Through active surveillance of febrile patients with recent tick bites, the authors identified a group of patients in northeastern China.

According to the International Committee on Taxonomy of Viruses (ICTV, <https://ictv.global/taxonomy>), the family *Nairoviridae*, which belongs to the order *Harevirales* and class *Bunyaviricetes*, comprises eight genera. Tick-borne nairoviruses pose a considerable threat to human health [3]. Crimean-Congo hemorrhagic fever virus, a representative viral species, can cause hemorrhagic fever in humans, with fatality rates exceeding 30%, and is widely distributed across Africa, the Middle East, Asia, and Europe [4]. Other nairoviruses, such as Nairobi sheep disease virus, Tacheng tick virus 1, Songling

virus (SGLV), and Yezo virus (YEZV), can cause mild, severe, or fatal diseases in humans and animals [3]. The identification of XCV in patients further expands the known spectrum of pathogenic nairoviruses.

Over the past decade, advancements in next-generation sequencing have accelerated the discovery of tick-borne viruses and led to the identification of potential agents causing febrile illness in tick-bitten patients. In northeastern China, next-generation sequencing has identified several viruses associated with febrile illness, including Jingmen tick virus, Alongshan virus (ALSV), SGLV, Beiji nairovirus (BJNV), YEZV, and Wetland virus (WELV) [5–11]. Among these, SGLV, BJNV, YEZV, and WELV belong to the *Nairoviridae* family.

Other tick-borne nairoviruses identified in northeastern China, including Yanbian Nairo tick virus 1 (YBNTV-1), Ji'an nairovirus, Shanxi tick virus 2, Huangpi tick virus 1, and Yichun nairovirus, exhibit close phylogenetic relationships with known pathogenic viruses, thereby underscoring the potential

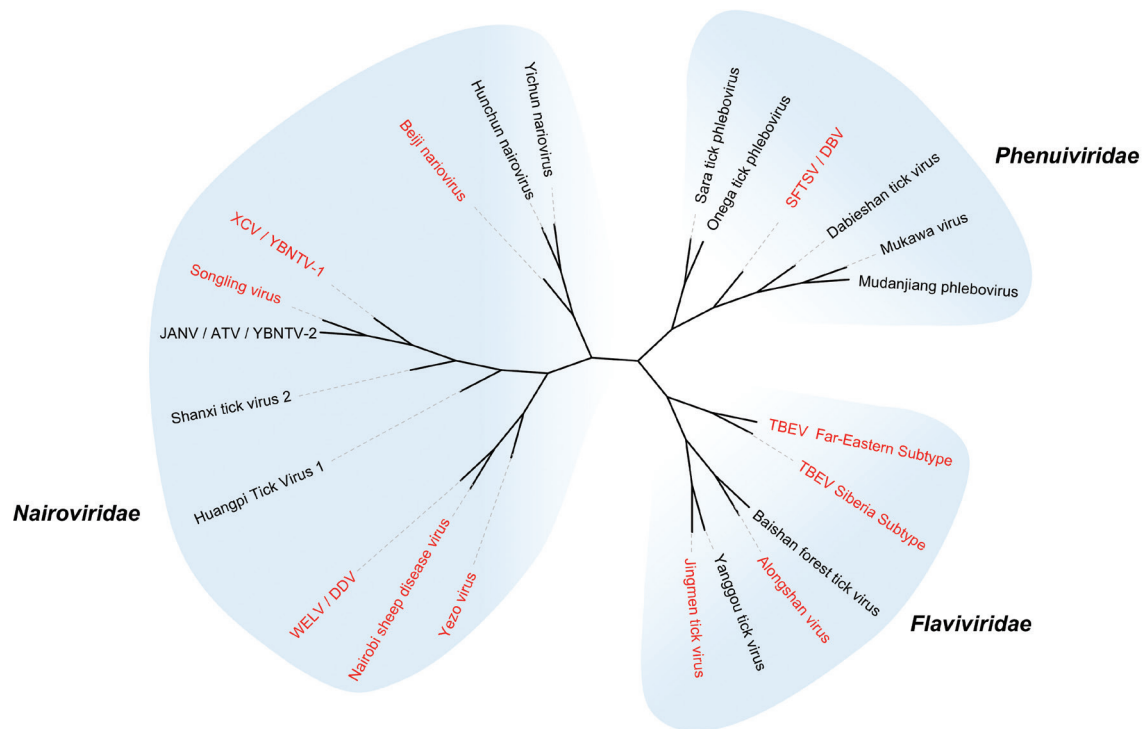


FIGURE 1 | Pathogenic and potentially pathogenic tick-borne viruses identified in northeastern China. Pathogenic tick-borne viruses are shown in red, and potentially pathogenic ones in black. A backslash indicates that the virus has an alternative name. Abbreviations: ATV, Antu virus; DBV, Dabie bandavirus; DDV, Dadong tick virus; JANV, Ji'an nairovirus; SFTSV, Severe fever with thrombocytopenia syndrome virus; TBEV, Tick-borne encephalitis virus; WELV, Wetland virus; XCV, Xue-Cheng virus; YBNTV-1, Yanbian Nairo tick virus 1; YBNTV-2, Yanbian Nairo tick virus 2.

health risks to humans and animals posed by these nairoviruses [12–15]. Notably, RNA-dependent RNA polymerase shares 92.9%–94.2% amino acid sequence identity between YBNTV-1 and XCV. According to the criteria for confirming a novel viral species, these two viruses should be classified as the same species [14].

To date, 10 pathogenic and at least 12 potentially pathogenic tick-borne viruses have been identified in northeastern China (Fig 1). The high diversity of tick-borne viral diseases poses significant clinical diagnostic challenges. The clinical manifestations of XCV infection range from nonspecific acute febrile illnesses to severe disease. As with other emerging viruses, such as ALSV, SGLV, BJNV, and YEZV, XCV lacks distinct clinical infection features and laboratory findings. Distinguishing infections on the basis of clinical symptoms alone is challenging, thus underscoring the need for the development of rapid molecular and serological diagnostic methods.

The key factors contributing to the high diversity of tick-borne viruses in northeastern China and making this region a hotspot for tick-borne diseases are concerning. First, the complex and diverse geographical environment that includes mountains, wetlands, and grasslands, along with many wild animals and grazing livestock, provides an ideal breeding habitat and abundant blood meals for ticks. Second, the geographical location of northeastern China is crucial for the spread of tick-borne viruses [15]. This region contains important stopover sites and natural

habitats for migratory birds in the East Asia/Australasia flyway.

Migratory birds play a crucial role in the dissemination of tick-borne viruses, because ticks can adhere to the birds and consequently achieve long-distance movement, thereby carrying the virus into northeastern China [16,17]. Moreover, northeastern China has a similar environment to Europe and the Russian Far East. The region is largely covered by coniferous-broadleaved mixed forests, which provide habitat for *Ixodes persulcatus* and *Ixodes ricinus*, and facilitate viral cross-transmission between these tick species. Some viruses vectored by *Ixodes persulcatus* in China, such as tick-borne encephalitis virus, YEZV, ALSV, and BJNV, have been found to originate from, or to be closely associated with, viruses identified in *Ixodes ricinus* ticks in Europe [18–20].

Finally, the robust tick-borne disease surveillance system in northeastern China has facilitated early detection of numerous pathogenic tick-borne viruses. Guided by a reverse microbial etiology strategy [21], Chinese researchers have actively assessed the pathogenic potential of identified tick-borne viruses in advance of their outbreaks, thus providing crucial data support for the rapid differential diagnosis and control of tick-borne viral diseases.

In summary, the discovery of numerous pathogenic and potentially pathogenic tick-borne viruses in northeastern China highlights the region's complex diversity of tick-borne viral diseases, which poses significant prevention and control challenges. However, limited research on the

pathogenic mechanisms of these newly identified viruses hinders progress in the development of vaccines and drugs for tick-borne diseases. Future studies should prioritize this area to provide a reliable basis for the prevention and treatment of tick-borne diseases.

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CONFLICTS OF INTEREST

The authors declare that there are no conflicts of interest.

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