

Ixodid ticks are recognized as key vectors of numerous zoonotic pathogens, yet their vector competency remains insufficiently understood in many regions. This research aimed to analyze findings from three significant studies to better understand the vector potential of ixodid ticks in Eastern Europe and Black Sea Region. By integrating field surveillance, molecular diagnostics and pathogen screening we assess the presence and diversity of potential pathogens within tick populations, identifying novel and known microorganisms of medical and veterinary importance.

Through the screening of over 1,800 ticks from 11 species, we identified orthonairoviruses, including **Sulina virus (SULV)** in *Ixodes ricinus* from Latvia (2.7% prevalence) and **Tacheng tick virus 1 (TCTV1)** in *Dermacentor reticulatus* from Poland (0.9%). Phylogenetic analyses revealed distinct clades of both viruses, indicating their geographic segregation and evolutionary divergence. Additionally, our surveillance confirmed the presence of **Tacheng tick virus 2 (TTV2)**, **Jingmen tick virus (JMTV)**, and **Haseki tick virus (HTV)**, further supporting the expansion of tick-borne viruses into Europe.

Parallel bacterial pathogen screening revealed high **Rickettsia** diversity, with *R. asiatica*, *R. raoultii*, *R. monacensis*, *R. helvetica*, *R. massiliae*, and *R. tillamookensis* detected across multiple tick species. Notably, *R. asiatica* was documented in Europe for the first time. Moreover, nanopore-based metagenomic sequencing (NS) enabled the detection of **Anaplasma phagocytophilum**, **Coxiella burnetii**, **Neoehrlichia mikurensis**, and co-infections with multiple bacterial taxa, underscoring the polymicrobial nature of tick-borne infections.

Our findings highlight the expanding diversity and geographic spread of both viral and bacterial tick-borne pathogens in Eastern Europe. The results reinforce the need for enhanced vector surveillance and diagnostic inclusion of these emerging pathogens in clinical settings. This study also demonstrates the power of metagenomic sequencing as a robust tool for the comprehensive detection and characterization of tick-associated microbes, providing critical insights into the evolving epidemiology of tick-borne diseases.