WEST NILE AT THE ONE HEALTH INTERFACE:
FROM GENOMIC SURVEILLANCE TO RNA PLATFORMS FOR RAPID RESPONSE – Review

Liliana Elena OLARIU JURCA[1], Daniela MOT[1], Florina POP[4], Cristian POP[4], Gabriela Ingrid NICOLAESCU[5], Adrian OLARIU JURCA[2], Ingrid DOLORES[2], Alexandra SIRMON[3]*

Corresponding author: Alexandra Sirmon, E-mail: alexandra.tudorica@umft.ro

[1] University of Life Sciences "King Mihai I" from Timișoara, Faculty of Bioengineering of Animal Resources, 300645, Calea Aradului, no. 119, Timișoara, Romania
[2] University of Life Sciences "King Mihai I" from Timișoara, Faculty of Veterinary Medicine, 300645, Calea Aradului, no. 119, Timișoara, Romania
[3] Victor Babeș University of Medicine and Pharmacy, Faculty of Medicine, Department of Epidemiology, 2 Eftimie Murgu Sq., 300041 Timișoara, Romania
[4] Politehnica University Timișoara, Faculty of Robotics, Artificial Intelligence and Autonomous Systems, Department of Mechatronics, 1 Mihai Viteazu Blvd., 300222 Timișoara, Romania
[5] University of Life Sciences "King Mihai I" from Timișoara, Faculty of Engineering and Applied Technologies, Timișoara, Romania

ABSTRACT

West Nile virus (WNV) remains a significant zoonotic threat, shaped by complex transmission cycles involving mosquito vectors, avian reservoirs, and incidental mammalian hosts. Its recurrent emergence, geographical expansion, and genetic diversity highlight the need for integrated surveillance systems capable of translating epidemiological and genomic information into timely public health action. Within the One Health framework, genomic surveillance can support the identification of circulating viral lineages, the investigation of viral introductions and evolutionary patterns, and the refinement of risk assessment. However, substantial gaps in geographical sampling, cross-sector data integration, and the translation of genomic findings into intervention strategies continue to limit its operational impact.

This critical review examines the interface between WNV genomic surveillance and emerging RNA-based technologies, with particular emphasis on the potential contribution of messenger RNA (mRNA) and self-amplifying RNA vaccine platforms to preparedness and rapid response. It critically evaluates the extent to which sequence-informed antigen design, modular platform development, and advances in RNA delivery could facilitate candidate vaccine development, while distinguishing WNV-specific experimental evidence from extrapolations based on other pathogens. Diagnostic applications, manufacturing constraints, immunological considerations, regulatory requirements, and implementation challenges are also considered.

Building on this evidence, the review proposes an integrated conceptual framework linking genomic intelligence, risk assessment, RNA platform development, and coordinated One Health response. Key priorities include representative genomic sampling, interoperable surveillance networks, rigorous preclinical and clinical evaluation, and equitable access to emerging technologies. Bridging genomic surveillance and RNA innovation may strengthen preparedness for WNV; however, its practical value will depend on demonstrated effectiveness, translational feasibility, and sustained coordination across human, animal, and environmental health sectors.

Keywords: West Nile virus, genomic surveillance, One Health, mRNA vaccine, self-amplifying RNA, vaccine preparedness

MATERIALS AND METHODS

This article is a **narrative critical review** of published literature on West Nile virus genomic diversity, integrated One Health surveillance, vaccine development and RNA-based vaccine platforms. Relevant publications were identified through **targeted searches of bibliographic and scientific literature resources**, without language restriction, covering the period from **2005 to October 2026**, with emphasis on evidence published during the last decade; reference lists of relevant reviews and original research articles were also screened.

Studies were included when they contributed to at least one of the main review areas: **WNV genomic surveillance and molecular epidemiology, One Health surveillance, vaccine development, or RNA-based technologies**. Evidence from RNA vaccine research involving other pathogens was considered only as **indirect, platform-level evidence** and was **not used as proof of WNV-specific safety, immunogenicity or efficacy**.

The selected literature was **analyzed qualitatively and synthesized thematically**, and **no meta-analysis was performed**.

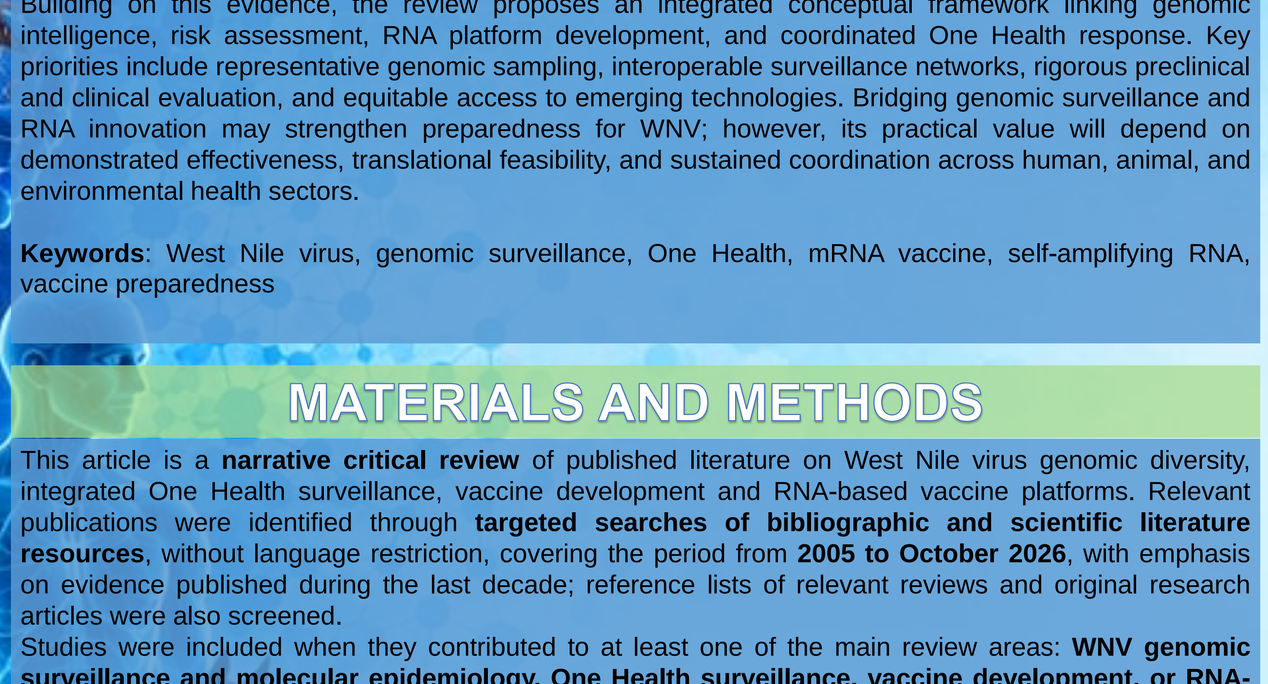


***Figure 2**. Integrated One Health framework for West Nile virus surveillance, risk assessment, and coordinated public health and veterinary response*

INTRODUCTION

West Nile virus (WNV) is a mosquito-borne zoonotic flavivirus maintained primarily in a transmission cycle between Culex mosquitoes and birds, with humans and horses acting as incidental hosts. While most human infections are asymptomatic or mild, **WNV** can cause severe neuroinvasive disease, including meningitis, encephalitis and acute flaccid paralysis.

WNV has become an important public health concern in Europe because of its wide geographic distribution, ecological adaptability and capacity to cause recurrent outbreaks. Lineages 1 and 2 are endemic in south-eastern Europe, and Romania represents one of the best-documented examples of sustained WNV circulation. In this context, genomic surveillance can complement conventional epidemiological monitoring by characterizing circulating lineages, identifying viral introductions and elucidating transmission patterns.

Within a One Health framework, integrating genomic data across human, animal, vector and environmental surveillance could improve understanding of WNV circulation, preparedness and risk assessment. This narrative critical review examines the role of WNV genomic surveillance within One Health and explores the potential application of RNA-based vaccine technologies, distinguishing WNV-specific evidence from broader technological advances reported for other pathogens.

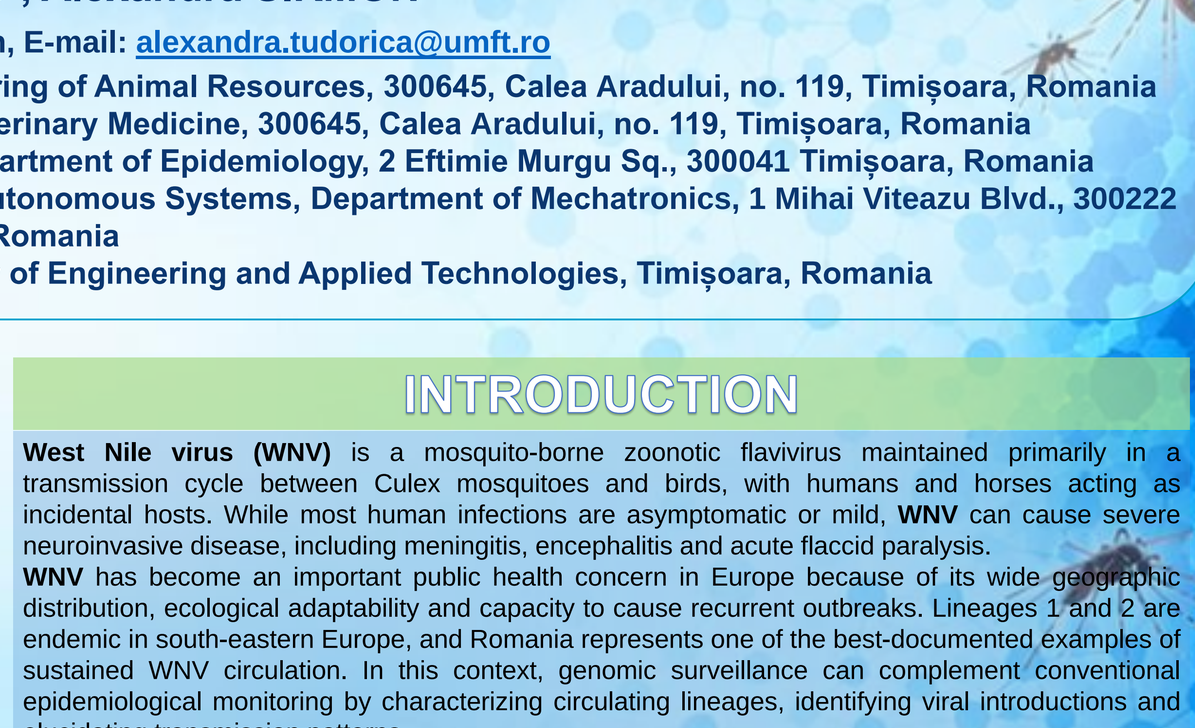


***Figure 1.** West Nile virus transmission ecology, illustrating the enzootic bird-mosquito-bird cycle, incidental hosts, and major environmental determinants of viral circulation*

RESULTS AND DISCUSSIONS

European circulation. At least 13 independent WNV introductions into Europe have been described (eight lineage 1a and five lineage 2), with multi-year persistence reported for seven. This estimate represents a minimum based on available genomic data.

Genomic surveillance gaps. WNV has been detected in 39 African countries, but molecular data are available from only 24, genomic sequences from 16, and only 63 whole genomes were available in the analyzed evidence, limiting phylogenetic resolution and viral dispersal reconstruction.

Evidence from integrated surveillance. In Romagna, Italy, WNV sequences from humans, mosquitoes and birds showed 99.82% nucleotide and 99.92% amino acid identity, supporting local lineage 2 circulation and overwintering, but not proving direct transmission.

Vaccine development. No human WNV vaccine is licensed. Nine clinical trials involving six candidates have been registered, none beyond phase II, whereas four vaccines are licensed for horses.

RNA platforms. In influenza models, 1.25 μg of self-amplifying RNA provided equivalent protection to 80 μg of conventional mRNA (64-fold dose reduction). This platform-level evidence does not establish WNV-specific safety, immunogenicity or efficacy.

CONCLUSIONS

WNV remains a **One Health challenge** because its transmission links **human, animal, vector and environmental systems**. **Genomic surveillance improves lineage characterization and exposes sampling gaps**, but its value depends on representative sampling, reliable metadata and integration with epidemiological and ecological evidence; it should be treated as **a component of broader preparedness rather than an independent solution**.

The **absence of a licensed human vaccine** and the platform-level maturity of RNA technology support **further WNV-specific evaluation rather than immediate clinical application**. Because humans are incidental hosts, **human immunization would provide individual protection rather than transmission control**, so **vaccine development and vector-based prevention must advance together**. As a narrative critical review, the synthesis is selective rather than exhaustive and the proposed framework remains **a conceptual contribution requiring empirical testing**.