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NGS-based genomic surveillance of West Nile virus in a One Health framework

Inhalt

West Nile virus (WNV) circulates primarily in an enzootic transmission cycle between Culex mosquitoes and birds, with mammals serving as accidental hosts. Humans infections can be asymptomatic or lead to flu-like symptoms, severe neurological disease and even death. WNV has been found almost worldwide, with the number of infections in humans and animals in Germany increasing over the last seven years. In addition to WNV hotspot areas such as Berlin, the virus spread also to other major cities such as Leipzig, Hamburg and Dresden. In the study presented here, we analysed the whole genomes of 86 WNV isolates from diseased birds collected in 2023 and 2024 by a nationwide bird surveillance network coordinated by the FLI. The sequencing results were assessed phylogenetically and -geographically. All WNV strains detected in 2023-2024 belonged to known lineage 2 clusters, with no evidence of new introductions. Most bird cases were linked to subcluster 2.5.3.4.3c. Phylogenetic analysis dates the most recent common ancestor to mid-2018, supporting a single introduction followed by local endemic spread. A few sequences clustered in subcluster 2.5.3.2, indicating additional independent introductions. The detection of novel mutations in certain samples raises the possibility of viral adaptation to local hosts or changes in transmission dynamics, underscoring the need for continued genomic surveillance and epidemiological monitoring as part of a One Health approach.

Keywords

NGS, surveillance, West Nile virus, phylogenetics

Registration ID

31

Professional Status of the Speaker

PhD Student

Junior Scientist Status

Yes, I am a Junior Scientist.

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