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Modeling the West Nile virus force of infection in the avian host population in Northern Italy

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Abstract

Background & aims of study

West Nile virus (WNV) is one of the most threatening mosquito-borne pathogens in Italy where hundreds of human cases were recorded during the last decade. In particular, in the Emilia-Romagna region (northern Italy) WNV has been present since 2008, leading to the establishment of an integrated surveillance network which aims at detecting the virus also in the avian host population. Here, we aimed at estimating the force of infection (FOI) of WNV in the avian population through a modeling framework which enabled us to eventually assess the fraction of birds that present WNV antibodies at the end of each epidemiological season.

Methods & results

We fitted a deterministic SIR model to ornithological data collected between 2013 and 2022: every year from May to November birds belonging to resident Corvidae species are captured via Larsen traps or shot by hunters and tested for WNV genome presence. The model was able to replicate the observed patterns of viral transmission. We found that the FOI peaks between mid-July and late August and that infected birds seem on average 31% more likely to be captured. We found evidence of spatio-temporal heterogeneity in predicted seroprevalence, and for 2018 we estimated the highest FOI (up to about 60% of the birds were infected), consistently with the anomalous number of recorded human infections.

Implications



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Implications

Thanks to our modeling study we quantified WNV infection dynamics in the avian host community, which is still poorly investigated despite being of paramount importance for virus persistence. To the best of our knowledge, this is among the first studies providing quantitative information on infection and immunity in the bird population, yielding new important insights on WNV transmission dynamics. Specifically, assessing avian antibody-mediated immunity will help predictive models to estimate the risk of WNV spillover to the human population.

Keywords

Mosquito

Seroepidemiologic Studies

Passeriformes

SIR model

SESSION DETAILS

Session 1: Vector-borne 1

📍 Europa

11:00-12:40

Wednesday, 29 November, 2023

IN THIS SESSION

11:00-11:20

Targeting vector control for dengue control: A modelling assessment of alternative approaches

11:20-11:40

Modeling the West Nile virus force of infection in the avian host population in Northern Italy

11:40-12:00

Uncovering mechanisms behind the spatial-temporal emergence of Usutu virus in the Netherlands

12:00-12:20

Linking antigenic diversity to dengue disease risk

12:20-12:40

Estimating the efficacy and likely population impact of TAK-003, a second-generation