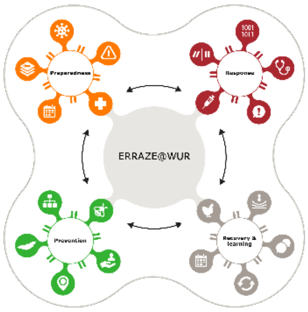
Paradigm Shifts for Global One Health

Greater resilience requires transformation and integration

Book of Abstracts

International symposium
23-25 April 2024
Wageningen, The Netherlands



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Uncovering mechanisms behind the spatial-temporal emergence of Usutu virus in the Netherlands in a multi-host context

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Problem statement: The Netherlands has recently seen the emergence of both West Nile and Usutu virus. Arboviruses circulating in wildlife species form a highly complex disease system. To understand transmission dynamics in such systems, high quality data on demographics, environment, and epidemiology are crucial but challenging to collect. By bringing together a multitude of data sources in a Bayesian inference framework, we aim to uncover which factors have shaped the spatio-temporal patterns of Usutu virus emergence in the Netherlands and how different host types contributed to this.
Methods: We developed a temperature-dependent, age-structured stochastic metapopulation model to simulate Usutu virus transmission between Culex pipiens sl. mosquitoes, blackbirds, and possible reservoir birds in the Netherlands. Random Forest models were fitted to predict relative abundance of birds and mosquitoes using mosquito trap count data (n=1544), blackbird point count data (n>500,000) and environmental predictors. Blackbird dispersal was parameterised by analysing ring-recovery data for their home range in breeding and non-breeding season as well as for natal and breeding dispersal. Using an Approximate Bayesian Computation approach, the model was fitted to multiple summary statistics based on several sources of surveillance data, including PCR and antibody-tested live blackbirds, and dead blackbird counts of which a subset was PCR-tested. We performed model comparison and parameter estimation to uncover which biological mechanisms were best supported by the data.
Results: Assuming blackbirds are the only relevant host species, we found that variation in environmental suitability and pre-existing immunity were insufficient explanations of the observed emergence pattern. While blackbirds are the most severely affected host species and the main target of surveillance, other bird host species, which do not die from infection and disperse further, contributed significantly to the spread of Usutu virus. Lastly, alternative overwintering routes, additional to vertically infected diapausing mosquitoes were needed to reproduce the observed multi-annual dynamics. The best fitting model was used to estimate spatiotemporal variation in R0 in the Netherlands and reconstruct the emergence across space and time.
Conclusions: Using a highly data-driven modelling approach, we identified several mechanisms that have shaped the emergence of Usutu virus, including the contribution of reservoir bird species. This framework allows us to evaluate the spatial spread and multi-year infection dynamics, features which have rarely been studied for Usutu and related arboviruses. It can be adapted to study other mosquito-borne pathogens, enhance surveillance programmes and evaluate the potential impact of future change scenarios on arbovirus transmission.

Keywords: mathematical modelling, arbovirus, Usutu virus, birds, mosquitoes