Understanding Usutu Virus Dynamics: Effects of Data and Model Structure Across Biological Scales

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Understanding the epidemiology of emerging pathogens, such as Usutu virus infections, requires systems investigation at each scale involved in the host-virus ecology, from individual bird infections to bird-to-vector transmissions to USUV incidence in bird and vector populations and eventually to spillover probability in humans. For new pathogens, wild data is sparse, and predictions are based on laboratory-type inoculation and transmission experiments combined with dynamical mathematical modeling. In this study, we developed a multiscale vector-borne epidemiological model of Usutu virus infection in birds and mosquitoes and used individual within-host viral load data and host-to-vector probability of transmission data to predict USUV incidence in bird and mosquito populations exposed to two different Usutu viral strains. We addressed the role of model structure, data uncertainty, and optimal experimental design on model predictions. We found that within-host peak viremia does not always correlate with infection incidence levels in host and vector populations and that uncertainty in predictions at one scale may change predicted results at another scale. We showed that optimal experimental design and increased frequency of data collection vastly improve these correlations. The results may be useful for predicting spillover events.

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