

Introduction: Current infectious disease models in Germany for SARS-CoV-2 often lack the ability to provide age-specific infection parameters and are not always based on known contact matrices of the population, do not usually include known setting-based information of reported cases, and do not account for age-specific underdetection of reported cases. Here, we develop an age-structured model to understand the age- and setting-specific contribution of contacts to transmission during all phases of the COVID-19 pandemic in Germany.

Methods: We develop a deterministic SEIR model using a pre-pandemic contact matrix. The model is optimized to fit reported age-specific SARS-CoV-2 incidences from Robert Koch Institute, includes information on setting specific reported cases in schools, and integrates age and pandemic period specific parameters for underdetection of reported cases deduced from a large population-based seroprevalence study (MuSPAD).

Results: We obtain an overview of the contribution of contacts to transmission within the population over time, which indicates among whom the disease spreads. The contribution of contacts to overall transmission in Germany varied across all phases of the pandemic. In the second wave, the contribution of contacts in the 80+ group to the transmission rate was highest. However, accounting for underreporting, a substantial proportion of infections was due to contacts in the young adult group. The contribution of contacts in the young adult group to the transmission rate was higher (range 5-10 times) compared with estimates without accounting for underreporting. We also estimated that the contribution of contacts in schools to the total cases in the population was quite varied below 10% during the third wave.

Discussion: Our model provides a tool to investigate the contribution of different age groups to the spread of SARS-CoV-2. In the future, we will aim to compare the current model with now emerging during-pandemic age-specific contact survey data.

P160

Monitoring of zoonotic West Nile virus and Usutu virus - two emerging arboviruses circulate in the German bird population

J. Ziegler¹, P. D. Santos², F. Bergmann¹, A. Günther², C. M. Holicki¹, B. Sadeghi¹, D. Höper², M. Keller¹, M. Eiden¹, M. Beer², F. J. Conraths³, M. H. Groschup¹

¹Friedrich-Loeffler-Institut, Institute of Novel and Emerging Infectious Diseases, Greifswald-Insel Riems, Germany, ²Friedrich-Loeffler-Institut, Institute of Diagnostic Virology, Greifswald-Insel Riems, Germany, ³Friedrich-Loeffler-Institut, Institute of Epidemiology, Greifswald-Insel Riems, Germany

Wild birds, as amplification and reservoir hosts as well as physical spreaders, are essential factors in transmission cycles of endemic or emerging arboviral zoonotic pathogens in Central Europe. Therefore, surveillance and pathogenesis studies of these animals can be an important early warning system for the occurrence and exposure to those zoonotic pathogens. Accordingly, we have been monitoring migratory and resident birds for zoonotic arthropod-borne viral infections for many years through systematic annual sampling in a unique nationwide wild bird surveillance network.

More than 2,300 blood samples from various wild birds from 22 bird orders and more than 2,900 bird carcasses were collected at more than 20 different collection sites by bird clinics, falconry centers, wild parks and bird sanctuaries distributed throughout Germany in 2019 and 2020. Diagnostic studies included in-depth molecular and/or serological methods particularly focussed on zoonotic flaviviruses, such as West Nile virus (WNV) and its close relative Usutu virus (USUV), and results were compiled annually update to reveal spatial spreading tendencies in the German bird population.

First, the epidemic spread of USUV, which has low zoonotic potential but high virulence to several bird species, was studied in great detail by this avian network. In 2018 a dramatic nationwide increase in the numbers of USUV positive birds was observed (based on the dead and live bird surveillance). Sequencing studies on all available USUV genomes revealed four distinct lineages from 2017 to 2020, two of which (Europe 3 and Africa 3) circulate throughout Germany. In eastern Germany, increased numbers were found for the USUV lineage Europe 2.