Novel Orthobunyavirus Identified in Snowy Owls from Berlin Zoo

Pauline Dianne Santos, Martin Beer, Ute Ziegler, Markus Keller, and Dirk Höper

Institute for Diagnostic Virology, Friedrich Loeffler Institute, Insel Riems Greifswald
Institute of Novel and Emerging Infectious Diseases, Friedrich Loeffler Institute, Insel Riems Greifswald

Next generation sequencing in tandem with RIEMS (Reliable Information Extraction from Metagenomic Sequence data sets) analysis confirmed the presence of both West Nile Virus and Usutu virus in two deceased snowy owl birds from Berlin zoo. In parallel, a few sequences of an unknown and unexpected Orthobunyavirus (67-89% nucleotide similarity) were detected in the owl samples. Further analyses generated the partial sequences of the L, M, and S segments of the virus, which have 30-41% amino acid sequence similarity with other Orthobunyavirus. Primers for reverse transcription -quantitative PCR (RT-qPCR) and long-range PCR assays were designed based on the preliminary L and S gene sequences. RT-qPCR assays detected CT-values of 18-28 in Snowy owl organ samples. Long-range PCR generated 642 bp product of the S segment and overlapping 3.996 bp and 4.003 bp products were generated of the L segment. The spleen samples will be processed for re-sequencing to generate the whole genome sequence of the novel Orthobunyavirus. Moreover, this RT-qPCR assay will be used for screening of bird and mosquito samples from Germany to determine the incidence and host-vector range of the virus. This study shows the importance of NGS-based-diagnostic-metagenomics for detection of known and unknown pathogens.

Contact:
Pauline Dianne Santos
Pauline.Santos@fli.de