

Negative Strand RNA Viruses

0097

Wide Distribution of Apparently Apathogenic Paramyxovirus Species in European Bats

L. Kwasnitschka¹, *A. Balkema-Buschmann¹, B. Ohlendorf², T. Müller³, R. Hoffmann⁴, G. Kerth⁵, M.H. Groschup¹

¹Friedrich Loeffler Institut, Institute of Novel and Emerging Infectious Diseases, Greifswald - Insel Riems, Germany

²Landesreferenzstelle für Fledermausschutz Sachsen-Anhalt, Landesverwaltungsamt Sachsen-Anhalt, Roßla, Germany

³Friedrich Loeffler Institut, Institute of Epidemiology, Wusterhausen, Germany

⁴Fledermausschutzverein Rumänien e.V., Arad, Romania

⁵Ernst Moritz Arndt University, Institute of Zoology, Greifswald, Germany

We have recently reported on the detection of Paramyxovirus RNA in German bats, namely Soprano Pipistrelle (*Pipistrellus pygmaeus*) and the Greater Mouse Eared Bat (*Myotis myotis*). After a more extensive continuation of our surveillance at different locations in Saxony-Anhalt, in Bavaria and to a lesser extent in Romania, the presence of a variety of Paramyxovirus species or subspecies can be reported for a number of indigenous bat species. Using a published Pan-Paramyxovirus PCR protocol, we were able to amplify sequences from the Paramyxovirus L-gene in oral swabs as well as in urine and fecal samples that were collected during population surveys of different bat colonies. Despite the wide geographic and zoologic distribution of these viruses, the overall prevalence among the analysed animals does not exceed three percent, while individual colonies display prevalences up to 23%. Phylogenetic analyses of the amplified sequences display a proximity to Jeilongvirus as well as to bat paramyxovirus that were detected by other groups in African and European bats. So far, no pathogenic potential of these viruses for animals or humans has been observed. Virus isolation is now attempted to facilitate the further analyses of these viruses.

Corresponding author:

Anne Balkema-Buschmann

anne.buschmann@fli.bund.de