

PRNA2-314

Detection of a J-Virus-like Paramyxovirus in European Bats

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Flying foxes (fruit bats, Macrochiroptera) have been identified as subclinical carriers of Nipah and Hendra Viruses belonging to the family of Paramyxoviridae in South-East Asia and in Africa. Since these agents may cause fatal diseases in humans and animals, we are interested to assess whether members of the paramyxovirus family are also present in European insectivore bats (Microchiroptera). For this purpose oral swab samples and urine samples were collected in the course of a population survey of Pipistrellus bats in Saxony-Anhalt. Using two published Pan-Paramyxovirus PCR protocols, we were able to amplify sequences from the L-gene of a paramyxovirus in bat samples collected from individuals of the Soprano Pipistrelle (*Pipistrellus pygmaeus*) and Nathusius' Pipistrelle (*Pipistrellus nathusii*). These sequences are closely related but not identical to J-Virus or Beilong virus, which have first been isolated from the house mouse (*Mus musculus*) in Australia and in a human kidney mesangial cell culture in China. Further detailed sequence analyses will reveal the exact phylogenetic relationship of this virus to other members of the family of paramyxoviridae. The epidemiological relevance of this virus still needs to be elucidated. However, no clinical signs were observed in the positive bats and no correlating viral infections were ever reported in Germany in activists involved in the Pipistrellus colony surveys or in humans in general.