Topic 1: Small mammals and their pathogens

Phylodynamic studies on astrovirus sequences detected in German bats

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Among the different viruses that circulate in bat populations, the family of the *Astroviridae* exhibits particular characteristics due to its high variant diversity and its high prevalence of up to 50% in insectivorous bats. The small, positive oriented single strand RNA viruses were first detected in 1975 in humans, and several variants have since been detected in various avian and mammalian species. Clinical symptoms associated with an astrovirus infection may, depending on the variant and affected species, range from mild to severe diarrhoea, hepatitis, nephritis, respiratory syndromes and encephalitis.

However, the pathologic effect of astrovirus infections in bats it is still unclear as no clinical signs could be observed so far. Moreover, the mechanisms of astrovirus transmission and elimination in bats are still obscure. Here, we assess the astrovirus phylodynamic characteristics by amplifying 400 nt fragments from the RNA-dependent RNA-polymerase (RdRp)-gene via nested RT-PCR followed by Sanger sequencing. The faeces and urine samples from individually tagged bats of the species *Myotis nattereri*, *Myotis bechsteinii*, *Myotis daubentonii*, and *Plecotus auritus* have been analysed since 2011 at three sampling regions in Germany. This gives us the unique opportunity to perform studies of individual bats over long periods of time. Individuals that were tested at several points in time, give an insight into virus persistence rates in individual bats. Different astrovirus variants differ in prevalence and regularity of occurrence between 2011 and 2016.

Overall, this study will help us to improve our understanding of the astrovirus transmission dynamics and phylodynamics within the observed bat colonies.

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