Research

The bat-derived mumps virus (batMuV) is a member of the genus Rubulavirus; its RNA genome has been detected in African flying foxes. This virus is of particular interest, because the viral genome organization is identical to that of human mumps viruses (MuV) and the amino acid sequences of each of its proteins are highly conserved in comparison to human MuV strains. Given that no infectious batMuV isolate is available, the surface glycoproteins, the fusion (F) and the hemagglutinin-neuraminidase (HN) protein, were expressed in cell culture systems and used for a first analysis of their functional characteristics.

One aim of this project is to analyze the role of the viral surface glycoproteins concerning virus entry, tropism, replication, and virulence. Therefore, recombinant MuV, in which the F and HN protein of a human MuV isolate are replaced by the corresponding glycoproteins of batMuV, will be generated and further used for the infection of immortalized cell lines. We are going to infect chiropteran cells, which belong to the same family as the host species of batMuV, as well as different mammalian cell lines, to answer the question if the replication of recombinant viruses differs between chiropteran and non-chiropteran cells.

The infection studies will provide new information about different key factors, which play an important role for the virus entry, such as the binding of viral particles to cellular receptors. The results, obtained for recombinant viruses which express the batMuV glycoproteins, will be compared to those obtained for recombinant MuV which contain only human proteins. Our results will provide a basis to understand the replication cycle of batMuV and enable the analysis of the zoonotic potential of these bat viruses.

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