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Molecular characterization of a novel mastadenovirus in harbor and grey seals

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The rate at which novel mammalian adenoviruses have been discovered has rapidly increased in recent years. However, there is still limited information regarding the diversity of adenoviruses in marine mammals. In this study, we used pan-adenovirus family primers targeting the DNA polymerase to perform PCRs on tissue samples originating from harbor and grey seals that were found stranded or dead in 2020 and 2021 on the Dutch North Sea coast. This resulted in the amplification of specific adenovirus amplicons in tissues from ten harbor seals and one grey seal with Sanger sequencing and NCBI-BLAST analysis of the resulting sequences confirming the presence of two closely related strains of a novel mastadenovirus species. A PCR-based strategy using primers designed to bind to conserved regions of the genome has been utilized to enable characterization of the full genome sequence. Based on ICTV species demarcation criteria, the seal adenovirus is a candidate new adenovirus species. Phylogenetic analyses were performed using full-length sequences of the DNA polymerase, hexon, and penton genes and showed that the seal adenovirus was most closely related to polar bear adenovirus 1. These findings extend our knowledge of the diversity of viruses in European seal populations and highlight the necessity for additional studies to better understand the virological and host determinants influencing transmission of seal adenovirus among and between phocid species.

Keywords

Virus discovery, Surveillance, Mastadenovirus, Phylogenetic analysis

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Professional Status of the Speaker

PhD Student

Junior Scientist Status

Yes, I am a Junior Scientist.

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