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Identification and comparison of adenoviruses in fecal samples from wild and captive non-human primates

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DNA viruses from the family Adenoviridae infect a wide range of animal hosts, including humans and non-human primates (NHP). Adenoviruses (AdV) infecting primates are classified into seven Human adenovirus subgroups (HAdV-A – HAdV-G) or Simian adenovirus A group with the remaining species unassigned to any subgroup allocated to the genus Mastadenovirus. In an attempt to study the molecular diversity and evolution of human and NHPAdV and the possibility of cross-species transmission, we have screened a community of savanna-woodland chimpanzees (*Pan troglodytes schweinfurthii*) living in their natural habitat in Ugalla, Tanzania and 17 species of NHP from one Slovak and 13 Czech ZOOS. The presence of AdV in non-diarrhoeal fecal samples (113 samples from Ugalla and 153 samples from ZOOS) was detected by nested PCR using degenerated primers targeting highly conserved DNA polymerase genes. From the AdV-positive samples nearly complete hexon gene sequences (hypervariable region responsible for serotype specificity) were amplified. Phylogenetic analyses based on both DNA polymerase and hexon gene sequences proved the presence of AdV grouped into HAdV-E and HAdV-C clades in wild chimpanzees. On the other hand, phylogenetic analyses of the samples from captive NHP showed much higher heterogeneity – we revealed the presence of AdV clustering to the HAdV-B, HAdV-E, HAdV-F and SAdV-A groups and also unassigned distinct species clustering to the genus Mastadenovirus. Here we reported the first detection of AdVs in *Mandrillus*, *Cercopithecus* and *Lophocebus* spp. Our data showed approximately 30% prevalence of AdV DNA in non-diarrhoeal fecal samples from wild chimpanzees in Ugalla and almost 40% prevalence of AdV in samples from ZOOS. The study confirmed the presence of various AdV species in the gastrointestinal tract of both wild and captive animals and gave a new insight into the diversity of AdVs infecting NHP.

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