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Genome analysis of human adenoviruses provides insights into their molecular evolution, zoonosis, and emergence of human viral pathogens.

Ten years of adenovirus genomics and bioinformatics provide remarkable insights into the molecular evolution of human and non-human simian adenoviruses, as well as into the emergence of new human viral pathogens through zoonosis. Remarkable findings include the recognition of HAdV coinfections, viral lateral gene transfer, and extraordinary and unexpected phylogenetic relationships. As an example, the lone HAdV type within the "human species E" clade appears to be a chimpanzee virus that has crossed host barriers and adapted to the human host recently. Bioinformatic analysis shows that the hexon hypervariable regions of HAdV-E4 have high sequence identity with the counterpart sequences from HAdV-B16, suggesting recombination with a human adenovirus. Recombination amongst other HAdV and SAdV genomes are also documented. This should be a consideration in using SAdVs as alternative gene transfer vectors for human gene therapy. (Received January 20, 2015)