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Assessing the suitability of adenoviral vectors for an improved vaccine against Devil Facial Tumour Disease

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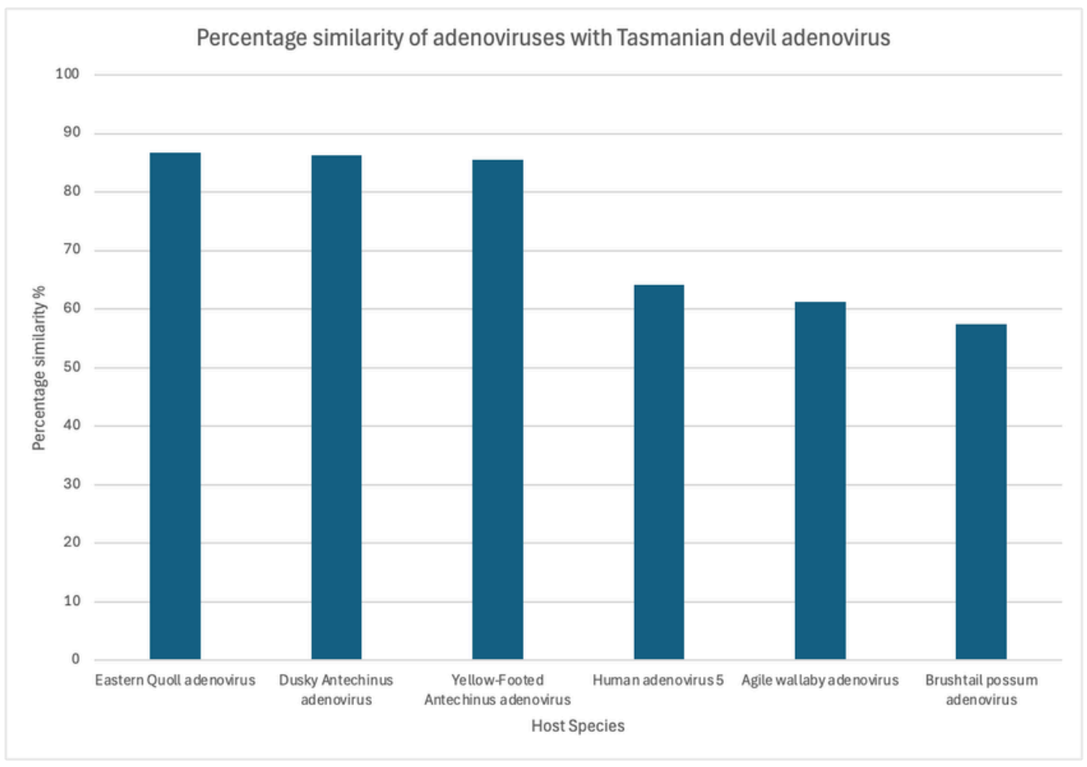
ABSTRACT

Devil Facial Tumour Disease (DFTD) is one of the few known transmissible cancers and has caused an estimated 80% decline in wild Tasmanian devil populations, making the development of an effective vaccine a priority for conservation. Current adenovirus-based vaccine vectors, which use human adenovirus 5 (HAdV5), have demonstrated the ability to deliver antigens and stimulate an immune response in devils. However, the transduction efficiency success has been limited, highlighting the need to identify a viral vector that will improve the delivery of antigens to target cells. This investigation aimed to determine the genetic differences in marsupial adenoviruses by comparing hexon gene sequences with a Tasmanian devil adenovirus sequence to identify the most genetically compatible adenovirus. This research was conducted using secondary sources, by using PCR amplified hexon sequences analysed and aligned in CLC Main Workbench. Eastern quoll adenovirus exhibited the greatest hexon sequence similarity with the Tasmanian devil adenovirus (86.82%), followed by yellow footed antechinus (86.25%) and dusky antechinus (85.57%), whilst human adenovirus 5 demonstrated substantially lower similarity (64.09%). These findings support the hypothesis that adenoviruses from closely related small marsupials are genetically more similar with Tasmanian devil adenovirus. This research contributes to the development of improved viral vectors for DFTD vaccines by identifying genetically compatible adenovirus that warrant further experimental investigation for vaccine delivery.

Image 1 - DFTD tumour, Ni Leathlobhair and Lenski, 2022

RESULTS



Graph 1 - Percentage similarities of host species adenovirus with devil Tasmanian devil adenovirus

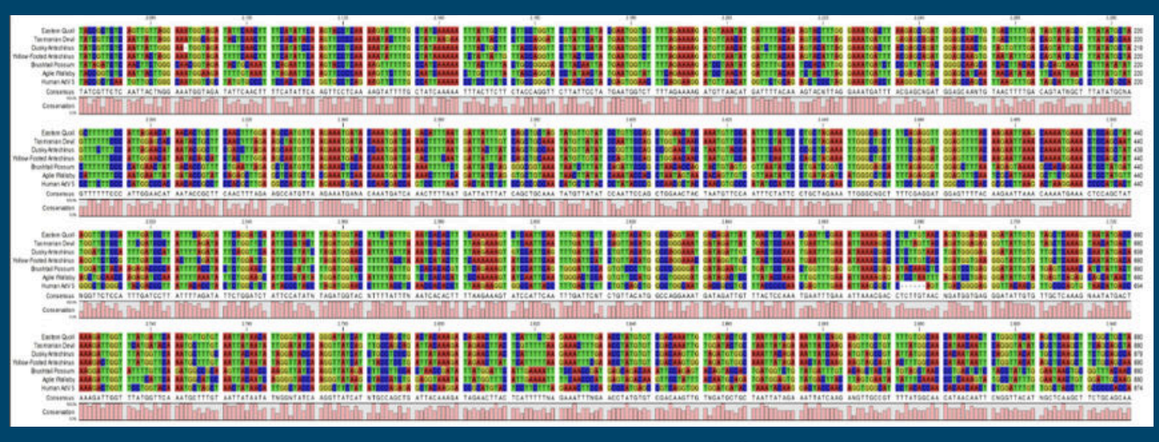


Figure 1 - Alignment of human adenovirus 5 (HAdV5) with the six marsupial adenoviruses – CLC Main Workbench, M. Fisher, personal communications, 2026

Conclusion

The results of this study showed that the eastern quoll adenovirus had the highest percent similarity with the Tasmanian devil adenovirus at 86.82%. The findings support the hypothesis, demonstrating that small marsupial adenoviruses have higher genomic compatibility with Tasmanian devil adenovirus than the human adenovirus 5. Based on this investigation the eastern quoll adenovirus is the best candidate as a viral vector for an updated vaccine against DFTD.