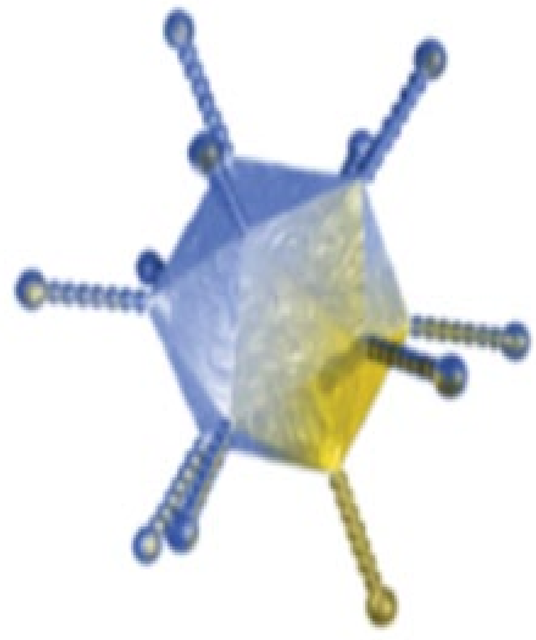
Molecular characterisation of human adenoviruses from environmental samples in Tshwane, Gauteng



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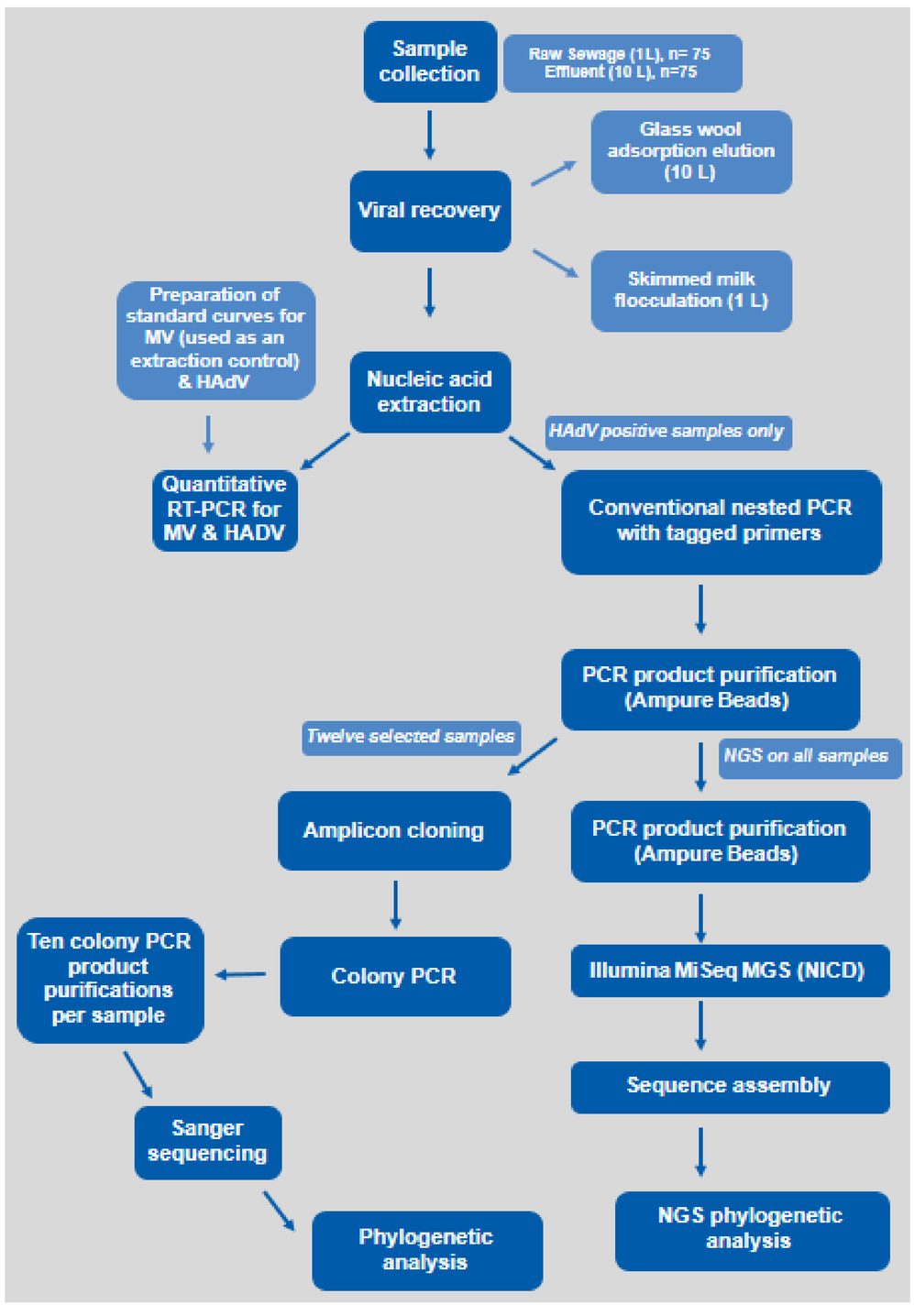
Introduction

- Human adenoviruses (HAdVs) are non-enveloped with linear, ds DNA genomes and are grouped into seven species (A-G)
- Transmitted via faecal-oral route, inhalation of respiratory droplets and direct contact with contaminated environments
- The HAdV is abundant in sewage water compared to other enteric viruses

Aim

- To investigate the presence and genotypes of human adenoviruses in environmental samples namely raw sewage and treated effluent, using molecular methods

Materials & Methods



Results

- 93% (140/150) positive for HAdV

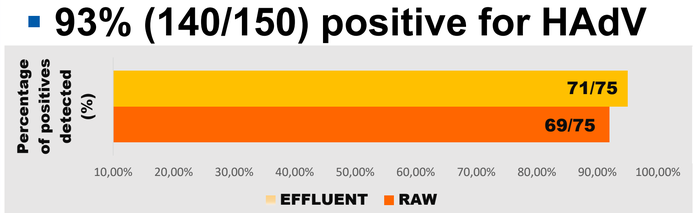
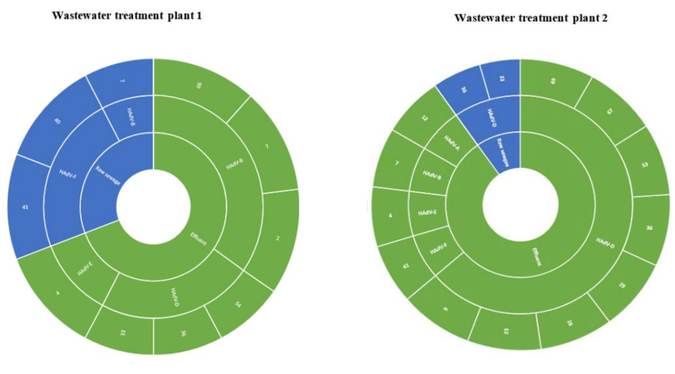


Figure A: Bar graph illustrating the percentage of positives detected in raw sewage and effluent samples.

Viral concentration:

		Lowest concentration (gc/L)	Highest concentration (gc/L)
WWTP 1	Raw	$1.38x10^5$	$4.50x10^9$
	Effluent	$5.08x10^3$	$4.30x10^8$
WWTP 2	Raw	$6.84x10^4$	$1.69x10^{12}$
	Effluent	$5.27x10^3$	$1.16x10^8$

Sanger sequencing



Next generation sequencing

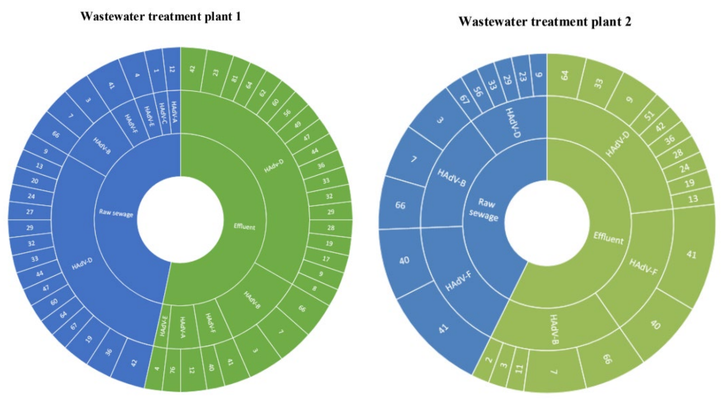


Figure B: Pie charts illustrating the distribution of HAdV species and genotypes for Sanger sequencing and Next generation sequencing. Key: Raw sewage ●, Effluent ●.

NGS Phylogenetic analysis

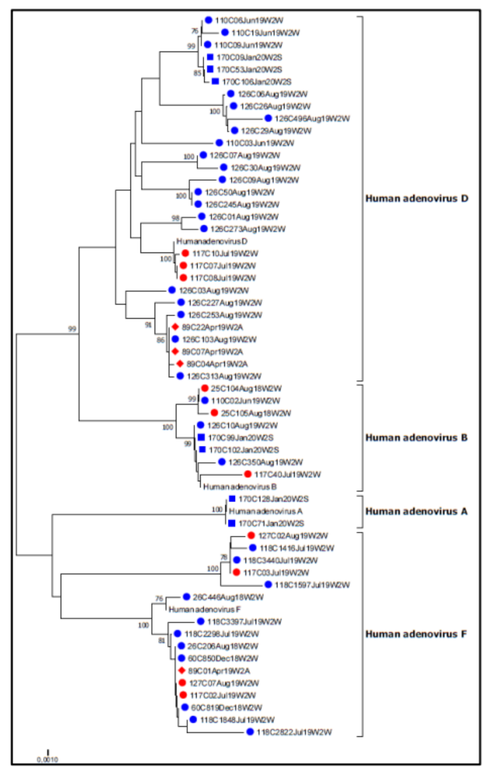


Figure C: The neighbour-joining phylogenetic tree of human adenovirus nucleotide sequences identified from wastewater treatment plant 1 using NGS. The evolutionary distances were determined using the Kimura 2-parameter method, conducted in MEGA6 (Tamura *et al.*, 2013). Closely related strains from GenBank indicated by accession numbers serve as reference. The percentage of replicate trees in which the associated strains clustered together in the bootstrap test (1000 replicates) is shown next to the branches. The tree is drawn to scale, with branch lengths in the same units as those of the evolutionary distances used to infer the phylogenetic tree. The analysis involved 73 nucleotide sequences. The scale bar indicates 0.05 nucleotide differences per site, over the indicated region. Key: Raw sewage samples (Red) and effluent samples (Blue). Each season is represented by a shape; Summer (Square ■), Autumn (Diamond ◆), Winter (Circle ●) and Spring (Triangle ▲)

Discussion & Conclusion

- Environmental surveillance successfully detected human adenovirus circulating in Tshwane, Gauteng
- These detected human adenovirus types gives us a better understanding of viruses currently circulating within our communities
- The results indicate adenovirus diversity within the Tshwane region of South Africa
- It is evident that the presence of these viruses are of environmental and public health concern

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