L-22

UNVEILING VIRAL DIVERSITY THROUGH WHOLE-VIROME SEQUENCING

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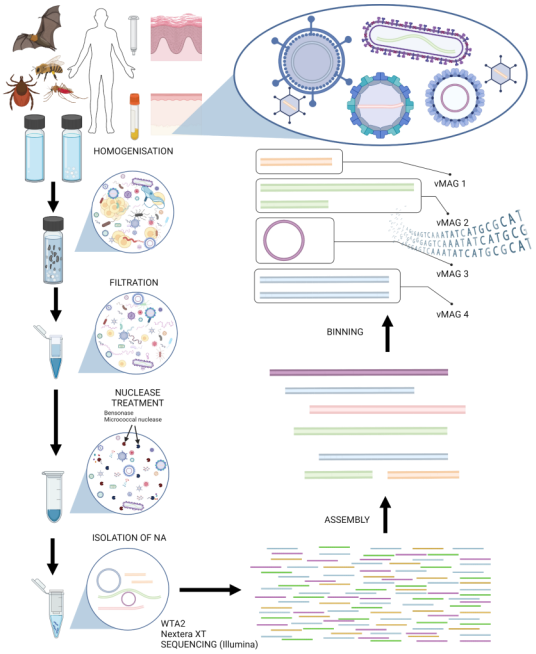
In the dynamic landscape of viral metagenomics, our research focuses on whole-virome sequencing using the Novel enrichment technique of viromes protocol (NetoVir protocol, 1), which we have adapted to diverse starting materials. The NetoVir protocol is a robust and fast approach for efficiently identifying DNA and RNA viruses without structural or genome preferences, ranging from small Picornaviridae to large viruses of the Mimiviridae family. The individual steps of the protocol allow for the enrichment of capsid-protected viruses, and through random nucleic acid amplification, sufficient reads can be obtained for subsequent bioinformatic analysis. Using a comprehensive bioinformatics, we can obtain information on a wide range of viruses without limiting our investigation to specific virus groups. This allows us to gain insight not only into known but also into unknown viruses.

Utilizing and modifying the NetoVir protocol for various samples (Scheme 1), we investigated the whole virome in samples obtained from humans and animals that either have a high economic impact on humans or are an important source of potential zoonotic infections.



Scheme 1. **Overview of sample preparation and analysis**

To characterise the full length of the newly discovered large DNA viruses, we have successfully combined bioinformatic analysis with classical laboratory techniques (2). Our focus includes the creation of viral Metagenome-Assembled Genomes (vMAGs), with a rigorous selection of high-quality sequences for further analysis, with an emphasis on completeness (complete or 50+% complete). Since viruses generally have much smaller genomes in comparison to cellular organisms, there are differences between non-viral and viral MAGs, especially in the number of contigs that make up the MAG. This feature provides an opportunity for consequent modification of the number of contigs using different computational analyses and to continue to complete the sequences using the wet lab approaches.

This interdisciplinary approach, combining wet-lab experiments and bioinformatics, provides a complex view of viral metagenomics and opens the way to a deeper understanding of viral diversity and evolution.

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