

UNDERSTANDING THE EVOLUTION OF HIV USING NEXT GENERATION SEQUENCING TECHNOLOGIES

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Next generation sequencing (NGS) technologies have enabled cost-effective generation of large volumes of sequence data that has altered our ability to capture host and pathogen diversity. For highly mutable pathogens such as HIV, the resultant high-resolution data from these NGS technologies has allowed a greater appreciation of the evolutionary dynamics of the virus within a host over time and at a host population level. In this presentation I will discuss the group's work on examining the influence of host immune factors on the evolution of HIV and how this information has informed studies on HIV transmission networks, viral adaptation, HIV replicative capacity and ultimately vaccine design.