Investigation of viral adaptation dynamics during early HIV infection yields important considerations for vaccine design

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Human immunodeficiency virus (HIV) remains a worldwide health risk, having claimed over 35 million lives to date. No cure for HIV exists, and this is partially due to the virus' high mutation and replication rate. Due to these characteristics, HIV has been shown to adapt and consequently evade an individual's immune response. Unfortunately, current HIV vaccine design approaches do not sufficiently incorporate these viral adaptations, and it has become increasingly apparent that these must be considered for an effective vaccine. Previous research has explored the detrimental impact of these adaptations in chronic HIV infection, however further research is needed to understand the early stage. Our study analysed the composition of the three most commonly considered HIV viral proteins in vaccine design (Gag, Pol and Nef) using next-generation sequencing across the early stage of infection from 13 individuals, in order to explore when these adaptations arise and how they change over time. We show that these adaptations appear early on during infection, increase in number over time, and may have significant implications at both the individual and population level. Pinpointing and understanding these early adaptations have become fundamental as individuals are being placed on treatment as soon as infection is suspected. Our research will aid current vaccine design prospects for HIV by improving the understanding of how quickly the virus can adapt in these early stages, which regions of the virus are more likely to adapt, and how these shape the genetic landscape of the virus over time.