



The Added Role of Phylogenetics in the Prevention of HIV-1 and Related Viral Diseases

Guest Editor:

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Message from the Guest Editor

Despite remarkable advances in the Fast-Track "90-90-90" treatment-as-prevention initiative, global HIV epidemic remain elusive with 1.5 million new infections annually over the last decade. Molecular phylogenetics is an exciting new direction to delineate the structure of transmission networks at an unprecedented detail, providing novel insights into regional epidemic drivers.

With this Special Issue, we wish to explore precisely what phylogenetics adds to the prevention of HIV-1 and related viral diseases. We welcome articles that describe phylogenetic insights into specific issues, including:

- Challenges in the identification of cluster types based on selected methodologies and genetic cut-offs.
- Epidemiological and virological predictors of the genesis and expansion of clustered outbreaks.
- The influence of migration and globalization in emerging patterns of viral spread.
- The mixing of epidemics among key vulnerable populations.
- The evolution of viral epidemics in the era of highly potent therapy, 90-90-90 Fast Track targets and COVID-19.
- Addressing ethical challenges in the implementation of phylogenetic strategies.





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Message from the Editor-in-Chief

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Electronic files or software regarding the full details of the calculation and experimental procedure, if unable to be published in a normal way, can be deposited as supplementary material.

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