Modelling the HIV epidemic in France using virus genomic data

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Résumé

Every time the Human Immunodeficiency Virus (HIV) replicates within a cell, errors can creep into its genome. These mutations make it possible to track an epidemic, because the more similar two virus sequences are, the closer the two individuals who bear them are likely to be in the chain of transmission. For more than twenty years, the field of phylodynamics has been analyzing this type of data to estimate, for example, epidemic growth rates or dispersion rates between regions. The SARS-CoV-2 pandemic illustrated the power of these methods, which remain marginal in France where routine sequencing performed during HIV screening is rarely used for epidemiological surveillance. However, this method is adapted to the HIV epidemic, it could inform us about the presence of clusters or the scale of the 'hidden' epidemic, which, by definition, is difficult to estimate because it is not screened. Thanks to the collaboration with leading national clinical virology teams, we analyze data from French cohorts, namely the national PRIMO cohort or the HIV-OE cohort at Montpellier University Hospital.

Preliminary results allow us to place the French epidemic in a global context and to successfully characterize homogeneous clades for the most common circulating subtype (HIV1-B). This better understanding of the structure of the French HIV epidemic will help guide future phylodynamic analyses to estimate variations in incidence and prevalence in overexposed populations over time. In particular, we will focus on assessing the proportion of the epidemic that is hidden to optimize public health policies.

Mots-Clés: Phylodynamics, HIV, modelling

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