Viral Evolution Used to Estimate Duration of Infection

Antoine Chaillon
University of California, San Diego
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Accurately estimating the duration of human immunodeficiency virus (HIV) infection for each individual would be important to understand rates of new infections (incidence) and to characterize factors accounting for these new transmissions to help design prevention strategies. Unfortunately, an accurate estimated duration of infection (EDI) is difficult to obtain because most infected individuals do not know when they were infected, and present too late for estimating the date of infection. Hence, the need to develop more reliable strategies to infer EDI is clear. During HIV transmission, one or a few closely related viral variants are transmitted from the donor, and the viral population within the recipient rapidly evolves and becomes more genetically diverse over time. For this project: (1) we will develop and optimize a method that takes advantage of the accumulation of HIV genetic variation over time to retrospectively estimate the date of infection; (2) we will validate this novel approach on a well characterized cohort off HIV1 infected subjects with known EDI; (3) we will develop an open source web-based system to estimate duration of HIV infection using HIV sequence data that could be freely used by other groups throughout the world (Aim 3). In summary, this study will provide important insights to the HIV research agenda, by developing an alternative approach to infer EDI, overcoming limitations of standard assays. The innovative technique that we will optimize during the course of the proposed project will likely be important for future studies in HIV epidemiology and transmission.