

Intra-patient evolutionary dynamics of immunodeficiency viruses across time and space

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Pelton Auditorium, B1-065

Fred Hutchinson Cancer Research Center

Refreshments will be served; registration not necessary to attend this event



Abstract: HIV's high mutation rates and large population sizes make it incredibly adaptable, especially to the antiretroviral drugs used in its treatment. However, as treatments have improved over the course of the epidemic, there has been a shift from HIV evolving resistance predictably and quickly in each patient to resistance emerging rarely, if at all. By studying the manner in which drug resistance emerges, we can gain broader insights into how HIV evolves within its host. I'll explore two questions: 1) how has intra-patient drug resistance evolution changed over the course of the epidemic and 2) what role does population spatial structure play in influencing the intra-patient dynamics. In answer to the first question, I will present data from 6717 historical HIV sequences from the Stanford HIV Drug Resistance Database that suggest that as treatments have improved over the decades, there has been a transition from soft sweeps of many drug resistance mutations simultaneously to hard sweeps of single drug resistant types. This supports more broadly a prediction from theory that when adaptation is likely (as when drugs failed frequently), sweeps should be soft. In answer to the second question, I will present data from four Simian-HIV infected macaques sampled in multiple tissues over the course of their infection and treatment. I will use these data to estimate selection, migration and population size and suggest how their interaction may explain equivocal evidence of compartmentalization from the HIV literature.



Contact: Jesse Bloom (jbloom@fredhutch.org) with questions
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