



Universität
Basel

Research Project

Recombination and reassortement in viral evolution

Third-party funded project

Project title Recombination and reassortement in viral evolution

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Organisation / Research unit

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Department

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Very few organisms evolve exclusively by asexual vertical transmission of their genomes. Instead, most populations exchange genetic information horizontally via a diverse set of mechanisms with profound effects on genetic diversity, the evolutionary dynamics, and adaptive potential.

Theoretical models predict that recombination accelerates adaptation and reduces mutation load. Recombination or horizontal transfer are hence expected to be beneficial on the long run despite its short-term costs.

Empirical evidence for this effect, however, is sparse and largely limited to short evolution experiments. RNA viruses like HIV and influenza are ideal systems to study the interplay of recombination and adaptive evolution since they evolve rapidly, are densely sampled, and their biology is well understood. Recombination rates of HIV and influenza viruses are high enough to matter, but low enough that substantial linkage and clonal interference remains. Hence the competing effects of recombination and selection are directly observable.

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In microbial evolution, recombination and reassortment are often the most impactful evolutionary events. Yet most phylogenetic analyses of viruses ignore recombination or seek to remove sequences with evidence of recombination. Here, we propose to develop computationally efficient and scalable methods to analyze recombination and reassortment in viruses and investigate how recombination facilitates adaptation and reduces recombination load. Insights from this undertaking will not only help to address pressing public health problems such as predicting future circulating influenza viruses, but will also shed light on fundamental problems in evolutionary biology.

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