

Dating the adaptation of H1N1 and H3N2 subtypes of Influenza A viruses in different hosts

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Influenza A viruses with very high mortality and morbidity rate, have the potential to be transmitted from nonhuman to human hosts, and *vice-versa*. But, following a host switch event, the nucleotide composition of the virus might differ from that of its new host, which is expected to lead to an inefficient replication of the virus and therefore a suboptimal viral fitness. Therefore, we predict that after a host switch event the nucleotide composition of the virus changes to reflect that of its new host. However, the dynamics of this evolutionary change across different hosts and viral subtypes remain unknown. To address this question, we designed a novel combination of phylogenetic approaches based on the analysis of whole viral genomes sampled in North America, and used change in GC3 content as a proxy for adaptation. We demonstrate that the time required for a virus to adapt to its new host depends on the direction of the host switch event, and that H1N1 viruses take on average longer than H3N2 viruses to adapt to their new hosts. More fundamentally, while different viral genes take different times to adapt to their new host, the pattern of this timing is similar across subtypes.