Abstract

Background: An influenza pandemic caused by a swine-origin influenza virus A/H1N1 [A(H1N1)pdm09] spread worldwide in 2009 and is estimated to have caused between 151,700 and 575,400 deaths globally. The spread of influenza is tradi¬tionally tracked by epidemiological data; however, this approach gives lit¬tle insight into the different viral circulating vari¬ants. Genome sequencing is emerging as a surveillance tool for evolutionary and phylogenetic mapping, and to explore the origins, molecular epidemiology, and genetic diversity of epidemic/pandemic viruses. Objective: To determine the origins, molecular epidemiology and genetic diversity of Kenyan influenza A(H1N1)pdm09 viruses.Methodology: A total of 40 influenza A/H1N1pdm09 viruses isolated between July 2009 and August 2010 were selected. The eight segments from each isolate were amplified and directly sequenced. The resulting gene segments were concatenated and these genomes used for subsequent analysis. A Bayesian Markov chain Monte Carlo (MCMC) approach implemented in the BEAST package v1.7.4 was used to reconstruct the most recent common ancestor (MRCA) sequences, time the introduction of infection in the country, rates of substitution and estimate a time-resolved phylogeny. Results: The Kenyan complete genome sequences clustered with globally distributed clade 2 and clade 7 sequences. However, local clade 2 viruses did not circulate beyond the introductory foci while clade 7 viruses disseminated country wide and were sustained by multiple introductions generating complex spatial patterns. Often, the local isolates clustered with isolates from the United Kingdom than with isolates from other countries. The time of the most recent common ancestor was estimated between April and June 2009, two months before the first laboratory confirmed case. The complete genome had an estimated rate of nucleotide substitution of 4.9 X 10-3 substitutions/site/year and fast population growths characterized the population dynamics. Conclusions: Adaptive evolution and viral migration seem to play a vital role in shaping the evolutionary dynamics of local A(H1N1)pdm09 viruses. Continuous monitoring is thus essential