

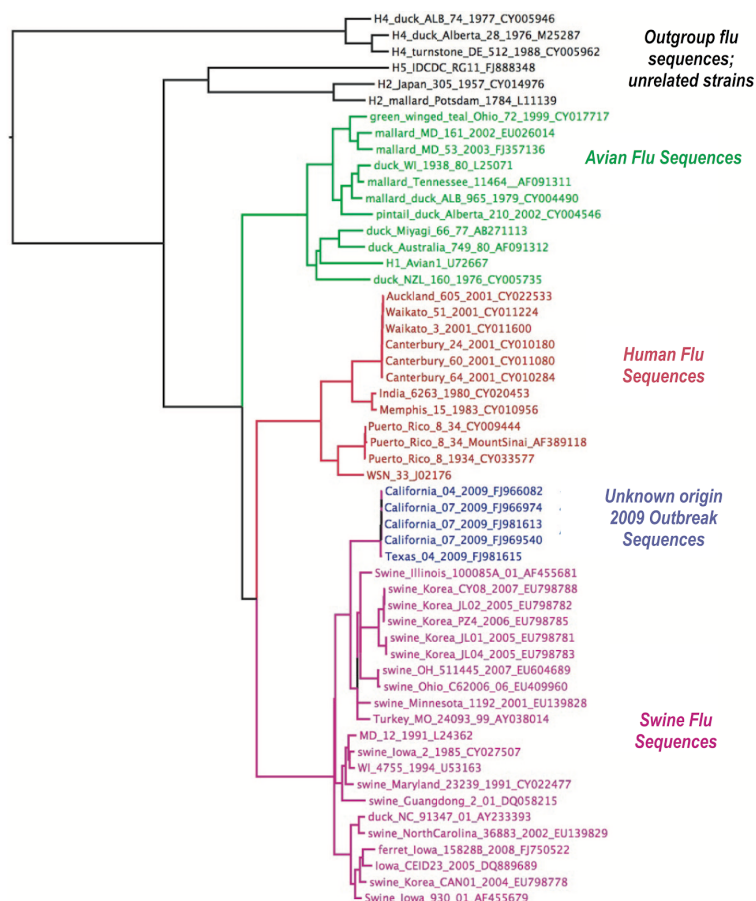
# Applications of Phylogenetics

## Epidemiological Investigations

Different strains of the influenza virus infect different species, most commonly birds (avian flu), pigs (swine flu), and humans (we just call this the flu). The seasonal influenza strain that most commonly infects humans is called H3N2, and we get vaccinated every year to try and protect ourselves and others from infection. Sometimes, new flu strains can emerge; most commonly, mutations in either a strain of swine flu or a strain of avian flu allow those strains to infect humans. Because these mutations create an entirely new strain of flu, these so-called "zoonotic" (host switching) events often lead to pandemics. Typically these new strains come from livestock who are in close contact with humans (chickens and pigs). Other times, new flu strains results from mutation of existing human flu strains.

The most famous flu pandemic was the Spanish Influenza of 1918 which killed between 20-50 million people around the globe. More recently in 2009, a new strain of H1N1 flu emerged and killed over 200,000 people across the globe. To prevent future outbreaks like this, it is crucial to understand the origins of these new flu strains.

Below is a phylogeny showing sequences from many samples of flu viruses including the 2009 H1N1 outbreak. Sequences are labeled based on their host. Based on this phylogeny, what is the most likely origin of the 2009 outbreak strain?



# Applications of Phylogenetics

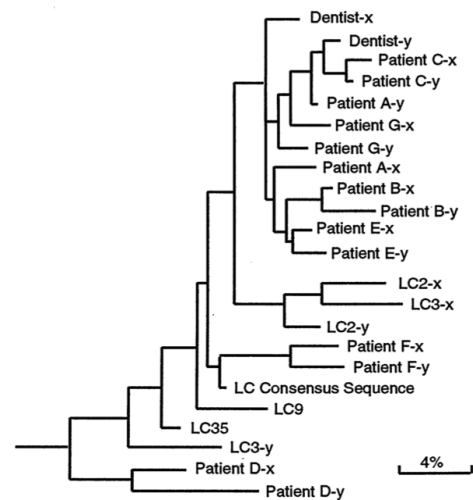
## Forensic Investigations

In the early 1990s, several individuals in Florida were diagnosed with HIV even though they had no known risk factors for contracting the virus. As is turned out, all six individuals were patients of the same dentist. **The question: Did they contract HIV from unclean dental practices, or is this just a coincidence?**

**The forensics approach** to investigate this case used phylogenetics! Blood was taken from many individuals:

- Six of the dentist's patients, named Patient A, B, C, D, E, F
  - Note, E and F were sex partners as well
- The dentist
- Many local individuals called "LC". *Think: why was this step done?*

The blood was searched for HIV sequences. For patient and dentist blood, scientists found the two most *different* HIV sequences (HIV evolves very rapidly within hosts). These are called -x and -y. So, each individual two sequences associated with them. For example, Patient A is Patient A-x and Patient A-y. A phylogeny was then made from all sequences<sup>1</sup>:



**Does this phylogeny provide evidence that the dentist gave HIV to any/all patients?** To answer this question, think what the phylogeny would look like if...

- Patients contracted HIV from non-dentist sources (like the local community individuals did)?
- Patients contracted HIV from the dentist?

## Other questions:

- Which individual has the most DIFFERENT HIV sequences inside their blood?
- Which individual has the most SIMILAR HIV sequences inside their blood?
- What about patients E and F? Did they give it to one another, or get from different sources? What phylogenetic pattern would each option look like?

<sup>1</sup> <https://www.ncbi.nlm.nih.gov/pubmed/1589796>