



Influenza virus A(H1N1)

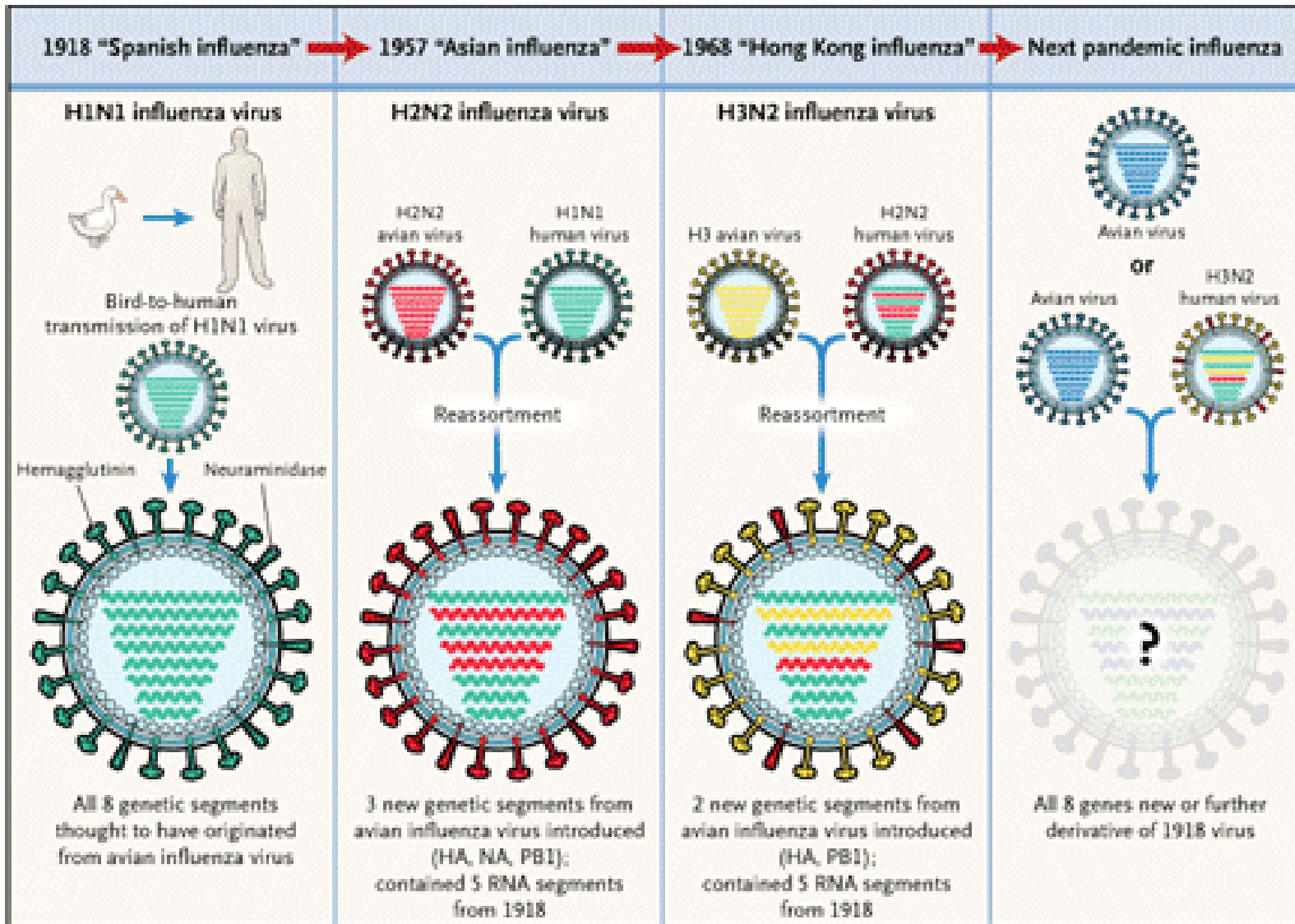
Origin of the virus

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Influenza A

- single stranded RNA virus with eight different genetic segments
- when two viruses co-infect the same cell, new viruses can be produced that contain segments from both parental strains (a *re-assortment*)





- One genetic segment codes for the haemagglutinine, one for neuraminidase
- Nine different Hs and 16 different Ns have been identified
- These decide the naming of the strain: H1N1, H5N1, H7N7, etc.
- In principle thus $9 \times 16 = 144$ different strains possible. Most are only avian.

- Extensive public databases of sequenced influenza viruses already available
 - New virus has been sequenced
 - And by:
 - sequence alignment,
 - cluster analyses by principal component analysis,
 - phylogenetic tree,
- we can trace the origin of the virus.

- Closest relatives to this new strain found in swine
- Six genetic segments from North America and two from European/Asian swine influenza
- One North American segment closely related to swine H3N2 isolates from 1998 that had human, swine and avian origin

- However, the virus has not been reported from pigs, neither in Mexico nor in the US
 - insufficient surveillance?
 - 'silent' infection in pigs?
 - very recent re-assortment?

