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SYNOPSIS

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Review of "Genomic characterisation and epidemiology of 2019 novel coronavirus: implications for virus origins and receptor binding"

Article citation: Lu R, Zhao X, Li J, Niu P, Yang B, Wu H, et al. Genomic characterisation and epidemiology of 2019 novel coronavirus: implications for virus origins and receptor binding. Lancet. 2020 Jan 29 [Epub ahead of print]. Available from: https://www.thelancet.com/journals/lancet/article/PIIS0140-6736(20)30251-8/fulltext

One-minute summary

- This study used **next generation and Sanger sequencing** to assemble **ten 2019-nCoV genomic sequences from nine patients**, including eight whole genomes and two partial genomes.
- Patients had symptom onset from December 22-27, 2019; eight patients visited the Huanan seafood market before symptom onset and one did not visit the market but stayed in a nearby hotel.
- Sequencing was performed from both bronchoalveolar lavage fluid and virus isolates.
- **Sequence identity:**
  - The eight complete genomes were nearly identical (>99.98%, the largest nucleotide difference was four mutations), indicating very recent emergence into humans.
  - **2019-nCoV was closely related (~88% nucleotide identity) to two bat-derived SARS-like CoV sequences;** had ~**79%** nucleotide identity to **SARS-CoV;** and only ~**50%** nucleotide identity to **MERS-CoV**. However, the **receptor binding domain of 2019-nCoV was phylogenetically closest to SARS-CoV.**
- Phylogenetic analysis:
  - The 2019-nCoV is a **novel betacoronavirus** from the subgenus Sarbecovirus. It has similar genomic organization to bat-derived SARS-like CoV and SARS-CoV, but with a longer spike protein.
  - Homology modelling indicated that **2019-nCoV had a similar receptor binding structure to SARS-CoV,** despite amino acid variation at some key residues. Authors suggest that 2019-nCoV may use angiotensin-converting enzyme 2 (ACE2) as a human binding receptor.

Additional information

- Phylogenetic analysis suggests that bats may be the original host, with an animal sold at the seafood market in Wuhan serving as an intermediary host. The authors note that most bats in Wuhan would be in hibernation in late December and that bats were not sold or found at the Huanan seafood market. Intermediate animal host are also associated with SARS-CoV (masked palm civet) and MERS-CoV (dromedary camels).

- The average evolutionary rate for coronaviruses is 10^{-4} nucleotide substitutions per site per year, and therefore constant surveillance for mutations is warranted.

- Since eight of the nine patients visited the seafood market in Wuhan and their 2019-nCoV isolates were nearly identical, the authors suggests that their viral isolates originated from one source and was detected relatively rapidly. The source of infection for the patient who stayed near the market (and also had an almost identical genome) is unknown.

Citation

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