

State of the Art in PID

Somsak Lolekha MD, PhD

President, the Royal College of Pediatricians of Thailand

Emerging infectious diseases are infections that have newly appeared in a population or have existed previously but are rapidly increasing in incidence or geographic or host species range.

- Most (approx. 75%) emerging infections emerge from wildlife.
- One in five are vector-borne diseases (transmitted from animal hosts to humans by arthropod vectors)
- Most are viral infections
- Most are caused by RNA viruses which have developed several ways to adapt mainly due to the lack of proofreading capacity of the viral polymerase.

Review

The origins of SARS-CoV-2: A critical review

Edward C. Holmes,^{1,2} Stephen A. Gardner,³ Angela L. Richardson,⁴ David L. Robertson,⁵ Alexander Gola-Christoph,⁶ Joel O. Wertheim,⁷ Simon J. Anthony,⁸ Nancy S. Danday,⁹ Marko F. Boni,¹⁰ Peter C. Doherty,¹¹ Jeremy Farrar,¹² James L. Geoghegan,¹³ Xuewei Jiang,¹⁴ Julian L. Lefcowitz,¹⁵ Stuart J.D. Neil,¹⁶ Tim Skow,¹⁷ Susan R. Weiss,¹⁸ Michael Worobey,¹⁹ Kristian G. Anderson,²⁰ Robert F. Garry,^{21,22} and Andrew Rambaut²³

The initial Covid-19 cases emerged at the **Huanan market**, most linked to the western section where most of the live-mammal vendors were located. The highest concentration of positive SARS-CoV-2 samples came from a single stall.



Three new studies build the case that COVID-19 originated at the Huanan Seafood Market in Wuhan, China. AP Photo/Dake Kang

PERSPECTIVE

COVID-19—lessons for zoonotic disease

Disease emergence is driven by human–animal contact in a global viral ecosystem

By Edward C. Holmes

Following exposure of humans to infected animals, a virus must establish a productive infection, transmitting within the human population.

Those animal viruses that by evolutionary chance can bind sufficiently well to human cell receptors will have an advantage in the game of emergence.

Main theories on the emergence of SARS-CoV-2 variants of concern

The VOCs have evolved:

- through accumulation of multiple mutations within patients with prolonged infection
- through multiple mutations in animal reservoirs
- gradually in parts of the world where there is less genomic surveillance but widespread circulation.

Need for **real-time molecular epidemiology** to gain information about virulence, pathogenesis, host range or immune escape and effectiveness of diagnostics and therapeutics.

Oude Munnink, et al. Nat Med. 2021