

# 2019 n-CoV Literature Situation Report (Lit Rep)

## January 28, 2020

### Key Takeaways

- ☒ **There is increasing evidence for person-to-person transmission both in and outside of China.**
- ☒ **While an origin for the virus has not been officially identified, current evidence points to bats with a reservoir in snakes.**
- ☒ **As more modelling and predictive studies are published, caution must be used when interpreting as the assumptions used to construct these models can be flawed.**

### Transmission

- A new case of illness was identified in a 27 year-old male from Vietnam who had not travelled to China. He had, however, spent three days with his parents in a shared hotel room after their return from travel in Wuhan, China. The father was diagnosed with 2019 n-CoV as well.
- Incubation period was estimated as  $\leq 3$  days for this case with strong evidence of person-to-person transmission.

*Importation and Human-to-Human Transmission of a Novel Coronavirus in Vietnam (Jan 28, 2020). NEJM Correspondence. DOI: 10.1056/NEJMc2001272*

- A hospital-based case study in Shenzhen, Guangdong province among six family members who travelled to Wuhan provides further evidence of person-to-person transmission.

*Fuk-Woo Chan et al. (Jan 24 2020). A familial cluster of pneumonia associated with the 2019 novel coronavirus indicating person-to-person transmission: a study of a family cluster. The Lancet. [https://doi.org/10.1016/S0140-6736\(20\)30154-9](https://doi.org/10.1016/S0140-6736(20)30154-9)*

### Modelling and Prediction

- Authors built a transmission model for the outbreak. Note that the model is limited by the assumptions made in constructing it. Key predicted measures are:
  - $R_0$  of 3.6 - 4.0
  - Only 5.1% (95% CI 4.8-5.5) of Wuhan infections are identified, meaning around 95% are going fully undetected.
  - By February 4, 2020 the model predicts:
    - Over 190 thousand cases in Wuhan alone.
    - Countries of greatest risk for imported infections will be Thailand, Japan, Taiwan, Hong Kong, and South Korea.
    - Even with near perfect travel restrictions to and from Wuhan, the outbreak outside of Wuhan would be reduced by only 24.9%.

*Read JM et al. Novel coronavirus 2019-nCoV: early estimation of epidemiological parameters and epidemic predictions. <http://dx.doi.org/10.1101/2020.01.23.20018549>*

- Authors used International Air Transport Association data to quantify traveler volume originating from Wuhan in 2018 from Jan-march, accounting for roughly 90% of all commercial travel. They present these data alongside Infectious Disease Vulnerability Index scores for high-volume-receiving countries. Authors identified no U.S. airports suggesting volume of travel from Wuhan to the U.S. is less than to many other regions.

*Bogoch et al. (Jan 2020). Pneumonia of Unknown Etiology in Wuhan, China: Potential for International Spread Via Commercial Air Travel. J Travel Medicine. <https://doi.org/10.1093/jtm/taaa008>*

## Origins, Reservoir, and Virus Background

- Researchers continue to note a gap in knowledge around disease transmission patterns, noting that while previous CoV outbreaks have often centered around nosocomial infections, this may not be the case for 2019 n-CoV. Apparent lower pathogenicity compared to SARS is called out as a potential threat for widespread transmission globally.

*Munster et al. (Jan 24, 2020). A Novel Coronavirus Emerging in China — Key Questions for Impact Assessment. NEJM. DOI: 10.1056/NEJMp2000929*

- Using various analytic techniques, researchers found that 2019 n-CoV falls into the betacoronavirus genus, along with SARS-CoV, vat SARS-like CoV, and other coronaviruses. Virus isolation, cytopathic effects, and morphology are described.

*Zhu et al. (Jan 24, 2020). A Novel Coronavirus from Patients with Pneumonia in China, 2019. NEJM. DOI: 10.1056/NEJMoa2001017*

- Chinese researchers conducted a sequence analysis and found that 2019-nCoV appears to be a recombinant virus between the bat coronavirus and a coronavirus of unknown origin, with the most likely wildlife reservoir being snakes. Study findings also suggest a “homologous recombination within the viral receptor-binding spike glycoprotein, which may determine cross-species transmission from snake to humans.”

*Ji et al. (Jan 2020). Homologous recombination within the spike glycoprotein of the newly identified coronavirus 2019-nCoV may boost cross-species transmission from snake to human. Med Virology. doi: 10.1002/fut.22099*

- In of 41 cases of 2019 n-CoV hospitalized by Jan 1, 2020 in Wuhan, clinical symptoms and diagnostic findings are described.

*Huang et al. (Jan 24, 2020). Clinical features of patients infected with 2019 novel coronavirus in Wuhan, China. The Lancet. [https://doi.org/10.1016/S0140-6736\(20\)30183-5](https://doi.org/10.1016/S0140-6736(20)30183-5)*

- A Chinese research team reports that a previously identified coronavirus of bat origin shares 96% of its genome with 2019 n-CoV. These two viruses differ substantially from other known coronaviruses, including SARS-CoV and MERS CoV, suggesting it is likely that 2019 n-CoV may also originate in bats.

*Zhou et al. (Jan 23 2020). PRE-PRINT. Discovery of a novel coronavirus associated with the recent pneumonia outbreak in humans and its potential bat origin. doi:*

*<https://doi.org/10.1101/2020.01.22.914952>*

*Cited by NY Times:*

*<https://www.nytimes.com/2020/01/28/opinion/coronavirus-china.html?smid=nytcore-ios-share>*

- China-based researchers provide background on general coronavirus genome structure, replication, pathogenesis, treatment, and prevention.

*Chen, Liu, and Guo. (Jan 2020). J Med Virology. Emerging coronaviruses: genome structure, replication, and pathogenesis. doi: 10.1002/jmv.25681*