

Journal Pre-proof

Recent insights into 2019-nCoV: a brief but comprehensive review

Qingmei Han , Qingqing Lin , Shenhe Jin , Liangshun You

PII: S0163-4453(20)30087-6
DOI: <https://doi.org/10.1016/j.jinf.2020.02.010>
Reference: YJINF 4453

To appear in: *Journal of Infection*

Accepted date: 11 February 2020

Please cite this article as: Qingmei Han , Qingqing Lin , Shenhe Jin , Liangshun You , Recent insights into 2019-nCoV: a brief but comprehensive review, *Journal of Infection* (2020), doi: <https://doi.org/10.1016/j.jinf.2020.02.010>



This is a PDF file of an article that has undergone enhancements after acceptance, such as the addition of a cover page and metadata, and formatting for readability, but it is not yet the definitive version of record. This version will undergo additional copyediting, typesetting and review before it is published in its final form, but we are providing this version to give early visibility of the article. Please note that, during the production process, errors may be discovered which could affect the content, and all legal disclaimers that apply to the journal pertain.

© 2020 Published by Elsevier Ltd on behalf of The British Infection Association.

Recent insights into 2019-nCoV: a brief but comprehensive review

Qingmei Han^{1,2,3*}, Qingqing Lin^{1,2,3*}, Shenhe Jin^{4*}, Liangshun You^{1,2,3#}

¹Department of Hematology, the First Affiliated Hospital, College of Medicine, Zhejiang University, Hangzhou 310003, Zhejiang, People's Republic of China

²Malignant Lymphoma Diagnosis and Therapy Center, the First Affiliated Hospital, College of Medicine, Zhejiang University, Hangzhou 310003, Zhejiang, People's Republic of China

³Institute of Hematology, Zhejiang University, Hangzhou 310003, Zhejiang, People's Republic of China

⁴Department of Hematology, Sir Run Run Shaw Hospital, College of Medicine, Zhejiang University, Hangzhou 310009, Zhejiang, People's Republic of China.

* Co-first author;

Corresponding author

Liangshun You.

Department of Hematology, The First Affiliated Hospital, College of Medicine, Zhejiang University, 79# Qingchun Road, Hangzhou, 310003, P. R. China.

Email: youliangshun@zju.edu.cn

Tel: 86-15088687797

Abstract

A novel coronavirus designated as 2019-nCoV hit the central Chinese city of Wuhan in late December 2019, and subsequently spread rapidly to all provinces of China and multiple countries. Up to 0:00 am February 9, 2020, a total of 37,287 cases have been confirmed infection of 2019-nCoV in China mainland, and 302 cases have also been cumulatively reported from 24 countries. According to the latest data, a total of 813 deaths occurred in China mainland, with the mortality reaching approximately 2.2%. At present, there is no vaccine or specific drugs for human coronavirus, so that it's critical to understand the nature of the virus and its clinical characteristics to response to the 2019-nCoV outbreak. Thus, we summarize the not much but timely reports on the 2019-nCoV in the present study, briefly but comprehensively.

Key words: 2019-nCoV; epidemiology; genomic; therapeutic

Introduction:

Coronaviruses (CoVs) are enveloped, single positive stranded RNA virus, which belong to the subfamily Coronavirinae. The CoVs genome, ranging from 26 to 32 kilobases in length, is probably the largest viral RNA known (1,2). Previously, there are six CoVs known to cause human diseases and can be divided into low pathogenic and highly pathogenic CoVs (2,3). The low pathogenic CoVs, including 229E, HKU1, OC43 and NL63, account for 10% to 30% of upper respiratory tract infections and typically cause mild respiratory diseases (3,4). In contrast, the highly pathogenic CoVs, including Severe Acute Respiratory Syndrome (SARS) and Middle East Respiratory Syndrome (MERS) CoV, predominantly infect lower airways and cause fatal pneumonia (2,5).

SARS-CoV emerged as a new human infection in South China in November 2002 and ended in July 2003. It infected 8,096 people and caused 774 deaths with an overall mortality rate of about 9.6% (6,7). MERS-CoV, another highly pathogenic CoV, first emerged in Saudi Arabiawas, has caused a total of 2494 laboratory-confirmed cases and 858 deaths from 27 countries (mortality rate, 34.4%) since September 2012. (<http://www.who.int/emergencies/mers-cov/en/>) (8). These two highly pathogenic β -CoVs have posed a substantial threat to public health.

In late December 2019, a novel CoV identified as the pathogen causing outbreaks of SARS-like illness in the Chinese city of Wuhan and was officially named as 2019-nCoV by the World Health Organization (WHO). Subsequently, the full genomic sequence from Shanghai Public Health Clinical Center argued for a bat origin for the 2019-nCoV (9). From the beginning, clusters of cases of novel CoV infection were reported that were epidemiologically linked to the Huanan Seafood Wholesale Market (10), and then evidence that human-to-human transmission of 2019-nCoV was further confirmed by the infection of 15 healthcare practitioners after close contact with 1 infected patient in a Wuhan hospital (11). As of February 9, 2020, 2019-nCoV has infected a total of 37590 cases from all over the world.

Despite several decades of research, specific vaccine or treatment for human CoVs is lack. In this review, we summarize the advance of the nature of the 2019-nCoV and its clinical characteristics and therapeutics, which may be critical for the response to the 2019-nCoV outbreak.

Genomic and structure

2019-nCoV belongs to lineage B β -COVs, subgenus Sarbecovirus, possessing a single-stranded positive-sense RNA surrounded by envelope (9,12). The RNA genome includes 29891 nucleotides (GenBank no. MN908947), encoding 9860 amino acids and is arranged in the order of 5'UTR-replicase(orf1a/b)- Spike(S)-Envelope(E) -Membrane

(M)-Nucleocapsid (N)-3'UTR, in which S, E, M, N encodes the structural proteins (9) (**Figure 1**). Recently, phylogenetic analysis has revealed that 2019-nCoV is most closely related to BatCoV RaTG13 from Yunnan, China in 2013 with 96.3% sequence identity, and is more related to two bat-derived SARS-like coronaviruses, bat-SL-CoVZC45 and bat-SL-CoVZXC21 (about 88% identity) which from Zhoushan, China in 2018, but is discordant with SARS-CoV (about 79% identity) and MERS-CoV (about 50% identity) (9, 12-14).

The genome of 2019-nCoV consists of 6 major functional open reading frames (ORFs), including ORF1a/b, S, E, M, N and several other accessory genes like ORF3b, ORF8. Replicase polyproteins pp1a and pp1ab encoded by ORF1a/b would be proteolytically cleaved into 16 non-structural proteins (nsps) which are involved in the transcription and replication of the virus (9). In addition, the ORF3b encoded a completely novel short protein without exact function. The new ORF8 likely encodes a secreted protein formed by an alpha-helix, followed by a beta-sheet containing six strands without known functional domain or motif similarly (9). The S gene of 2019-nCoV was less than 75% sequence identity to those of two CoVs, bat SARS-like CoVs (SL-CoVZXC21 and ZC45) and human SARS-CoV (14). And likewise, the spike glycoprotein encoded by the S genes of 2019-nCoV was longer than that of SARS-CoV (12,14). The spike protein, composed of S1 and S2 domain,

was crucial to determine host tropism and transmission capacity through mediating receptor binding and membrane fusion (12). Of which the S2 subunit of 2019-nCoV is highly conserved and has 99% identity with that of SARS-CoV (12). The receptor-binding domain, commonly located in the C-terminal domain of S1 to directly contact the human receptor.

Although, S1 domain of 2019-nCoV is only approximately 70% identity with SARS-CoV, homology modelling revealed that 2019-nCoV has a similar receptor-binding domain structure to that of SARS-CoV (9, 12).

Notably, Zhou et al found that 2019-nCoV just like SARS-Cov may also use ACE2 as an entry receptor in the ACE2-expressing cells, majority of which are type II alveolar cells (AT2) in human lung (14,15). Therefore, further investigation is worth to carry out whether ACE2 targeting drugs will be effective for the treatment of 2019-nCoV.

Since the genomic sequences of 2019-nCoV obtained from different patients were extremely similar to each other, exhibiting more than 99.9% sequence identity (12,14), we could reasonably believe that 2019-nCoV originated from one source rather than a mosaic and could be detected relatively rapidly. However, mutations need to be constantly monitored when the virus is transmitting to an increasing number of individuals.

Epidemiology

On the basis of initial investigation, the shared history of exposure to the

Wuhan Seafood Wholesale Market highly suggested that wild animals sold in the market such as bamboo rats, raccoons, and snakes would be the original source of the novel virus (16). Soon afterwards, traceability analysis supported that 2019-nCoV would be from *Rhinolophus*, consistent with the phylogenetic analysis results that 2019-nCoV was most related to BatCoV RaTG13 from the bat (13,17). However, intermediate host is likely to exist between bats and humans which is similar to masked palm civet for SARS-CoV35 and dromedary camels for MERS-CoV. The newest research suspected pangolins are potential intermediate hosts for novel coronavirus but may not be the only.

Epidemiologically, 2019-nCoV is highly contagious with about 2 hours survive time in the air. The incubation period after infection is generally 4-8 days (10,18,19). All age groups are susceptible to the virus, of which elderly patients with comorbidities are more likely to experience severe illness (10,18,19). Importantly, the people who are primary, asymptomatic and in incubation period are the main sources of infection, which is of critical significance to the epidemic prevention and control (16). Up to now, respiratory droplets is the major route of transmission. Besides, the fecal-oral route of transmission is considered but unconfirmed because 2019-nCoV nucleic acids could be detected in the stool samples of pneumonia patients with abdominal symptoms (20). Vertical transmission between mothers and infants is another possible

route based on the finding that a 30-hour-old newborn was confirmed with 2019-nCoV in Wuhan Children's Hospital. Some researchers also warn that the transmission through the ocular surface must not be ignored considering human conjunctival epithelium can be contaminated easily by infectious droplets and body fluids (21).

To our knowledge, basic reproduction rate (R_0), as the rate reflecting the speed of disease transmission, differs in time periods estimated by researchers and is also substantially affected by reporting rate. The latest R_0 is 2.68 estimated by Wu et al, roughly identical to the rate published by WHO and Chinese Center for Disease Control, all of which indicate that the number of infected patients will increase as long as R_0 is greater than 1 (16,22,23). As a result, the WHO has declared the outbreak of 2019-nCoV pneumonia to be a public health emergency of international concern on January 30 and adopted control measures to reduce R_0 rate to below 1 globally.

Clinical characteristics

The current clinical observation from Wuhan showed that 2019-nCoV shared many clinical features with SARS-CoV (24, 25). The mean age of the patients is 55 years old, with a predominance of male patients 54.3%. The mean incubation time is 4.1 to 7 days (12, 24). The most common symptoms are fever (98.6%), fatigue (69.6%), dry cough (59.4%) and myalgia (34.8%), accompanied with rhinobyon, rhinorrhoea,

pharyngalgia and diarrhea in a few patients (24) (**Table 1**). Notably, fever may not necessarily be the first manifestation. A part of patients are characterized by dyspnea and hypoxemia, which can rapidly progress to acute respiratory distress syndrome (ARDS), septic shock, metabolic acidosis, coagulation dysfunction and even multiple organ dysfunction syndrome (MODS) in one week (13,24).

Some laboratory tests could provide some hints of the early forms of the disease, such as leukocytopenia, lymphopenia and mild elevated C-reactive protein (CRP). Besides, severe cases could have increasing levels of leukocyte, granulocyte as well as D-dimer, creatine kinase and creatine(13,24). All suspected patients are recommended to be examined by chest computerized tomography (CT). Most confirmed patients suffered to bilateral pneumonia (75-98%), characterized with multiple patchy shadows, ground-glass opacity and interstitial infiltrations in chest CT, and even subsegmental consolidation in severe patients (10,13,26). So far most of patients show a good prognosis. However, the mortality rate is higher in the elder patients with chronic diseases, approximately 17% in recent report (24).

The diagnosis is based on the epidemiological risks, clinical features and laboratory tests. Patients who have a history of travel from Chinese city of Wuhan or close contact with confirmed or suspected case of 2019-nCoV, and then present with fever or respiratory symptoms within

incubation period should be suspected. In addition, due to the discovery of asymptomatic CoVcarriers and negative of viral nucleic acid test in many times before confirmed, the typical pulmonary imaging performance can not be ignored, and even can be used as a preliminary screening method. Positive of viral nucleic acid by real-time RT-PCR detection with specimens from the respiratory tract or serum are confirmed 2019-nCoV infection (14).

Treatments for 2019-nCoV

Despite several therapeutic options have been experimented in 2019-nCoV infected patients, there are still no specific therapies. As one kind of RNA virus, 2019-nCoV may possess some similar functional proteins for processing virus replication and assembly to human immunodeficiency virus (HIV). Thus, the HIV protease inhibitors may also effective to 2019-nCoV. At present, lopinavir/ritonavir (LPV/r) combination, which was previously confirmed effective in SARS-Cov and MERS-Cov, has been recommended for the treatment of 2019-nCoV in the latest guideline (27,28). Besides, by homology modelling and molecular docking, another anti-HIV drug nelfinavir was predicted to be active against 2019-nCoV and could be a potential drugs (29).

Remdesivir (RDV, GS-5734), a novel nucleotide analogue prodrug in development, has been proved to be a potential effective pan-CoV antiviral (30,31). Wang et al showed that RDV could inhibit 2019-nCoV

infection in vitro (32). And the successful use of RDV in the first case of 2019-nCoV in the United States posted the bright perspective (33). More promisingly, a randomized, double-blind, parallel-controlled phase 3 clinical trial of safety and efficacy of RDV is ongoing in Wuhan (NCT04252664). Meanwhile, Wang and his colleagues also provided evidence of the potential that chloroquine was also effective in the control of 2019-nCoV infection (32). Arbidol has a broad-spectrum antiviral activity against respiratory viruses. Recent news reported that arbidol can inhibit 2019-nCoV in vitro. A phase 4 clinical trial of arbidol for new coronavirus pneumonia had been registered (NCT04246242).

As for monoclonal antibody (mAb), several researches showed that the combination of RDV and mAb would likely to be the ideal treatment for 2019-nCoV. Tian et al reported for the first time that a SARS-CoV-specific human mAb, CR3022, could bind potently with 2019-nCoV receptor binding domain (34). Therefore, CR3022 may be developed to prevent and treat new coronavirus infection. Additionally, The janus kinase inhibitor baricitinib, which can disrupt receptor mediated endocytosis and interrupt the passage of the virus into cells, was identified to reduce the ability of the virus to infect lung cells and be a potential treatment for 2019-nCoV (35).

In addition to the therapeutics discussed above, Chinese healthcare practitioners also have started clinical trails of stem cell infusion and

traditional Chinese medicine for severe patients. We expect that these therapies will improve clinical outcomes in 2019-nCoV patients.

Discussion

The world has experienced three outbreaks of highly pathogenic CoVs, including the emergence of SARS-CoV in 2002, MERS-CoV in 2012 and now, the outbreak of 2019-nCoV (6-8). It is clear that 2019-nCoV is another lineage B β -CoV and has been postulated that bat is the primary host (9). Despite only 75% similarity in genetic sequence to SARS-CoV(9,14), 2019-nCoV shares many features with SARS-CoV, such as epidemiology, clinical characteristics, and the entry receptor ACE2 and so on (14,15,24,25).

The 2019-nCoV jumps unpredictably, spreads rapidly and has posed severe threat to public health. Although the overall mortality rate is lower than SARS-CoV and MARS-CoV, the mortality in the elder patients who with chronic diseases is as high as 17% (25). As yet, no specific therapy of proven efficacy has been recommended for human CoVs infection. Retrospective analysis showed that most deaths of the CoVs infection patients were due to severe pneumonia (2,5). Previous studies indicated that viral evasion of host maladjusted immune responses are believed to play critical roles in acute lung injury (ALI), in addition to CoVs-induced direct cytopathic effects (5). Indeed, changes of some immune index have been detected in the CoVs infection patients, such as lymphopenia,

monocytosis and elevated cytokine levels (2,5,25). The treatment of corticosteroids may reduce the risk of lung inflammation but also delay CoVs clearance in addition to other side effects (36-38). Thus, the topic of corticosteroid use in patients with CoVs has been a matter of debate for years. The available clinical data tends to argue for no net benefit derived from corticosteroids in the treatment of SARS-CoV and MERS-CoV (38-40). Recently, the study of the largest case series of 2019-nCoV from Wuhan showed that there was no effective outcomes were observed with usage of varied dose of methylprednisolone (25).

The outbreak of 2019-nCoV poses a serious challenge to China. Currently, the most effective measures to 2019-nCoV are still early detection and quarantine of new sources of infection, and early diagnosis and supportive treatments for confirmed patients. We have made considerable advances in preventing and controlling emerging infectious diseases since the SARS-CoV epidemic 17 years ago. Besides, based on the successful therapy of SARS-CoV, a series of effective treatments have been adopted in the patients with 2019-nCoV. Therefore, we have the confidence to effectively curb the outbreak of 2019-nCoV. The epidemic peak may reach soon and the final victory is not far away.

Acknowledgement

The correspondence author doctor You participate in the fight against the 2019-nCoV on the frontline. The authors gratefully acknowledge and in

memory of doctor Wenliang Li who first stepped up to warn the public about the outbreak of the novel virus, as well as thousands of unsung heroes in the fight against the epidemic of 2019-nCoV.

Funding

The research was supported by National Natural Science Foundation of China (No. 81873451).

Competing interests

The authors declare that they have no competing interests.

References

1. Fehr AR, Perlman S. Coronaviruses: an overview of their replication and pathogenesis. *Methods Mol Biol* 2015;1282.
2. Li G, Fan Y, Lai Y, et al. Coronavirus Infections and Immune Responses. *J Med Virol* 2020.
3. Cui J, Li F, Shi Z-L. Origin and evolution of pathogenic coronaviruses. *Nat Rev Microbiol* 2019; 17: 181-192.
4. Su S, Wong G, Shi W, et al. Epidemiology, Genetic Recombination, and Pathogenesis of Coronaviruses. *Trends Microbiol* 2016; 24: 490-502.
5. Channappanavar R, Perlman S. Pathogenic human coronavirus infections: causes and consequences of cytokine storm and immunopathology. *Semin Immunopathol* 2017; 39: 529-539.
6. Drosten C, Günther S, Preiser W, et al. Identification of a novel coronavirus in patients with severe acute respiratory syndrome. *N Engl J Med* 2003; 348: 1967-1976.
7. Ksiazek TG, Erdman D, Goldsmith CS, et al. A novel coronavirus associated with severe acute respiratory syndrome. *N Engl J Med* 2003; 348: 1953-1966.
8. WHO. Middle East respiratory syndrome coronavirus (MERS-CoV). 2020.
9. Chan JF-W, Kok K-H, Zhu Z, et al. Genomic characterization of the 2019 novel human-pathogenic coronavirus isolated from a patient with

atypical pneumonia after visiting Wuhan. *Emerg Microbes Infect* 2020; 9: 221-236.

10. Huang C, Wang Y, Li X, et al. Clinical features of patients infected with 2019 novel coronavirus in Wuhan, China. *Lancet* 2020.

11. Wang R, Zhang X, Irwin DM, et al. Emergence of SARS-like Coronavirus poses new challenge in China. *J Infect* 2020.

12. Lu R, Zhao X, Li J, et al. Genomic characterisation and epidemiology of 2019 novel coronavirus: implications for virus origins and receptor binding. *Lancet* 2020.

13. Paraskevis D, Kostaki EG, Magiorkinis G, et al. Full-genome evolutionary analysis of the novel corona virus (2019-nCoV) rejects the hypothesis of emergence as a result of a recent recombination event. *Infect Genet Evol* 2020; 79: 104212.

14. Zhou P, Yang X-L, Wang X-G, et al. A pneumonia outbreak associated with a new coronavirus of probable bat origin. *Nature* 2020.

15. Zhao Y, Zhao Z, Wang Y, et al. Single-cell RNA expression profiling of ACE2, the putative receptor of Wuhan 2019-nCoV. *bioRxiv* 2020: 2020.2001.2026.919985.

16. Li Q, Guan X, Wu P, et al. Early Transmission Dynamics in Wuhan, China, of Novel Coronavirus-Infected Pneumonia. *N Engl J Med* 2020.

17. Zhou P, Yang X-L, Wang X-G, et al. Discovery of a novel coronavirus associated with the recent pneumonia outbreak in humans and its

potential bat origin. *bioRxiv* 2020: 2020.2001.2022.914952.

18. D W, B H, C H, et al. Clinical Characteristics of 138 Hospitalized Patients With 2019 Novel Coronavirus-Infected Pneumonia in Wuhan, China. *JAMA* 2020.

19. Chen N, Zhou M, Dong X, et al. Epidemiological and clinical characteristics of 99 cases of 2019 novel coronavirus pneumonia in Wuhan, China: a descriptive study. *Lancet* 2020.

20. Zhang H, Kang Z, Gong H, et al. The digestive system is a potential route of 2019-nCov infection: a bioinformatics analysis based on single-cell transcriptomes. *bioRxiv* 2020: 2020.2001.2030.927806.

21. Lu C-w, Liu X-f, Jia Z-f. 2019-nCoV transmission through the ocular surface must not be ignored. *The Lancet*.

22. Mahase E. China coronavirus: what do we know so far? *BMJ* 2020; 368: m308.

23. Wu JT, Leung K, Leung GM. Nowcasting and forecasting the potential domestic and international spread of the 2019-nCoV outbreak originating in Wuhan, China: a modelling study. *Lancet*. 2020.

24. Wang D, Hu B, Hu C, et al. Clinical Characteristics of 138 Hospitalized Patients With 2019 Novel Coronavirus-Infected Pneumonia in Wuhan, China. *JAMA* 2020.

25. Michael DC, Susan MP, Mona RL, ea al. Severe Acute Respiratory Syndrome. *Clin Infect Dis* 2004; 38: 1420-1407.

26. Carlos WG, Dela Cruz CS, Cao B, et al. Novel Wuhan (2019-nCoV) Coronavirus. *Am J Respir Crit Care Med* 2020.
27. Chu CM, Cheng VCC, Hung IFN, et al. Role of lopinavir/ritonavir in the treatment of SARS: initial virological and clinical findings. *Thorax* 2004; 59: 252-256.
28. Momattin H, Al-Ali AY, Al-Tawfiq JA. A Systematic Review of therapeutic agents for the treatment of the Middle East Respiratory Syndrome Coronavirus (MERS-CoV). *Travel Med Infect Dis* 2019; 30: 9-18.
29. Xu Z, Peng C, Shi Y, et al. Nelfinavir was predicted to be a potential inhibitor of 2019-nCoV main protease by an integrative approach combining homology modelling, molecular docking and binding free energy calculation. *bioRxiv* 2020: 2020.2001.2027.921627.
30. Sheahan TP, Sims AC, Leist SR, et al. Comparative therapeutic efficacy of remdesivir and combination lopinavir, ritonavir, and interferon beta against MERS-CoV. *Nat Commun* 2020; 11: 222.
31. Agostini ML, Andres EL, Sims AC, et al. Coronavirus Susceptibility to the Antiviral Remdesivir (GS-5734) Is Mediated by the Viral Polymerase and the Proofreading Exoribonuclease. *mBio* 2018; 9: pii: e00221-218.
32. Wang M, Cao R, Zhang L, et al. Remdesivir and chloroquine effectively inhibit the recently emerged novel coronavirus (2019-nCoV)

in vitro. Cell Research 2020.

33. Holshue ML, DeBolt C, Lindquist S, et al. First Case of 2019 Novel Coronavirus in the United States. N Engl J Med 2020.

34. Tian X, Li C, Huang A, et al. Potent binding of 2019 novel coronavirus spike protein by a SARS coronavirus-specific human monoclonal antibody. bioRxiv 2020: 2020.2001.2028.923011.

35. Richardson P, Griffin I, Tucker C, et al. Baricitinib as potential treatment for 2019-nCoV acute respiratory disease. The Lancet 2020.

36. orneli HM, Zorc JJ, Mahajan P, et al. A multicenter, randomized, controlled trial of dexamethasone for bronchiolitis. N Engl J Med 2007; 357: 331-339.

37. Ni YN, Chen G, Sun J, et al. The effect of corticosteroids on mortality of patients with influenza pneumonia: a systematic review and meta-analysis. Crit Care 2019; 23: 99.

38. Clark DR, Jonathan EM, Baillie JK. Clinical evidence does not support corticosteroid treatment for 2019-nCoV lung injury. Lancet 2020.

39. 2Arabi YM, Mandourah Y, Al-Hameed F, et al. Corticosteroid therapy for critically ill patients with middle east respiratory syndrome. Am J Respir Crit Care Med 2018; 197: 757-767.

40. Stockman LJ, Bellamy R, Garner P. SARS: systematic review of treatment effects. PLoS Med 2006; 3: e343.

Legends to figure and table

Figure 1

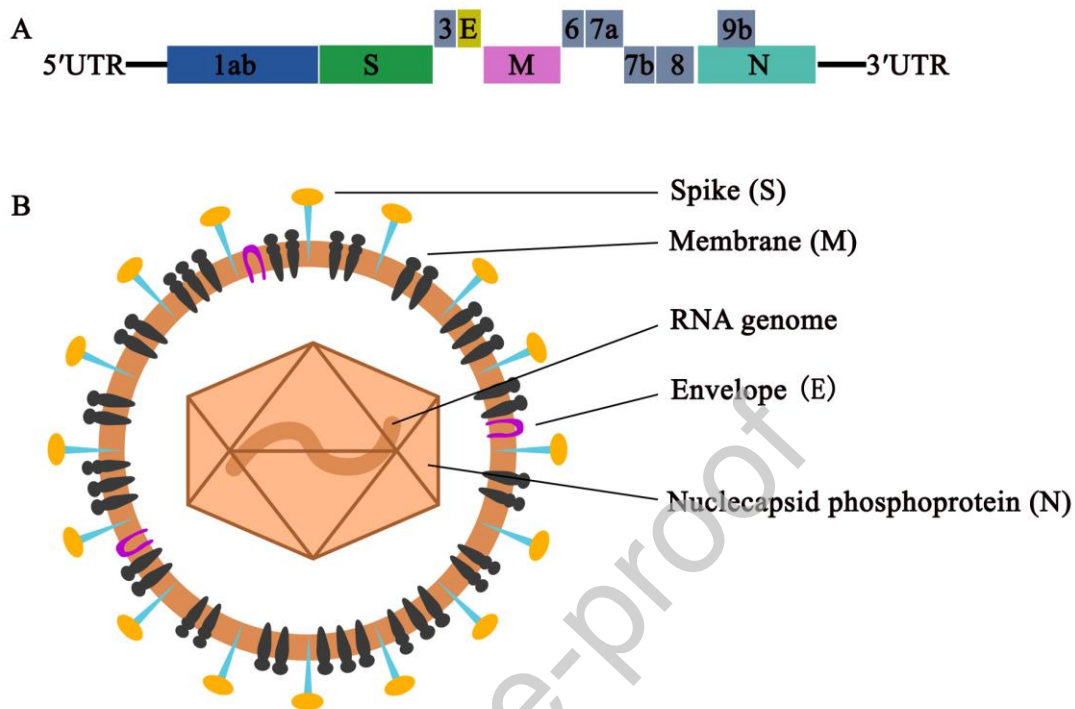


Figure 1. Genomic organization and virus structure of 2019-nCoV. (A)

2019-nCoV genome comprises of 5' untranslated region (5' UTR) including 5' leader sequence, open reading frame (ORF) 1a/b, envelop, membrane and nucleoprotein, accessory proteins such as orf 3, 6,7a, 7b, 8 and 9b and 3' untranslated region (3' UTR) in sequence. **(B)** 2019-nCoV structure consists of single-strand, positive-sense RNA as the genetic material surrounded by nucleocapsid protein in the core and an envelope containing four proteins: Spike protein, Envelope protein, Membrane protein.

Table 1. Clinical Characteristics of patients with 2019-nCoV and SARS-CoV.

	2019-nCoV*	SARS-CoV
Epidemiology		
Outbreak date	December, 2019	November, 2002
Location of first case	Wuhan, China	Guangdong, China
Confirmed cases	37590 (Feb9, 2020)	8096
Mortality	813 (2.2%) (Feb9, 2020)	744 (10%)
Healthcare practitioners	29%	23.1%
Characteristics		
Age, years (range)	56 (42-68)	39.9 (1-91)
Male: female ratio	1: 1.19	1: 1.25
Fever	98.6%	99-100%
Fatigue	69.6%	31.2%
Nonproductive cough	59.4%	25%-75%
Myalgia	34.8%	49.3%-60.9%
Dyspnea	31.2%	40-42%
Expectoration	26.8%	NR
Sorethroat	17.4%	12.5%
Diarrhea	10.1%	20-25%
Nausea and/or vomiting	6.3%-10%	19.4%-19.6%
Dizziness	9.4%	4.2%- 42.8%
Headache	6.5%	35.4%- 55.8%
Abdominal pain	2.2%	3.5%

Data are n, age (range), or n (%) unless otherwise stated.

2019-nCoV=2019 novel coronavirus. SARS-CoV=severe acute respiratory syndrome coronavirus.

* Epidemiology and characteristics for 2019-nCoV infection are based on the data from the 138 patients reported by Dawei Wang and colleagues (reference 24). The date of SARS-CoV is from the review by Michael DC (reference 25). Case numbers and mortalities are updated up to 0:00 am Feb 9, 2020) as disclosed by the Chinese Health Commission.