

## REVIEW ARTICLE

# Biochemical Dynamics and Clinical Features of Novel Corona Virus (2019-nCoV)

Taha Nazir, BPharm, MPhil, PhD; Saeed Ur Rashid Nazir, BPharm, MPhil, MBA, PhD;

Misbah Sultana, BPharm, MPhil, PhD; Nida Taha, PharmD, MPhil; Humayun Riaz, BPharm, MPhil, PhD; Azharul Islam, BSc, MSc, MPhil; Ruqaiya Rasheed Kayani, Pharm D, MPhil; Saba Manzoor, PharmD, MPhil

### ABSTRACT

**Context** • The novel Corona Virus (nCoV-19) was initially reported in Wuhan, China during December 2019, and later people with nCoV-19 were identified in different parts of the world. Infected people had shown symptoms resembling pneumonia, but about 50% of patients were asymptomatic.

**Objective** • The study intended to examine the data from studies on nCoV-19.

**Design** • The research team performed a literature review, searching relevant literature databases. The sources of data included bioRxiv, medRxiv, Google Scholar, Embase, PsychINFO, WanFang Data and PubMed. The search terms were novel Corona Virus, and nCoV-19 structure.

**Setting** • The study took place in the main library of the University of Sargodha, Sargodha, Pakistan.

**Results** • The study identified 22 studies that had reported and confirmed over 2000 cases of nCoV-19 by January 26, 2020. The studies found that the virus was transmitted through respiratory droplets. The virus has two serotypes, OC43 and 229E.

**Conclusions** • No specific curative therapy is available for CoVid-19. However, certain precautionary measures may potentially reduce the transmission, including washing hands, using sanitizers frequently, avoiding public gatherings, and quarantining or isolating patients. This virus has spread globally and immunocompromised individuals, and especially older individuals, are at significant risk. Community and healthcare professionals have a positive role to play in controlling the spread of the disease. (*Altern Ther Health Med.* 2020;26(S2):50-53)

**Taha Nazir, BPharm, MPhil, PhD**, is a CEO of Microbiology and Molecular Biology Research Group, Advanced, Advanced Multiple Incorporation, Mississauga, Ontario, Canada. **Saeed Ur Rashid Nazir, BPharm, MPhil, MBA, PhD**, is an Assistant Professor in the College of Pharmacy, University of Sargodha, Sargodha, Pakistan. **Misbah Sultana, BPharm, MPhil, PhD**, is an Associate Professor in University College of Pharmacy, University of the Punjab, Lahore, Pakistan. **Nida Taha, PharmD, MPhil**, is a scientist in Microbiology and Molecular Biology Research Group, Advanced Multiple, Incorporation Mississauga, ON, Canada. **Humayun Riaz, BPharm, MPhil, PhD**, is a professor in Rashid Latif College of Pharmacy, Lahore, Pakistan. **Azharul Islam, BSc, MSc, MPhil**, is a scientist in Department of Internal Medicine, University of Texas Medical Branch, Galveston, Texas, USA. **Ruqaiya Rasheed Kayani, PharmD, MPhil**, is a Clinical Pharmacist and Pharmacologist in Lahore, Pakistan. **Saba Manzoor, PharmD, MPhil**, is a Community Pharmacist at Fazal Din Pharma Plus, Lahore, Pakistan.

Corresponding author: Saeed Ur Rashid Nazir, BPharm, MPhil, MBA, PhD

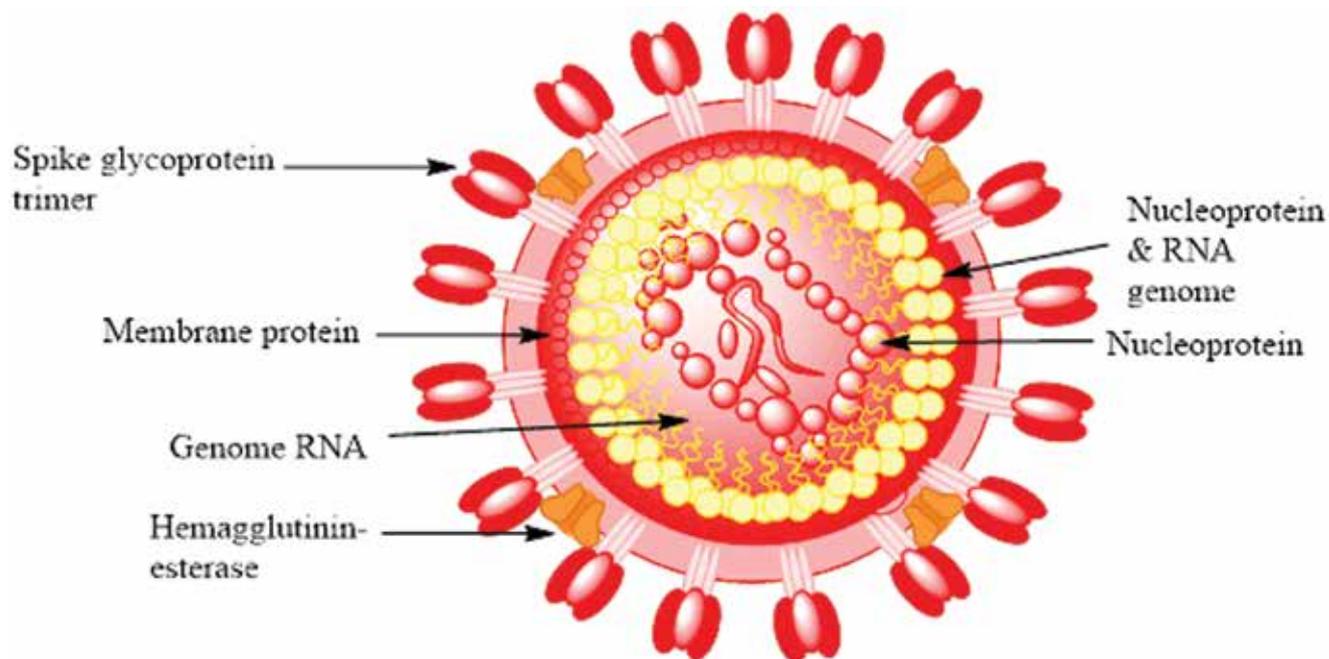
E-mail address: [srnazir@yahoo.com](mailto:srnazir@yahoo.com)

A novel coronavirus was initially reported in Wuhan, China during December 2019, and the causative agent was originally unknown. Often, infected people showed symptoms resembling pneumonia. Subsequently, the virus was provisionally named nCoV-19.<sup>1</sup> Medical practitioners had reported and confirmed 2000 cases of nCoV-19 by January 26, 2020; infected individuals had been visiting or living in the city of Wuhan.<sup>2</sup> Now people with nCoV-19 have been identified throughout the world.

CoVid-19's symptoms are severe acute respiratory syndrome in addition to those of the common cold, and it's transmitted through respiratory droplets.<sup>3</sup> Infection in humans may have originated from an animal coronavirus.<sup>4</sup> The virus has a helical nucleocapsid, has RNA with a positive polarity and is single stranded, is enveloped, and has no polymerase viron.<sup>5</sup>

In one study, researchers found that CoVid-19 has two serotypes OC43 and 229E.<sup>6</sup> Those researchers indicated that the pathogenesis includes the respiratory tract which targets the epithelial cells of the respiratory tract, resulting in diffuse alveolar damage and that infections were asymptomatic 50% of the time. Another study found that reinfection can occur because immunity to the virus is brief and laboratory

**Figure 1.** The figures shows the molecular structure of nCoV-19 with its predominant features



diagnosis revealed that antibodies were produced but then the levels slowly decline and people become susceptible again.<sup>7</sup> PCR-based and antibody-based tests were available but often were not performed.<sup>2</sup>

No specific curative therapy is available for CoVid-19. However, certain precautionary measures may potentially reduce the transmission including washing hands, using sanitizers frequently, avoiding public gatherings, and quarantining or isolating patients.<sup>7</sup>

## METHODS

### Procedures

The research team searched the relevant literature databases in Feb, 2020. The sources of data included bioRxiv, medRxiv, Google Scholar, Embase, PsychINFO, as well as WanFang Data and PubMed. The search terms were novel Corona Virus, and nCoV-19 structure.

These online databases contain archives of most English and Chinese biomedical journals. Only papers that were published in English were considered, and all available years in each database were searched. The initial search identified 28 published articles, for which the research team obtained full texts and independently read them in full to identify those papers suitable for inclusion in the review. Studies included above mentioned terms were all considered. Eventually, 22 unique academic publications were included in this study. Non-scientific commentary, reports, and news articles were excluded from the analysis. Disagreements on the inclusion or exclusion of literature were resolved through discussion. Using a Microsoft Excel spreadsheet, data were extracted from the chosen studies. No blinding regarding a journal or author was done.

## RESULTS

### Etiology and Phylogeny

Rhinoviruses and coronaviruses cause the common cold, with rhinoviruses being its most significant cause. Severe acute respiratory syndrome (SARS), with atypical pneumonia was traced in late 2019 at a seafood wholesale market in Wuhan of China. Another study showed that an epidemic of severe acute respiratory syndrome (SARS) has been associated with an outbreak of atypical pneumonia originating at China in 2002.<sup>8</sup> One more study demonstrated that Middle east respiratory syndrome (MERS), with severe pneumonia emerged in 2012.<sup>9</sup> One more study found that the genome sequence for 2019-nCoV was different than that of CoV-SARS but that it has some similarity in different isolates to SARS.<sup>10</sup> Those researchers found that angiotensin converting enzyme 2 is the receptor surface for the SARS coronavirus.

Although 2019-nCoV has some similarities to SARS-CoV, researchers initially deliberated whether it was a new beta-coronavirus in humans. Although phylogenetic analysis has indicated that the original viral host may have been bats, the seafood market in Wuhan sells animals that might have acted as intermediate hosts, expediting the virus' appearance in humans.<sup>11</sup>

Significantly, structural analysis of 2019-nCoV has indicated that the virus may be able to bind to the angiotensin-converting enzyme 2 receptor in humans.<sup>12</sup> Its advancement, alteration, and extent of spread deserves urgent investigation and research.

The corona virus binds to cells through spikes on its surface, known as hemagglutinin, and enters the cytoplasm and uncoats itself there.<sup>12</sup> Translation of the positive-strand

genome occurs in the cytoplasm, becoming 2 large replicase polyproteins expressed by two open reading frames (ORF1a and ORF1b) that are linked together by a ribosomal frameshift.<sup>12</sup> Then the protease, into which the virus encoded itself, cleaves the replicase polyproteins at 11 conserved sites.<sup>13</sup>

An RNA-dependent RNA polymerase, a 3C-like serine proteinase (3CLpro), a papain-like proteinase (PL2pro), and a superfamily 1-like helicase (HEL1) that is responsible for replicating the viral RNA genome.<sup>11</sup> Structural proteins are formed by synthesis and translation of mRNA. Virus assembly and envelope is obtained from endoplasmic reticulum.<sup>14</sup>

### Epidemiology and Transmission

The mode of transmission of coronaviruses is respiratory aerosol. These infections occur globally in early life, and antibodies are found in almost half of children. Viral epidemics occur predominantly in the winter, with 2 to 3 years between occurrence of specific viruses.<sup>15</sup>

In November 2002, SARS appeared in China and rapidly spread to other countries. Of the 8300 reported cases, 785 patients died, with a fatality rate of 9%.<sup>1</sup> The mode of transmission was from human to human. Some patients who carried the virus were known as super-spreaders.<sup>16</sup>

In the primary outbreak of SARS, most hospital personnel were infected, but control through respiratory-infection techniques significantly abridged the spread. Animals were suspected to be the source of CoV-SARS. The natural host for CoV-SARS appears to be the horseshoe bat, and the intermediate host the civet cat.<sup>14</sup>

### Challenges

Other coronaviruses that cause respiratory illnesses in humans and 2019-nCoV aren't closely related. The 2019-nCoV translated proteins may be affiliated with the supplementary species Orthocoronavirinae. Su et al used genome sequences to construct a phylogenetic tree.<sup>17</sup> By analyzing the absence or presence of 10 homolog proteins of 2019-nCoV, the researchers established a cluster tree from the retrieved profiles.

Li et al used the data that Su et al's study retrieved to characterize the association between the 10 translated 2019-nCoV proteins and those of other species of Orthocoronavirinae.<sup>18</sup> That study intended to evaluate whether the 2019-nCoV is related most closely to BatCoV RaTG13, which belongs to the subgenus Sarbecovirus of Betacoronavirus, and to the SARS coronavirus and Bat-SARS-like coronavirus.

From the 10 homolog proteins of 2019-nCoV, Li et al found two clades by sequencing genomes through a phylogenetic profiling cluster of homolog proteins, and one 2019-nCoV protein was revealed. The Clade 1 Group of conserved protein of Clade 1 comprised Spike glycoprotein, Orf1lab polyprotein, membrane proteins, and nucleocapsid proteins. The Clade 2 group comprised 6 proteins, which excluded Hypercovers and Sarbeovirus.

Two nonstructural proteins for the Clade 2 group were NS7b and NS8, and they were absolutely conserved by 2019-nCoV, BatSARS-CoV and BetaCoV\_RaTG. One earlier study had found that NS7b and NS8 affected human immune-response signaling in an experimental model of SARS-CoV.<sup>2</sup> Knowledge of the functional variations in NS7b and NS8 proteins through advancement may offer significant evidence in efforts to discover the human infective property of 2019-nCoV.<sup>19</sup>

### Recommendations

The research team suggests that the public and patients be advised to follow the recommendations below strictly:

- Avoid close contact with patients suffering from respiratory infections, which may be acute or chronic.
- Wash your hands hourly for 20 seconds with soap and water.
- Avoid unprotected contact with wild or farm animals.
- If you have symptoms of an acute respiratory infection, cover your mouth with a disposable cloth or tissue papers while coughing or sneezing, remain at a distance from other people, and wash your hands frequently.
- If you are immunocompromised, avoid public gatherings and exposure. If you find it necessary to be in contact with other individuals in a closed space, use gloves, masks, and antiseptic soap, and make sure the room has been cleaned with antiseptic agents prior to exposure. Such a gathering should occur only in a true emergency.
- Practice strict measures for personal hygiene for the control and prevention of the disease.<sup>20</sup>

Instructions for survivors of SARS-COV-2 with long-term complications who now are suffering from 2109-nCoV. are not available yet. Globally the mortality rate is between 1-2%.

### CONCLUSIONS

Since the epidemic of 2109-nCoV in the city of Wuhan, China, the disease has spread globally. Immunocompromised individuals and the elderly are at significant risk. Healthcare providers should play a role in presenting the facts related to the disease, provide supportive care and should adopt as their explicit purpose to continually reduce the burden of illness and also improve the health and functioning of the people. Furthermore, the community and healthcare professionals should play a positive role in controlling and reducing the spread of the disease.

### AUTHORS' DISCLOSURE STATEMENT

The authors received no funding for and have no conflicts of interest with respect to the review.

## REFERENCES

1. Wang C, Horb PW, Hayden FG, Gao GF. A novel coronavirus outbreak of global health concern. *The Lancet*. 2020; 395(10223), 470-473.
2. Zhu N, Zhang D, Wang W, Li X, Yang B, Song J, et al. A novel coronavirus from patients with pneumonia in China, 2019. *N Engl J Med*. 2020; 382: 327-33.
3. Assiri A, McGeer A, Perl TM, Price CS, Al Rabeeah AA, Cummings DA, et al. Hospital outbreak of Middle East respiratory syndrome coronavirus. *N Engl J Med* 2013; 369: 407-416.
4. Wu F, Zhao S, Yu B, Chen Y-M, Wang W, Song Z-G, et al. A new coronavirus associated with human respiratory disease in China. *Nature*. 2020; 579(7798):265-269.
5. Zhao L, Jha BK, Wu A, Elliott R, Ziebuhr J, Gorbalenya AE, Silverman RH, Weiss SR. Antagonism of the interferon-induced OAS-RNase L pathway by murine coronavirus ns2 protein is required for virus replication and liver pathology. *Cell host & microbe*. 2012;11(6):607-616.
6. Chan JF-W, Yuan S, Kok K-H, To KK-W, Chu H, Yang J, et al. (). A familial cluster of pneumonia associated with the 2019 novel coronavirus indicating person-to-person transmission: A study of a family cluster. *Lancet*. 2020; 395(10223):514-523.
7. Christian MD, Loutfy M, McDonald LC, Martinez KE, Ofner M, Wong T Low DE, et al. (2004). Possible SARS coronavirus transmission during cardiopulmonary resuscitation. *Emerging infectious diseases*, 10(2), 287-93.
8. Zhong N, Zheng B, Li Y, Poon L, Xie Z, Chan K, et al. Epidemiology and cause of severe acute respiratory syndrome (SARS) in Guangdong, People's Republic of China, in February, 2003. *Lancet*. 2003; 362(9393):1353-1358.
9. Assiri A, McGeer A, Perl TM, Price CS, Al Rabeeah AA, Cummings DA, Madani H, et al. (2013). Hospital outbreak of Middle East respiratory syndrome coronavirus. *N Engl J Med*. 369(5), 407-416.
10. Peng, X., Xu, X., Li, Y., Cheng, L., Zhou, X., & Ren, B. (2020). Transmission routes of 2019-nCoV and controls in dental practice. *International Journal of Oral Science*, 12(1), 1-6.
11. Zhou P, Yang X-L, Wang X-G, Hu, B., Zhang L, Zhang W, et al. A pneumonia outbreak associated with a new coronavirus of probable bat origin. *Nature*. 2020; 579, 270-73.
12. Ziebuhr J, Siddell SG. (1999). Processing of the human coronavirus 229E replicase polyproteins by the virus-encoded 3C-like proteinase: identification of proteolytic products and cleavage sites common to pp1a and pp1ab. *Journal of virology*, 73(1), 177-185.
13. Chan JFW, Kok KH, Zhu Z, Chu H, To KKW, Yuan S, Yuen KY. (2020). Genomic characterization of the 2019 novel human-pathogenic coronavirus isolated from a patient with atypical pneumonia after visiting Wuhan. *Emerging Microbes & Infections*, 9(1), 221-236.
14. Weiss SR and Leibowitz JL. Coronavirus pathogenesis. *Advances in virus research*. 2011; 81:85-164.
15. Gao GF. From "A" IV to "Z" IKV: Attacks from emerging and re-emerging pathogens. *Cell*. 2018; 172(6):1157-1159.
16. Phan LT, Nguyen TV, Luong QC, Nguyen TV, Nguyen HT, Le HQ, et al. Importation and human-to-human transmission of a novel coronavirus in Vietnam. *N Engl J Med*. 2020; 382(9):872-874.
17. Su S, Wong G, Shi W, Liu J, Lai AC, Zhou J, et al. Epidemiology, genetic recombination, and pathogenesis of coronaviruses. *Trends in Microbiology*. 2016; 24(6):490-502.
18. Li C, Yang Y, Ren L. Genetic evolution analysis of 2019 novel coronavirus and coronavirus from other species. *Infection, Genetics, and Evolution*, 2020; 104285.
19. Wang L, Su S, Bi Y, Wong G, Gao GF. Bat-origin coronaviruses expand their host range to pigs. *Trends in Microbiology*. 2018; 26(6):466-470.
20. Li DKT. Challenges and responsibilities of family doctors in the new global coronavirus outbreak. *Family Medicine and Community Health*. 2020; 8(1).