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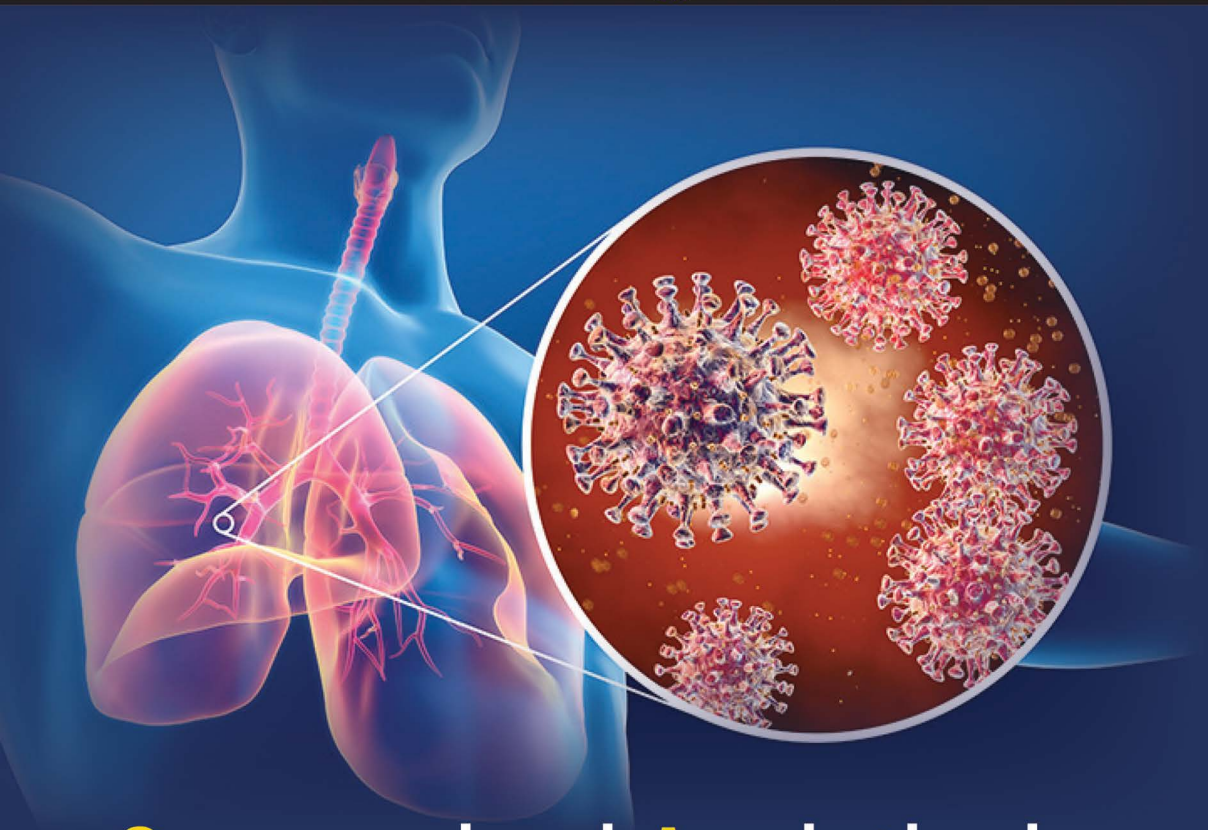

Summarized Analytical Review of System Involvement in COVID-19



Jayanthi Rangarajan

Forewords
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JAYPEE

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CHAPTER 2

COVID-19 and its Variants

N Rathna Priya

INTRODUCTION

Viruses infecting the respiratory tract are many. Coronaviruses infect humans causing mild to severe respiratory infections. They also cause infections in many different animals. Severe Acute Respiratory Syndrome coronavirus (SARS-CoV) was detected in 2002. Middle East Respiratory Syndrome coronavirus (MERS-CoV) emerged in 2012. Both the viruses were of zoonotic origin. These two highly pathogenic coronaviruses emerged to cause fatal respiratory illnesses in humans. It is one of the major public health concerns in the 21st century.[1,2]

SARS-CoV-2 emerged in 2019 as a novel coronavirus, during an outbreak of an unusual pneumonia,[3] which was reported from the city of Wuhan in China. This outbreak posed a global public health threat surpassing SARS and MERS and was known as coronavirus disease 2019 (COVID-19). The incidence rate was higher and the spread was faster due to the high transmissible nature of the novel virus, which overwhelmingly surpassed SARS and MERS viruses.[4]

Some microbes have the unique characteristic of changing their antigenic nature themselves. The modified forms are identified as their variants. Similarly, SARS-CoV-2 has many variants. One of its variants has acquired such a characteristic that enabled the virus to cause infections leading to a high mortality rate. That particular variant has been named as COVID-19[5] and has features that help it to survive in extremes of environment without losing its infectivity.[6]

EMERGENCE AND SPREAD

Clusters of patients with pneumonia of an unknown cause were reported from the health facilities in Wuhan, Hubei Province, China, in late December 2019.[7] Symptoms of pneumonia were similar to SARS and

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MERS virus infection, such as fever, cough, and chest discomfort, which worsened to cause difficulty in breathing due to bilateral lung infiltration. Epidemiological analysis of the first 27 documented hospitalized patients suggested the possibility of the SARS-CoV-2 to have originated from the Huanan Seafood Wholesale Market[1] in the downtown Wuhan. This is a wet market that sells seafood along with animals and birds of all kinds. A study has suggested that the first known case of COVID-19 disease had occurred most probably on December 8, 2019. On December 31, 2019, it was declared to the public by the Wuhan Municipal Health Commission. The notification reported it as a pneumonia outbreak of unidentified cause and also informed the World Health Organization (WHO).[1,8]

Independent teams of scientists collected samples from patients with symptoms of severe pneumonia in China. Betacoronavirus was identified in the bronchoalveolar lavage fluid samples by molecular analysis using metagenomic ribonucleic acid (RNA) sequencing and virus isolation methods.[9] The scientists in various independent teams identified and reported betacoronavirus as the causative agent, which had never been found before. This scientific evidence of the causative virus was made known to the public on January 9, 2020. Genomic sequences of the novel coronavirus identified by the various research institutes in China were published first on January 10, 2020, on the Virological Website, and almost complete genome sequences were released in the Global Initiative on Sharing All Influenza Data (GISAID) database on January 12, 2020.[2]

The spread of SARS-CoV-2 was identified when several family clusters of pneumonia were reported in the community and many cases of healthcare-associated pneumonia occurred in the healthcare facilities. The infection was found to occur in individuals who had never been to the Huanan Seafood Wholesale Market. Human-to-human transmission of the new virus was finally concluded after a careful study of the above events. The reason for the spread to other countries is the travel between cities before the celebration of the lunar New Year festival in China, which facilitated the spread to other cities and within a short duration of less than a month a massive spread to 34 provinces of China occurred, including Hubei province. As thousands of confirmed cases of newly diagnosed novel coronavirus were reported every day causing a spread to other parts of China as well as to other countries, a clear picture of a pandemic in evolution was identified.[2] The WHO declared it to be a public health emergency and named the novel virus as a Variant of International Concern. The nomenclature was decided by the International Committee on Taxonomy of Viruses as "SARS-CoV-2" on February 11, 2020. The WHO named the disease as "COVID-19" and officially declared it as a pandemic on March 11, 2020.[1] The spread of SARS-CoV-2 to other parts of the world occurred rapidly due to the high transmissible nature of the virus along with an easy access and low cost of the international air travel.[4,9,10] Although the spread of COVID-19 was controlled in China by March 2020, the number of infected individuals was on the rise in Europe, the United States, and other regions of the world.[1,2]

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The Center for Systems Science and Engineering at Johns Hopkins University updates the statistics periodically in their dashboard. According to their statistics, as on August 11, 2020, COVID-19 has seeded 216 countries. Approximately 20 million cases were diagnosed at that point of time.[1] The center has also stated that when there was an overwhelming need for the healthcare resources, the mortality rate increased very much, causing the overall death toll to be more than 733,000, with the United States topping the list with the highest number of cases.[2]

Many scientific reports were published from many countries. One report from France mentioned the detection of SARS-CoV-2 virus in a sample collected and stored in December 2019 from a patient with pneumonia, which implies that the spread to France had occurred much earlier than the actual outbreak. There were few reports stating the detection of SARS-CoV-2 virus in cases from Wuhan, who had never been to the market selling seafood, which rules out the possibility of the origin of the virus from the seafood market.[2]

TAXONOMY

Severe acute respiratory syndrome coronavirus 2 belongs to the family Coronaviridae. Its genus is *Betacoronavirus*. Its subgenus is *Sarbecovirus*. Although there is not much evidence to conclude when and where the novel virus first entered into humans, genomic analysis has proven that SARS-CoV-2 is a natural virus and has most likely originated in animals. Similar to SARS-CoV virus, the novel SARS-CoV-2 virus is also a positive sense, enveloped virus with a single-stranded RNA. The genome size is approximately 30 kb.[2,11,12]

The genome encodes four basic structural proteins needed to form the morphology of the virus. The spike (S) protein is found on the outer surface of the envelope (E) protein and gives the appearance of crown (meaning of Corona). The nucleocapsid (N) is held inside the membrane (M) protein. There are enzymes and a few other proteins, including RNA-dependent RNA polymerase (RdRp), which are known as nonstructural proteins. Each microbe has a unique genomic sequence. The genotype of the virus is studied through gene sequencing, which helps to identify novel pathogens. Once this virus enters into the respiratory tract, the viral S protein enters the host cell after attaching to the angiotensin-converting enzyme 2 (ACE2) receptor. There are many domains within a protein molecule. The receptor-binding domain (RBD) of the spike protein is similar to a key that has to fit into the lock present on the target cell of the host. This binding helps the virus to enter into the host cell. This binding is the key mechanism for natural immunity. This key step has been made use of to design vaccines and their immunity.[11]

Ribonucleic acid viruses commonly exhibit antigenic variations compared to deoxyribonucleic acid (DNA) viruses. Mutations occur in the bacteria and viruses periodically. Few mutations occurring at the nucleotide

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level that does not have an evolutionary disadvantage are retained in the microbe. Such useful mutations occur at a rate of 1×10^{-3} substitutions/site/year. The mutation in the genome occurring at this relatively low rate produces approximately one substitution every 2 weeks.[11]

GENOMICS AND PHYLOGENY

Severe acute respiratory syndrome coronavirus 2 has 79% genomic similarity with SARS-CoV. However, it has only 50% genomic similarity with MERS-CoV.[1] Accessory proteins are interspersed with structural proteins in such a way that the overall length matches with the SARS-CoV. Out of the four structural proteins, S protein alone is different in SARS-CoV and SARS-CoV-2. Otherwise, the structural proteins and nonstructural proteins of SARS-CoV-2 have 90 and 85% similarity in the amino acid sequence with SARS-CoV, respectively. Approximately two-thirds of the 5' genome is occupied by the replicase gene, which encodes a large polyprotein (pp1ab). The polyprotein helps in transcription and viral replication.[13-15]

The whole genome sequencing of SARS-CoV-2 placed it under the genus *Betacoronavirus* and subgenus *Sarbecovirus*, clustering close to the SARS-CoV and SARS-related coronaviruses (SARSr-CoVs) found in bats.[1,16] The four horse-shoe bat coronavirus isolates (RaTG13, RmYN02, ZC45, and ZXC21) are grouped together with SARS-CoV and other SARSr-CoVs. But SARS-CoV-2 alone is placed in a distinct lineage within this clade, as it is phylogenetically related to SARS-CoVs.[2,3]

The amino acid sequence of the S protein matched to about 90.7–92.6% with the coronaviruses that infected the pangolins. But with the coronaviruses that infected the bats and humans, SARS-CoV-2 showed 75–97.7% and 76.7–77% similarity, respectively. When the amino acid sequence of the receptor-binding protein of S protein was analyzed, there was only 73% similarity. Further analysis of the S protein identified a four amino acid residue (PRRA). This residue was inserted at the junction of the S1 and S2 subunits.[1,2,17]

In phylogeny of viruses, the evolution of the lineages is analyzed with reference to the lines of descent, and the contact tracing is done, which helps in understanding the dynamics of virus transmission. A phylogenetic tree is constructed to understand how close is a variant to the original virus. Such an analysis of the phylogenesis provides adequate information about any outbreak.[11]

NOMENCLATURE

The variants of SARS-CoV-2 are placed together considering their lineage and component mutations. The variants were named after the country in which they were detected initially.

The WHO considered the stigma faced by those countries, whose name was used to identify the variant. Therefore, to name them in a

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nonstigmatizing fashion, the WHO consulted its experts and concluded on May 31, 2021, that the Greek letters will be used hereafter to refer to the important strains.[5,6,18]

The variants of SARS-CoV-2 were named using the Greek letters from Alpha to Mu. After Mu, the letters Nu and Xi were omitted, and a totally new term "Omicron" was coined in November 2021. The reason for the omission of the Greek letter Xi was to prevent any reference to Xi Jinping, the President of China. The WHO explained the reason for skipping the letter Xi as it is a common last name, and in order to prevent confusion with the word "new," the letter Nu was not used. The members of the WHO have agreed upon naming the future variants after constellations when all the Greek letters have been utilized for the nomenclature.

Similar to Paramyxoviruses, SARS-CoV-2 shows continuous variation due to frequent genetic mutations and/or viral recombinations. This causes a change in the genetic code, which gets carried to the daughter virions during the biosynthesis and assembly of the virus.

The term lineage refers to all the virus variants derived from a common ancestor, which are also genetically closely related to each other.

The term variant refers to those viruses that resemble each other closely except for one or more mutations in few regions.[19]

KEY DEFINITIONS

According to the Center for Disease Control (CDC), the definitions of key words are as follows:

- *Mutation*: "When a change in a virus's genome occurs at only one place, which do not always change the characteristics of the virus."[19]
- *Recombinant*: "When the genomes of two SARS-CoV-2 variants (that have infected a person at the same time) combine during the viral replication process to form a new variant that is different from both parent lineages."[19]
- *Lineage*: "A lineage is a group of closely related viruses with a common ancestor. SARS-CoV-2 has many lineages; all cause COVID-19."[19]
- *Variant*: "A variant is a viral genome (genetic code) that may contain one or more mutations. A group of variants with similar genetic changes belonging to a single lineage or a group of lineages are designated as a Variant Being Monitored (VBM), Variant of Concern (VOC), or a Variant of Interest (VOI) due to shared attributes and characteristics that may require immediate public health action for the control of the spread to other places."[19]

SALIENT POINTS

According to the CDC, the points for identifying a variant are as follows:

- Many lineages of SARS-CoV-2 have been identified through genome sequencing during the COVID-19 pandemic. Newer lineages have emerged around the world.[19]

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- These genetic lineages were routinely monitored through periodical epidemiological analysis, virus genetic sequence-based surveillance, and other laboratory studies.
- On November 30, 2021, the United States government SARS-CoV-2 Interagency Group (SIG) decided to give a new name to the variant. This decision for classifying Omicron as a VOC was based on the following features:
  - Omicron identified in multiple countries
  - Omicron identified in those without any history of recent travel
  - Delta variant was replaced in South Africa
  - Number of substitution mutations and their location in the spike protein
  - Reduced susceptibility to routine treatments
- On April 14, 2022, the Delta variant was downgraded from a VOC to a VBM. This decision was based on the following features:
  - When evidences suggested that there was a significant and sustained reduction in its national and regional proportions over time
  - When the Delta variant did not pose a significant risk to the public[19]
- The four classes of SARS-CoV-2 variants identified as per the SIG variant classification scheme are as follows:
  1. VBM
  2. VOI
  3. VOC
  4. Variant of High Consequence (VOHC)

The VBM is further divided as follows:

- Alpha, which includes B.1.1.7 and Q lineages
- Beta, which includes B.1.351 and its descendent lineages
- Gamma, which includes P.1 and its descendent lineages
- Delta, which includes B.1.617.2 and AY lineages
- Epsilon, which includes B.1.427 and B.1.429
- Eta, which includes B.1.525
- Iota, which includes B.1.526
- Kappa, which includes B.1.617.1
- Not allotted (B.1.617.3)
- Mu, which includes B.1.621, B.1.621.1
- Zeta, which includes P.2

VOC has:

- Omicron, which includes (first B.1.1.529, then BA.1, BA.1.1, then BA.2, BA.3, later BA.4 and BA.5 lineages).

VOHC:

- Such variant has not yet been reported under this category.[10,19]

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CLASSIFICATION OF VARIANTS

Among the microorganisms causing infections worldwide, only a few microbes have the property to undergo antigenic variation, for example, influenza virus and Trypanosoma. The WHO is the authority that oversees the functions of all the healthcare bodies and issues directions to the public as and when needed. The terms VOC and VOI were also used by the WHO. The classifications used in United States are almost similar to that of the WHO, but with a few differences, as it may require a different action plan for its location to assess the impact of the variants and execute the changes made in the control measures immediately. There was a need for a uniform nomenclature during public discussions while referring to the variants. Therefore, the WHO, in consultation with their committee members, suggested the use of Greek letters. From then on, the labels consisting of Alpha, Beta, Gamma, etc., were used to refer to the variants for the nonscientific audiences.[19,20]

Variant status is not fixed, but there is always a chance that the variant might get upgraded or downgraded in position based on the emerging scientific evidences. When a VOC is classified, it always has the features of VOI in it. Therefore, at any point of time, a VOI can change into VOC or vice versa.[19]

The impact of the SARS-CoV-2 pandemic was so devastating on the various aspects of human life that it required a coordinated effort from the various departments to decide and implement appropriate control measures. Therefore, the Department of Health and Human Services (HHS) of the United States established SIG to enhance systematic coordination among the CDC for diagnostics, National Institutes of Health (NIH) for therapeutics, Food and Drug Administration (FDA), and the Biomedical Advanced Research and Development Authority (BARDA) for vaccine production, and the Department of Defense (DoD) for intercontinental and intracontinental safety of the public.[4,8,19,21]

Recommendations are made by the SIG periodically after thorough analysis of the emerging variants. The expert committee evaluates and analyzes the variants reported at the national and regional levels. The team of experts also evaluate in depth the possible impact of the mutations on the public and on the various aspects, such as the need for any other control measures and the transmissible nature of the virus, and reclassify them accordingly. The role of SIG is to detect, identify, and characterize the variants of SARS-CoV-2. The SIG holds discussions, guides, and actively monitors the ways available to control the pandemic.[2,5,19]

Variants being Monitored

All the variants that have been associated with more severe disease or increased transmissibility at some point of time but currently not detected,

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or are found in very low levels only, are grouped under VBM. When the VOI or VOC has almost lost its potential to cause an outbreak or severe disease, it gets downgraded to VBM, and there should also be a significant reduction in their detection in all regions. Therefore, these variants have to be consistently monitored to prevent any adverse impact on the public and also help the public health authorities to immediately carry out the appropriate control measures.[2,19]

Variants under this category were not of any risk to the United States. Continuous analysis of the new data is done by experts. They identify the changes and reclassify the variant accordingly. If the variant is of concern, it will be notified, and the necessary action for curtailing the spread will be initiated.[19]

Variant of Interest

This is characterized by a change in the genetic coding of the virus, especially in the region corresponding to the receptor-binding protein, along with a reduced ability of neutralization by antibodies generated against previous infection or vaccination, nonresponsiveness to the usual treatment protocols, and/or increase in rate of transmission or morbidity and mortality.[19]

Possible features of a VOI are as follows:

- The variant has specific genetic markers that affect its transmission, help in diagnostics, support treatment, or exhibit immune escape mechanism.
- Data suggest this variant as the only cause for the increased proportion of cases.
- Spread can be either limited to a region or to other regions or other countries.

The steps to be taken when a VOC has been identified include numerous initiatives such as appropriate public health measures, including surveillance through genomic sequencing of samples collected from various regions and specific tests for laboratory characterization of the virus. Also, the characteristics of the virus are epidemiologically analyzed thoroughly for implementing the use of any authorized vaccines available or yet to be approved.[19]

Variant of Concern

This is characterized by faster transmission, increase in hospital stay days, slower recovery, increased mortality and less protection from antibodies formed through previous infection or administration of vaccines, nonresponsiveness to the usual treatment protocols or ineffectiveness of the vaccines, or failure to detect by the diagnostic techniques.[19]

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Possible features of VOC are as follows:

- It has the characteristics of the VOI along with the below-mentioned possible features as stated by the CDC:[19]
  - Evidence of impact on diagnostics, treatments, or vaccines:[19]
    - Widespread interference with diagnostic test targets
    - Evidence of substantially decreased susceptibility to one or more classes of therapies
    - Evidence of significantly decreased neutralization by antibodies generated during previous infection or vaccination
    - Evidence of reduced vaccine-induced protection from severe disease
- Evidence of increased transmissibility[19]
- Evidence of increased disease severity[19]

When a VOC is detected, global authority such as the WHO has to be notified first. Other measures required for controlling an outbreak has to be followed as per the International Health Regulations. The efforts to prevent the spread among the community have to implemented without delay. The number of samples collected from the infected individuals must be increased. Newer vaccines have to be designed for the protection of the society. Various treatment modalities have to be tried for eliminating the virus. Depending on the features of the circulating variant, newer diagnostic techniques should be considered, including the modification of vaccines or implementation of newer treatment protocols.[19]

Phylogenetic Assignment of Named Global Outbreak (PANGO) lineages is a software tool developed by members of the Rambaut Lab. The Centre for Genomic Pathogen Surveillance in South Cambridgeshire referred the SARS-CoV-2 lineages with the PANGO nomenclature.[22]

Variants of Significance

Lineage B.1.1.207 was first sequenced in Nigeria in August 2020. It was considered as an emerging threat by the CDC. Alpha variant and this variant share a common mutation at P681H. Until May 2021, this lineage was identified in 10 countries.[5]

Lineage B.1.616 was identified in early January 2021 in Brittany, Western France, and designated by the WHO as "Variant under investigation" in March 2021. The virus was detected only in samples from the lower respiratory tract.[5,23]

Lineage B.1.618 was first isolated in October 2020. This variant has been found in West Bengal, India, with the E484K mutation, which is also found in several other variants. The PANGOLIN database showed 135 sequences as being detected causing a significant spread in April 2021 whereas eight other countries situated worldwide reported only single-figure numbers.[6]

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Scientists reported the detection of SARS-CoV-2 lineages in the sewage water surveillance performed in the city of New York. It was reported in a preprint in July 2021 and got published in a journal in February 2022 that "these lineages are derived from unnamed unsampled human COVID-19 infections or that they indicate the presence of a nonhuman animal reservoir."[5,6]

Lineage B.1.640.2 was named after the Institut Hospitalo-Universitaire (IHU) in Marseille as an IHU variant. In October 2021, a traveler has infected 12 individuals. He was on his return journey to France. Although the WHO considered this lineage as VBM on November 22, 2021, it also stated that the transmissibility was less than the Omicron variant. Therefore, it is not much of a concern.[5]

The team of researchers reported the SARS-CoV-2 variant recombinant viruses. In March 2022, it was identified to contain elements of Delta and Omicron; hence, it was named as Deltacron (also called "Deltamicron"). Recombination is a process by which a virus combines with parts of a related virus, using up the genetic sequence of both the viruses during the process, so as to assemble its own copies. As of July 2022, only the Omicron variant is designated as a circulating VOC by the WHO.[5,6]

Variant of High Consequence

Those variants that show a clear evidence of non-responsiveness to the preventive measures or medical counter measures (MCMs) when compared with the already circulating variants are placed under this category.[19]

Features of a VOHC: Characteristics of the VOC along with the below-mentioned possible features constitute the VOHC:

- MCMs are insufficient
- Unable to detect using the usual diagnostic tests
- Data analysis shows that the protection offered by existing vaccines is ineffective. There is also a sudden increase in the infection rate in vaccinated individuals
- Proven treatment methods are ineffective, leading to an increase in the duration of hospital stay
- Many individuals requiring hospitalizations due to rapid progress of the infection

The VOHC when identified should first be notified to the WHO under the International Health Regulations and also has to be reported to CDC. The strategies required to prevent or contain transmission must be announced to the public along with the recommendations to update the treatment protocols and vaccine production.[19]

LABORATORY DIAGNOSIS

Early diagnosis can be achieved through appropriate laboratory investigations. Identifying the infection helps in initiating the control

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measures for preventing the spread of COVID-19. Molecular detection methods, including polymerase chain reaction (PCR), are the gold standard for the detection of SARS-CoV-2 nucleic acid. Viral nucleic acid detection kits targeting the important genes of the SARS-CoV-2 are commercially available. The structural proteins *RdRp* and open reading frame 1b (*ORF1b*) are the target genes in the PCR kits. The total time duration for processing of samples and final time detection of the virus take almost few hours, depending on the technology, whether manual extraction of the RNA or automated extraction is performed. Ideally, swabs are collected from the throat and nasopharyngeal mucosa. Viral load gradually drops from its peak level over the next few days until the onset of the disease. Therefore, false negatives are common with the oral swabs. To overcome this drawback, multiple detection methods are used, and correlations with other blood parameters are usually done. Computerized tomography (CT) scan of chest is performed to radiologically identify the pattern of lung involvement and helps in quick diagnosis. The typical feature on initial CT was the diffuse bilateral multilobar ground-glass opacities, usually distributed in the periphery or posterior part of the lung fields in patients with suspected SARS-CoV-2 infection. Thus, it has been suggested that for those who test negative in the initial nucleic acid screening, other methods can be combined with molecular detection methods for repeat swabs collected from the individuals with high clinical suspicion of COVID-19. Serological tests are available for detecting antibodies to N or S protein of the SARS-CoV-2 virus.[1,2,4]

CONCLUSION

Microbes, especially viruses, mutate, recombine, and reassort to cause pandemics. Constant vigilance by the regulatory bodies will help to detect outbreaks faster and to implement control measures immediately. Serological tests could complement molecular diagnosis, particularly in late phases after disease onset or for retrospective studies only. However, the extent and duration of immune responses are still unclear, and available serological tests differ in their sensitivity and specificity, all of which need to be taken into account when one is deciding on serological tests and interpreting their results. There is also a possibility of assessing the T-cell responses in the future.[24]

REFERENCES

1. Nature. [online] Available from www.nature.com. [Last accessed February, 2023].
2. SARS-CoV-2 variants overview. [online] Available from www.ncbi.nlm.nih.gov/activ. [Last accessed February, 2023].
3. BINASSS. [online] Available from www.binasss.sa.cr. [Last accessed February, 2023].
4. New Look, New Capabilities. [online] Available from v3r.esp.org. [Last accessed February, 2023].
5. WikiMili, the best Wikipedia reader. [online] Available from wikimili.com. [Last accessed February, 2023].

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6. COVID-19. [online] Available from en.wikipedia.org/wiki/COVID-19. [Last accessed February, 2023].
7. Liu J, Zheng X, Tong Q, Li W, Wang B, Sutter K, et al. Overlapping and discrete aspects of the pathology and pathogenesis of the emerging human pathogenic coronaviruses SARS-CoV, MERS-CoV, and 2019-nCoV. J Med Virol. 2020;92:491-4.
8. Internet Archive. [online] Available from archive.org. [Last accessed February, 2023].
9. Treviño S, Cortezano-Esteban S, Hernández-Fragoso H, Díaz A, Vázquez-Roque R, Sarmiento-Ortega VE, et al. Clinical monitored in subjects metabolically healthy and unhealthy before and during a SARS-CoV-2 infection: a cross-sectional study in Mexican population. Cytokine. 2022;153:155868.
10. Common sense and ramblings in America. [online] Available from common-sense-in-america.com. [Last accessed February, 2023].
11. World Health Organization. [online] Available from apps.who.int. [Last accessed February, 2023].
12. The Cureus Journal of Medical Sciences. [online] Available from www.cureus.com. [Last accessed February, 2023].
13. Hu B, Guo H, Zhou P, Shi ZL. Characteristics of SARS-CoV-2 and COVID-19. Nat Rev Microbiol. 2021;19:141-54.
14. Jurnal Online Universitas Gadjah Mada. [online] Available from humaniora.journal.ugm.ac.id. [Last accessed February, 2023].
15. www.nature.com
16. KAUST repository. [online] Available from repository.kaust.edu.sa. [Last accessed February, 2023].
17. eLIFE. [online] Available from elifesciences.org. [Last accessed February, 2023].
18. Mahilkar S, Agrawal S, Chaudhary S, Parikh S, Sonkar SC, Verma DK, et al. SARS-CoV-2 variants: impact on biological and clinical outcome. Front Med. 2022;9:995960.
19. www.cdc.gov/coronavirus/2019-ncov/variant-classifications.html
20. Virginia Department of Health. [online] Available from www.vdh.virginia.gov. [Last accessed February, 2023].
21. National Library of Medicine. [online] Available from www.nlm.nih.gov. [Last accessed February, 2023].
22. Understanding influence in the digital information environment and the impact on audiences and actors. [online] Available from https://cradpdf.drdc-rddc.gc.ca/PDFS/unc357/p811493_A1b.pdf. [Last accessed February, 2023].
23. The Free Encyclopedia. [online] Available from findatwiki.com. [Last accessed February, 2023].
24. GitHub. [online] Available from github.com. [Last accessed February, 2023].

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Jayanthi Rangarajan is the Dean of Government Medical College, Omandurar Government Estate, Chennai, Tamil Nadu, India. She has over three decades of teaching experience in Internal Medicine, and is an astute physician, and clinician. She has been in the forefront during the 3 years of COVID-19 pandemic in leading the team in the war against COVID-19 and saving thousands of lives. She is the principal investigator of the WHO Solidarity Trial I and II. She is the recipient of several awards and accolades. She is fellow (FRCP) of the Royal Colleges of Physicians of Glasgow, Edinburgh, and London. She has to her credit several publications and research papers in renowned journals.

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