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COVID-19 and animal infection: A review

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Abstract

The outbreak of the deadly virus (novel coronavirus or Severe Acute Respiratory Syndrome Coronavirus-2) that emerged in December 2019, remained a controversial subject of intense speculations regarding its origin, became a worldwide health problem resulting in serious coronavirus disease 2019 (acronym COVID-19). The concern regarding this new viral strain "Severe Acute Respiratory Syndrome Coronavirus-2" (acronym SARS-CoV-2) and diseases it causes (COVID-19) is well deserved at all levels. The incidence of COVID-19 infection and infectious patients are increasing at a high rate. Coronaviruses (CoVs), enclosed positive-sense RNA viruses, are distinguished by club-like spikes extending from their surface, an exceptionally large genome of RNA, and a special mechanism for replication. Coronaviruses are associated with a broad variety of human and other animal diseases spanning from enteritis in cattle and pigs and upper respiratory disease to extremely lethal human respiratory infections. With World Health Organization (WHO) declaring COVID-19 as pandemic, we deemed it necessary to provide a detailed review of coronaviruses discussing their history, current situation, coronavirus classification, pathogenesis, structure, mode of action, diagnosis and treatment, the effect of environmental factors, risk reduction and guidelines to understand the virus and develop ways to control it.

Keywords: Coronaviruses, RNA viruses, SARS-CoV-2, COVID-19, biocidal agents

Introduction

Coronavirus disease (COVID-19) is an infectious disease caused by the SARS-CoV-2 virus. The epicentre of the virus outbreak is Wuhan city, Hubei province, where several pneumonia cases with an unknown cause were reported on December 31st, 2019. The Novel Coronavirus has officially been named COVID-19 by the WHO. "co" stands for "corona", "vi" for "virus" and "d" for "disease", while "19" stands for the year when the outbreak was first identified (on December 31, 2019).

Globally, as of 4 March 2022, there have been 440,807,756 confirmed cases of COVID-19, including 5,978,096 deaths, reported to WHO. As of 26 February 2022, a total of 10,585,766,316 vaccine doses have been administered. Cases from WHO region includes about 181,275,264 confirmed cases from Europe, 147,655,931 confirmed cases from America, 56,001,277 confirmed cases from South-East Asia, 26,179,245 confirmed cases from Western Pacific, 21,252,125 confirmed cases from Eastern Mediterranean and 8,443,150 confirmed cases from Africa (WHO, 2022) ^[39]. In India as of 14th March 2022, there have been 4,29,96,062 confirmed cases of COVID-19, including 5,15,974 deaths reported (Government of India, 2022) ^[14]. The maximum number of cases were reported from Maharashtra (78,71,359) followed by Kerala (65,21,907), Karnataka (39,43,912) and Tamil Nadu (34,51,996); and the minimum number of cases were reported from Andaman and Nicobar (10,027) followed by Lakshadweep (11,402) and Dadra and Nagar Haveli and Daman and Diu (11,440) (Government of India, 2022) ^[14].

Coronaviruses (CoVs) are enveloped +ve-sense single-stranded RNA viruses that belong to the Coronavirinae subfamily of the Coronaviridae family. The name coronavirus comes from its appearance as a crown-like structure under electron microscopy. Coronaviruses are divided into four genera: alpha (α), beta (β), gamma (γ), and delta (δ). They are predominantly found in animals. Natural hosts of α - and β -CoVs are mammals, particularly bats, while pigs and birds are natural hosts of γ - and δ -CoVs. SARS-CoV-2 is not like the coronaviruses that cause the common cold (229E, OC43, NL63, and HKU1), but it is similar to the zoonotic severe acute respiratory syndrome (SARS) coronavirus (SARS-CoV) that emerged in 2002 and the Middle East respiratory syndrome (MERS) coronavirus that emerged in 2012. SARS-CoV-2, like many other coronaviruses, is thought to have originated in bats because it shares 89% to

96% nucleotide identity with bat coronaviruses (Anderson *et al.*, 2020) ^[3]. SARS-CoV-2 is thought to have spread from bats to an intermediate host (perhaps a Malayan pangolin, which has 91% nucleotide identity) and subsequently to humans, similar to SARS and MERS (Abd El-Aziz and Stockand, 2020) ^[2].

The binding of the viral surface spike protein (S protein) to the human angiotensin-converting enzyme 2 (ACE2) receptor causes SARS-CoV-2 infection. Lower expression of ACE2 in the lungs (mostly type II alveolar cells), heart, kidneys, vascular endothelium, and gut can lead to cardiovascular (hypertension, congestive heart failure, and disease atherosclerosis). When an infected person speaks, sings, or breathes, coughs, or sneezes, the virus can spread (symptomatic patient has higher viral load in the nasal cavity in comparison with the throat, which can predict that sneezing has the highest probability of infection than coughing) (Shivangi, 2021)^[32]. The majority of those infected with the virus will have mild to moderate respiratory symptoms and will recover without the need for medical attention. Some, on the other hand, will become extremely unwell and require medical assistance. Serious sickness is more likely to strike the elderly and those with underlying medical disorders such as cardiovascular disease, diabetes, chronic respiratory disease, or cancer. COVID-19 can make anyone sick and cause them to get very ill or die at any age. Being thoroughly informed on the disease and how it spreads is the best strategy to avoid and slow down transmission. Stay at least 1 metre away from people, wear a well fitted mask, wash your hands or massage them with an alcohol-based rub frequently, and practise respiratory etiquette to protect yourself and others from infection.

CoVs are an uncovered worldwide threat to health, as evidenced by their occasional arrival and pandemic. Novel CoV development may become unavoidable in the future as a result of changes in the genome, environment, and ecosystem, as well as greater human-animal interactions (Chan-Yeung and Xu, 2003)^[8]. As a result, developing innovative and effective treatments and vaccines against CoVs is an absolute must.

Historical Perspective

The first scientific annotations were most likely produced by Baudette and Hudson in 1933, when they described "gasping disease" in chickens and then transmitted the disease to embryos. This virus was later identified as an infectious bronchitis virus (IBV), which served as the template for the entire virus family (Baudette and Hudson, 1933)^[4]. Gledhill and Andrewes' isolation of the mouse hepatitis virus paved the way for further research (Gledhill *et al.*, 1952)^[12]. They claimed in their article that in the event of gasping death, the infectious agent they named mouse hepatitis virus (MHV) would not have caused such widespread destruction.

Coronaviridae, a novel family containing one genus coronavirus, was named by the International Committee on Virus Taxonomy in 1975. Canine coronavirus, feline peritonitis virus, human enteric coronavirus, transmissible pig gastroenteritis virus (TGEV), neonatal calf diarrhoea coronavirus (BCV), and rat coronavirus (RCV) are among the new viruses discovered (Sturman *et al.*, 1983) ^[34]. Since the First International Congress in Germany in 1980, the importance of the coronavirus family in both medical and commercial terms has grown dramatically. "Coronavirus come of age," a review of the First International Congress on

Coronaviruses in 1980, was written by Mahy (Mahy, 1980) ^[20]. This symposium advances the science of animal virology by establishing criteria for coronavirus molecular biology that will be followed by researchers investigating the pathogenesis of both human and animal virus illnesses (Weiner *et al.*, 1987).

HKU1, NL63, 229E, and OC43 are four corona viruses that have been found in humans and cause moderate respiratory illness. Crossover of animal beta-corona viruses to humans has resulted in severe sickness in humans twice in the last two decades. The first time this happened occurred in the Guangdong province of China in 2002-2003, when a novel coronavirus from the genera and with origins in bats moved over to humans via the intermediary host of palm civet cats. Before being contained, the virus known as the severe acute respiratory syndrome coronavirus infected 8422 people, predominantly in China and Hong Kong, and caused 916 fatalities (11% mortality rate) (Chan-Yeung et al., 2003)^[8]. In 2012, the Middle East respiratory syndrome coronavirus (MERS-CoV), which was likewise of bat origin, emerged in Saudi Arabia with dromedary camels as the intermediate host, infecting 2494 people and killing 858. (fatality rate 34%) (Memish et al., 2020)^[21].

In December 2019, a novel coronavirus (dubbed 2019-nCoV) was discovered in clinical samples from patients with viral pneumonia in Wuhan, China. The primary viral pneumonia patients were connected epidemiologically to the Huanan seafood market in Wuhan City, Hubei Province, China, where various non-aquatic animals such as bats, pangolins, and rabbits were on sale prior to the epidemic (Dietz *et al.*, 2019) ^[11]. A new human-infecting coronavirus, tentatively named 2019 novel coronavirus (2019-nCoV), was discovered using next-generation sequencing. The outbreak, originally known as "new coronavirus" or 2019-nCoV, was renamed COVID-19 on February 11, 2020, and the causal virus was called "Severe acute respiratory syndrome-related coronavirus 2" or SARS-CoV-2 (WHO, 2020) ^[38].

Structure, properties and classification of SARS CoV-2

Coronaviruses are enclosed single-stranded RNA viruses with spike-like projections (S protein) on their surface that range in size from 60 nm to 140 nm in diameter. SARS-CoV-2 contains a 30 kb RNA genome that codes for 16 nonstructural proteins (the most important of which is RNAdependent RNA polymerase protein (RdRp) encoded by the nsp12 gene) and four structural proteins: spike (S), envelope (E), membrane (M), and nucleocapsid (N). In non-structural and structural proteins, genomic sequence alignment analyses revealed 58% and 43% sequence identity among distinct CoVs species, respectively. This demonstrates that the virus's non-structural parts are more conserved than its structural parts, which have more variable characteristics. RNA viruses' genomes are typically smaller (less than 10 kb) than DNA viruses' genomes, but this is not the case with CoVs (genome size - 30 kb). The vast genomic size of CoVs increases their mutational capability, which is already higher than that of RNA viruses, which is a major worry in designing antiviral drugs.

Virus classification

Coronaviruses get their name from the crown-like spikes that cover the virion particle's outermost surface. These viruses comprise one of the largest virus families in the Nidovirales order. Coronaviridae, Arteriviridae, Mesoniviridae, and Roniviridae are the families that make up Nidovirales. Coronavirinae and Toronavirinae are two subfamilies of the Coronaviridae family. Coronavirinae is divided into four genera: alpha, beta, gamma, and delta (Zhang *et al.*, 2020)^[41]. Human coronavirus 229E (HCoV-229E), Human coronavirus OC43 (HCoV-OC43), Human coronavirus NL63 (HCoV- NL63, New Haven coronavirus), SARS-CoV, Human coronavirus HKU, Middle East respiratory syndrome coronavirus (MERS-CoV), Novel coronavirus (2019-nCoV) / COVID-19 are the seven strains of human coronaviruses. SARS-CoV-2 is a member of the beta CoV cluster, which also includes SARS CoV and MERS CoV.

| Table 1: | Classification | of Cor | onavirus |
|----------|----------------|--------|----------|
|----------|----------------|--------|----------|

| Realm | Riboviria |
|----------|---|
| Kingdom | Orthornavirae |
| Phylum | Pisuviricota |
| Class | Pisoniviricetes |
| Order | Nidovirales |
| Family | Coronaviridae |
| Genus | Betacoronavirus |
| Subgenus | Sarbecovirus |
| Species | Severe acute respiratory syndrome-related coronavirus |
| Strain | Severe acute respiratory syndrome coronavirus-2 |

Comparative and contrasting feature of SARS-CoV, MERS and SARS-CoV2: Studies have shown that SARS-CoV2 has significant genomic similarity to SARS-CoV, which was a pandemic in 2002 (Zhou *et al.*, 2021) ^[42] (Table 01).

Table 2: Features of SARS-CoV, MERS and SARS-CoV2

| Characteristic features | SARS-CoV | MERS | SARS-CoV2 |
|--|--|------------------|--|
| Countries | 29 | 23 | 165 |
| Mean incubation period (days) | 4.7 | 5.8 | 5.6-6.7 |
| Location of first case | Guangdong, China | Saudi Arabia | Wuhan, China |
| Outbreak beginning date | November 2002 | April, 2012 | December 2019 |
| Fatality rate | 10% | 36% | 6.8% |
| Time to infect first 1000 people (days) | 130 | 903 | 48 |
| Incidental Host | Masked palm civet | Dromedary camels | Malayan pangolin |
| ACE2 binding affinity | Receptor binding domain (RBD) has a lesser ACE-2 binding affinity. | Nil | Receptor binding domain (RBD) has a higher ACE2-binding affinity, leads to more efficient cell entry. |
| States of RBD | RBD is mostly in 'stand up' state | Nil | RBD is mostly in 'lying down' position, a state associated with ineffective receptor binding, may favor the immune evasion |
| Furin-like cleavage site | Furin-like cleavage site is absent in the S protein | Nil | S proteins contains a furin-like cleavage site |

Variants of COVID-19

A variation is a virus with one or more mutations in its genome (genetic code). Due to shared qualities and characteristics that may necessitate public health action, public health organisations may designate a set of variations with similar genetic alterations, such as a lineage or group of lineages, as a Variant of Concern (VOC) or a Variant of Interest (VOI).

Classifications of the variants

1. Variant under Investigation: When mutations occur and

there is any past relationship with any other similar variant that is thought to have an influence on public health, a variant becomes a variant under research.

2. Variant of Interest (VOI): Variants with specific genetic markers have been linked to changes in receptor binding, less neutralisation by antibodies developed against vaccination/previous infection, reduced therapeutic efficacy, potential diagnostic effects, and a predicted increase in transmissibility or disease severity (CDC, 2021)^[6].

| Table 3: List of | Variant of Interest |
|------------------|---------------------|
|------------------|---------------------|

| Name | PANGO lineage | First Outbreak | |
|---------|---------------|------------------------------------|--|
| Epsilon | B.1.427 | United States of America, Mar-2020 | |
| | B.1.429 | | |
| Zeta | P.2 | Brazil, Apr-2020 | |
| Eta | B.1.525 | Multiple countries, Dec-2020 | |
| Theta | P.3 | Philippines, Jan-2021 | |
| Iota | B.1.526 | United States of America, Nov-2020 | |
| Kappa | B.1.617.1 | India, Oct-2020 | |
| Lambda | C.37 | Peru, Dec-2020 | |
| Mu | B.1.621 | Colombia, Jan-2021 | |

3. Variant of Concern (VOC): A variant becomes a VOC when there is evidence of enhanced transmissions from field and clinical investigations. Higher transmissibility, changes in virulence/disease presentation, evidence of increasing illness severity, evasion of diagnostics, medicines, and vaccinations are all features of VOC. There are five different types of concern that have been discovered so far. WHO has given them the names Alpha, Beta, Gamma, and Delta (CDC, 2021)

| Name | PANGO lineage | First outbreak |
|---------|------------------|----------------|
| Delta | B.1.617.2 | India |
| Alpha | B.1.1.7 | United Kingdom |
| Gamma | P.1 (B.1.1.28.1) | Brazil |
| Beta | B.1.351 | South Africa |
| Omicron | B.1.1.529 | South Africa |

4. Variant of High Consequence: In comparison to previously circulating variants, a variant of high consequence has clear evidence that preventative efforts or medical countermeasures (MCMs) have dramatically reduced effectiveness. Evidence of diagnostic failure, increased disease severity and hospitalizations, reduced susceptibility to therapy, evidence of diminished vaccination efficiency, a significant number of vaccine breakthrough cases, or extremely low vaccine protection against severe disease are all possible features (CDC, 2021)^[6].

Incubation period

The incubation period varies from 2 to 14 days (median 5 days). The basic case reproduction rate (BCR) is estimated to range from 2 to 6.47 in various modelling studies (Sharma *et al.*, 2020) ^[31].

Reservoir Host

Bats: Bats have been identified as the primary natural reservoir host of numerous CoVs. The horseshoe bat is the reservoir of SARS-like-CoVs among the 1100 different species of bats (Michelitsch *et al.*, 2021)^[22].

Pangolins: Pangolin-CoV, which was isolated from a Malayan pangolin (*Manis javanica*), has a genome that was very similar to SARS-CoV-2 and bat CoV. (Michelitsch *et al.*, 2021)^[22].

Reptiles: Turtles (*Chrysemys picta bellii*, *Pelodiscus sinensis*, and *Chelonia mydas*) and snakes (*Chrysemys picta bellii*, *Pelodiscus sinensis*, and *Chelonia mydas*) may operate as intermediary hosts that transmit SARS-CoV-2 to people, according to an analysis of the virus's structural binding mechanism (Michelitsch et al., 2021)^[22].

SARS-CoV2 and Animal infection

Cats: Based on the finding of SARS-CoV-2 specific antibodies in 14.70% of collected cats during the COVID-19 outbreak, SARS-CoV-2 infects cat populations in Wuhan. Infection of cats that were raised in the wild after coming into contact with SARS-CoV-2 infected patients or a SARS-CoV-2-polluted environment, and generated an antibody response to the virus (Michelitsch *et al.*, 2021)^[22].

Dogs: Despite the fact that dogs have a low vulnerability to SARS-CoV-2 infection, contact with SARS-CoV-2 infected

people resulted in the infection of two pet dogs from Hong Kong and another from North Italy.

Minks: The first intensively farmed species to be infected by the COVID-19 outbreak was mink, demonstrating that mustelids are more susceptible to SARS-CoV-2. SARS-CoV-2 has infected several mink farms, initially in the Netherlands, then in Denmark, the United States, and Spain.

Rodents: Vaccines and antiviral medicines can be evaluated using mouse models. Although various rodent models have been described as prospective COVID-19 models, none of these models accurately replicated all of COVID-19's characteristics in humans (Michelitsch *et al.*, 2021) ^[22].

Ferrets: Ferrets are commonly used to study human respiratory virus infection as an animal model. They were extremely vulnerable to SARS-CoV-2 infection.

Treeshrew: The treeshrew (*Tupaia belangeris*) is a primatelike mammal that is not a rodent. It has been utilised as a viral infection animal model in scientific research.

Transmission

1. Human to animal transmission

Infected individuals can distribute respiratory droplets when sneezing, coughing, or even talking, which play a key role in virus transmission to animals. Some favourable risk factors, such as kissing, caressing, licking, or cuddling pet animals, can help spread the virus from infected individuals (Salajegheh *et al.*, 2020) ^[29]. The maximum transmission distance is up to 4 meter (Abbasi-Oshaghi *et al.*, 2020) ^[1].

2. Animal to human transmission

Mink to human transmission in the Netherland and Denmark has been reported.

3. Animal to animal transmission

Cats, Golden hamsters, Ferrets, Racoon dogs, and Minks have all been infected with the virus and have been able to spread it to naive animals by direct touch and aerosols. More than 100 SARS CoV-2-infected mink escaped from Danish fur farms, boosting the risk of the novel coronavirus spreading to wild animals and creating a new reservoir for the virus (Singla *et al.*, 2020)^[33].

Clinical Sign and lesion

In general, hospitalized patients are classified in two categories,

- 1. The general COVID-19 patients: Those patients who have obvious relief of respiratory symptoms after treatment, maintain normal body temperature for more than three days without corticosteroids or antipyretics, improve radiological abnormalities in the chest scanner or X-rays after treatment, and stay in the hospital for less than ten days.
- 2. COVID-19 refractory patients: A serious illness was defined as meeting at least one of the following criteria in the admission severity assessment: respiratory rate of 30 minutes, pulse oximeter oxygen saturation (SpO₂) of 93% at rest, and partial arterial oxygen pressure (PaO₂) at the inspired oxygen fraction (Fio2) 300 millimetres of mercury (Mo *et al.*, 2020) ^[24]. Small, subpleural, unilateral, or bilateral frosted glass opacities in the lower

lobes characterise typical moderate COVID-19 pneumonia, which progress to a crazy-paving pattern and eventual consolidation. After more than two weeks, the lesions are gradually absorbed with residual frosted glass opacities and subpleural parenchymal bands.

| Table 5: Persistence | of COVID-19 in | the environment |
|----------------------|----------------|-----------------|
|----------------------|----------------|-----------------|

| Object and surface | COVID-19 duration |
|--------------------|-------------------|
| Air | Up to 24 h |
| Cardboard | Up to 24 h |
| Plastic | Up to 2-3 days |
| Stainless steel | Up to 2-3 days |
| Copper | Up to 4 h |

Risk factors associated with COVID-19

- 1. Gender susceptibility for COVID-19 infection: SARS-CoV infects people under the age of 50, COVID-19 infects people in their forties and fifties, and MERS-CoV infects people beyond 50. Because of extensive alveolar injury, infected older males with co-morbid conditions were more likely to develop lung disease, indicating that men are more vulnerable than women. The increased vulnerability to COVID-19 infection in men may be explained by differences in sex hormones and immunitylinked genes on the X chromosome that affect both adaptive (acquired) and innate (non-specific) immune responses (Habibzadeh *et al.*, 2021) ^[16].
- Temperature: COVID-19 PCP (percentage of cases to 2. population) and PDP (proportion of deaths to population) were shown to be greater in northern countries, including sections of North America, Asia, and Europe, which are located at higher latitudes and have a colder temperature and better socio-economic conditions. A higher temperature may be useful against different forms of coronaviruses, such as SARS, according to several studies (Van Doremalen et al., 2013; Chan et al., 2011; Bi et al., 2007) ^[36, 7, 5]. In the study by Ma et al. (2020) ^[19], it has been reported that there is a negative between COVID-19 mortality association and temperature, because lower temperatures reduce the immune system's and liver's performance, making the environment more suitable to infectious agent activity and virus transmission.
- **3.** Age: Older populations in the northern hemisphere, especially in Europe and North America with a higher income, have a higher death rate from respiratory infections (Cristea *et al.*, 2020)^[10].
- **4. Densely populated area:** Densely populated areas could contribute to the spread of the disease in European and Asian megacities (Sajadi *et al.*, 2020)^[28].
- 5. Air Pollution: COVID-19 outbreaks and death are increased by air pollution. In Italy, for example, daily fluctuations in pollutant concentration were positively related to the number of infected people; similarly, the number of confirmed cases was significantly higher in cities with more than 100 days of air pollution than in areas with cleaner air (Coccia, 2020)^[9]. Furthermore, it has been demonstrated that air pollutants such as nitrogen oxide and particulate matter produced by vehicles and industry might impact viral infection emission and increase the number of hospital admissions due to respiratory virus bronchiolitis and asthma (Glencross *et al.*, 2020)^[13].
- 6. Vitamin D deficiency: Vitamin D insufficiency in

people living in high-latitude places with colder climates may play a role in disease development in those areas (Grant *et al.*, 2020) ^[15]. Although vitamin D supplementation is strongly recommended for preventing acute respiratory infections, more research into the usefulness of vitamin D for coronavirus infection is urgently needed (Sarmadi *et al.*, 2020) ^[30].

Pathogenesis

When viral particles enter the human body, they bind with the ACE2 receptor and release an RNA particle into epithelial cells (ECs), where viral proteins are replicated, and infection spreads to neighbouring cells, such as the alveolar portion of the lung. Because of increased permeability and leakage, the gaseous exchange driven by alveoli is significantly harmed as a result of this infection. Pulmonary oedema, activation of disseminated intravascular coagulation, pulmonary ischemia, hypoxic respiratory failure, and progressive lung destruction are all symptoms of this illness. The virus particles can also spread to other regions of the body, including as the brain, gastrointestinal tract, heart, kidneys, and liver, causing cerebral haemorrhage, neurological dysfunction, ischemic stroke, coma, paralysis, and death. The viral infection also activates the immune system, causing the release of cytokines such as MCP-1 and IL-8, as well as reduced expression of Ecadherins on ECs, which promotes leakage and vascular permeability. In Acute Respiratory Distress Syndrome (ARDS), these factors cause hypotension and pulmonary dysfunction. The majority of COVID-19 patients die from ARDS. Increased vascular permeability and leakage in the case of SARS-CoV-2 infection are caused by direct contact with ECs, binding with ACE2 receptor and activation, activation of the Kallikrein bradykinin pathway, activated neutrophils that produce ROS, activation of immune cells, and release of cytokines IL-1B and TNF that degrade glycocalyx (Jin et al., 2020)^[17].

Epidemiology

Global distribution of Covid19

The first case outside of mainland China was recorded in Thailand on January 11, and the disease had spread to all continents except Antarctica within months. On January 30, 2020, the WHO labelled the outbreak a "public health emergency of worldwide concern," and on March 11, 2020, it was declared a pandemic. There are more than 29 lakh confirmed cases worldwide as of April 28, 2020, with more than 2 lakh verified deaths

The coronavirus COVID-19 is affecting 226 countries and territories. Globally, as of 8 April 2022, there have been 494,587,638 confirmed cases of COVID-19, including 6,170,283 deaths, reported to WHO. The maximum number of cases were reported from United States of America (79,544,396), followed by India (43,033,067), Brazil (30,067,249), France (916,667), Germany (22,441,051), United Kingdom (21,508,550). Minimum number of cases were reported from Micronesia (1), Saint Helena (2), Nauru (3), Marshall Island (4), Niue (7). No cases were reported from Tuvalu, Turkmenistan, Tokelau, Pitcairn Island, Democratic People's republic of Korea (WHO, 2022) ^[39].

Distribution of Covid-19 in India

On January 30, 2020, the first incidence of COVID-19 in India was reported from Kerala; the patient was a female student at Wuhan University in China. By February 3, 2020, there were three cases. In February 2020, no new cases were recorded. However, by mid-March, the number of infected cases had begun to rise, with numerous cases recorded across India. On March 12, 2020, the first COVID-19-related death in India was recorded in Bangalore, when a 76-year-old man died. The disease's case fatality rate was 1.70% in March 2020, rising to 2.80% by June 2020. Despite the fact that the death rate is modest when compared to the global infection rate of 6.13%, the severity is substantially higher in the country due to the big population (Shivangi *et al.*, 2020) ^[32]. n light of the rising number of COVID-19 incidents in India, India implemented a 14-hour "Janata Curfew" on March 22, 2020, as our honourable Prime Minister Narendra Modi requested.

India reported a total of 43,029,839 confirmed cases and 5,21,416 deaths as of 5 April 2022, with a case fatality rate (CFR) of 1.21%. COVID-19 deaths were highest in Maharashtra (1,47,789), Kerala (68,130), and Karnataka (68,130). (40,055). Maharashtra, Kerala, Karnataka, Tamil Nadu, and Andhra Pradesh accounted for 56%t of the total cases in the country.

Diagnosis

Early diagnosis is crucial for controlling the spread of COVID-19. Molecular detection of SARS-CoV-2 nucleic acid is the gold standard. Many viral nucleic acid detection kits targeting ORF1b (including RdRp), N, E or S genes are commercially available.

Sample collection: Although SARS-CoV-2 has been found in throat swabs, posterior oropharyngeal saliva, nasopharyngeal swabs, sputum, and bronchial fluid, the virus load is higher in lower respiratory tract samples. The sample vial must be correctly labelled and sealed and preserved in an outer covering of absorbent material (primary container) before being placed in a secondary container. The secondary container should then be placed in the thermocol box containing frozen gel packs (outer container). All processes, including packaging, labelling, and shipping, must be carried out in accordance with the guidelines (MOHFW, 2020)^[23].

Various methods for diagnosis of COVID-19 CT Scan

On initial CT, patients with COVID-19 had typical characteristics, such as bilateral multilobar ground-glass opacities with a peripheral or posterior distribution. For people with a high clinical suspicion of COVID-19 but who test negative in initial nucleic acid screening, it has been proposed that CT scanning along with recurrent swab tests be employed.

Virus culture

The virus can be cultured using standard methodology, as described by Kim *et al.*, (2020) ^[18]. Briefly, Vero cells were cultured in Dulbecco's modified Eagle's medium (DMEM) supplemented with 2% foetal bovine serum at 37° C with 5% CO₂ and used for inoculation of nasopharyngeal and oropharyngeal samples. The specific cytopathic effects were detected after 3 days of inoculation.

Immunological assay

ELISA: Various investigations established that the detection of virus specific IgM and IgG are valid for serological diagnosis during the severe acute respiratory syndrome

(SARS) outbreak. In a study conducted in China, researchers discovered that COVID-19 serodiagnosis based on IgM and IgG ELISA has high specificity for COVID-19 diagnostic (Xiang *et al.*, 2020)^[40].

Lateral Flow Assay: In a quick point-of-care immunoassay, the lateral flow assay is used. This assay might be useful for detecting COVID-19 quickly and on-site, especially in an emergency. These assays were created to detect SARS CoV-2 virus antigens as well as IgG and IgM antibodies against SARS CoV-2 virus infection. Tang et al. (2021) [35] emphasized that the detection of IgM and IgG antibodies by rapid lateral flow assay will play an important role in COVID-19 infections and help us to assess the burden of infections, find out asymptomatic patients etc. The COVID-19 IgM/IgG Rapid Test from BioMedomics is a point-of-care device that has an 88.66% sensitivity. Despite the quickness and low cost of these immunoassays based on antigen detection for SARS-CoV-2, past experience with this type of assay for influenza (Flu) viruses has limited its applications. When using this form of antigen detection test, keep in mind that we may miss the case due to sampling variability and low viral load in the infected person. Serological tests, which measure the host immune response to invading infections, are rapidly developed. Serological assays were previously employed in SARS and other corona virus outbreaks, and they were crucial. According to a Chinese study, we can detect the antigen in the patients' lung tissue using immunohistochemical analysis, and the discovery of IgM and IgG antiviral antibodies in the blood can provide additional evidence to confirm the COVID-19 cases. A recent Chinese study that looked at a family cluster of SARS-CoV-2 infections found that serology testing can help with early diagnosis and screening in close connections. Although the WHO has suggested that serology testing be utilised when molecular testing is unavailable.

Nucleic acid testing assay

RT-PCR

The molecular-based technique known as real-time reverse transcriptase-polymerase chain reaction (RT-qPCR) is used worldwide to identify SARS-CoV-2 RNA in clinical samples. The viral RNA is assessed using the cycle threshold (Ct), which is defined as the number of cycles required for the fluorescent signal to cross the threshold and become visible in this real-time PCR test. Different Ct values have been used to diagnose COVID-19, ranging from 16.90 to 38.80 for varied clinical samples. Ct values less than 40 are typically considered to be a good predictor of SARS-CoV-2 RNA positive. Strong positive samples have Ct values ranging from 15-24, and moderately positive samples have Ct values ranging from 25-30, according to RT-qPCR studies on remaining patient samples. The molecular testing is still a "gold standard" for relevant case diagnosis. Other approaches that have been developed and assessed around the world include loop-mediated isothermal amplification, clustered regularly interspaced short palindromic repeats, and multiplex isothermal amplification followed by microarray detection. A number of molecular targets within the RNA of Corona viruses have been discovered for use in the PCR assay, including helicase (Hel), nucleocapsid (N), transmembrane (M), envelope (E), and envelope glycoproteins spike (S). Other structural proteins that can be used for the COVID-19 diagnostic include hemagglutinin-esterase (HE), open reading frames ORF1a and ORF1b, and RNA-dependent RNA polymerase (RdRp) (Prajapat et al., 2020) [27]. The E gene assay, followed by a confirmatory assay utilising the RdRp gene, was recommended by the WHO for first-line screening of COVID-19 cases, while the CDC in the United States requested that two nucleocapsid protein targets [N1 and N2] be used as molecular assays. Among the three created innovative real-time RT-PCR assays targeting the RdRp/Hel, S, and N genes of SARS-CoV-2, the RdRp/Hel assay exhibited the lowest limit of detection in vitro and had superior sensitivity and specificity, according to a study published in Hong Kong, China. To eliminate the possibility of SARS-CoV-2 genetic drift and cross-reaction with other endemic coronaviruses, at least two molecular targets should be used. The LAMP is a nucleic acid amplification technique, which amplifies the DNA in isothermal condition with rapidity and high specificity. This method can be utilised for the diagnosis of COVID-19 without the need of specialized equipments and trained analysts. Recently; Prof. Feng Zhang & co-workers gave a CRISPR-Cas13 (clustered regularly interspaced short palindromic repeats- and associated Cas proteins13) based SHERLOCK (specific high-sensitivity enzymatic reporter unlocking) protocol, which is accurate and rapid method for Novel Coronavirus (COVID-19).

Prevention and control of COVID-19 By Vaccination of human population

Covaxin: This is the first COVID-19 vaccine developed in India. It was created by Bharat Biotech in conjunction with the National Institute of Virology of the Indian Council of Medical Research (ICMR) (NIV). The vaccine has been approved for phase I and II human trials, which will begin in July 2020. The vaccine was then approved for restricted use in emergency situations by the Drug Controller General of India (DCGI) in January 2021, following phase III studies (Ndwandwe *et al.*, 2021) ^[26].

Covishield: Covishield was developed in conjunction with the Serum Institute of India by the University of Oxford and the British-Swedish corporation AstraZeneca (SII). This vaccination has also been approved for use in emergency situations with restrictions. The Indian government has placed an order with SII for 11 million doses of Covishield (Ndwandwe *et al.*, 2021)^[26].

ZyCoV-D: This vaccine has been developed by pharmaceutical company Zydus Cadila and it is the third vaccine in India to receive the DCGI nod for phase III human trials. This is India's first DNA plasmid vaccine.

Sputnik V: Sputnik V is the first Covid-19 vaccine developed using a human adenoviral vector technology. It was created by the Gamaleya Research Institute in Russia. Russia's sovereign wealth fund, the Russian Direct Investment Fund (RDIF), is investing in the vaccine's manufacture and promotion abroad. It has partnered with Dr. Reddy's Laboratories in India. Human phase II trials are now underway (Ndwandwe *et al.*, 2021)^[26].

Biological E's novel Covid-19 vaccine: Biological E. Ltd is a Hyderabad-based vaccine and pharmaceutical company and it has entered into an exclusive license agreement with the Ohio State Innovation Foundation. Phase I/II phase human trial is going on.

By following standard precautions and measures

Precautions on Pet Animals: Although there is no proof that pets played a part in the spread of the SARS-CoV-2 epidemic, researchers believe that pets may be susceptible to infection with the virus. It's also a good idea to keep the sick owner away from the pets, avoid kissing them, practise basic cleanliness, and keep pets from associating with other animals or people outside. Despite the fact that the CDC does not suggest routine testing of animals for SARS-CoV-2, companion animals that have been exposed to SARS-CoV-2 infected individuals and have shown clinical symptoms of new illness should be screened for SARS-CoV-2 as a precaution. In addition, general hygiene precautions should be taken after interaction with animals and animal products, such as handwashing with soap on a frequent basis.

By maintaining personal and environmental hygiene: To maintain appropriate personal and environmental hygiene, standard preventative measures should be followed at all times. Regular handwashing with water and soap/detergent, using a disinfectant, wearing masks, avoiding close contact with affected individuals, avoiding crowded places, covering the mouth with a tissue during sneezing or coughing, avoiding touching the eye and nose, food hygiene practice, and thorough cooking of animal-based food items are all examples of these precautions (Mahy *et al.*, 2020) ^[20].

One Health Approach for prevention of COVID-19: From local to global levels, the One Health concept comprises joint planning and collaborative efforts of diverse sectors and disciplines to preserve optimal health and welfare of humans, animals, and plants in shared settings. It recognises that human health is intertwined with the health of animals and the environment. To understand the mechanism of COVID-19 and battle its spread, a complete understanding of the links between pathogen, native hosts, intermediate hosts, and environment, as well as the tendency of mutations, characteristics of animal-to-human, and human-to-human transmission, is required.

Mission Covid Suraksha: The Government of India has sanctioned Rs.900 crores for the Phase I of the Mission COVID Suraksha, for a period of 12 months. This mission will accelerate the development of approximately 5-6 vaccines for coronavirus. However, a total of 10 vaccine candidates have been supported by DBT till now.

Conclusion

The SARS CoV-2 spike protein binds to the ACE2 receptor on the host cell, which is the major determinant of coronavirus tropism. The homology of complete ACE2 in dogs, cats, tigers, minks, and bats is nearly identical to that of humans. The virus is now spreading from person to person, resulting in one of the most serious pandemics in modern history. SARS CoV-2 infection has been recorded in animal hosts (dog, cat, tiger, lion, and mink), and it has been transmitted to humans. SARS COV-2 is highly contagious in ferrets, minks, rabbits, racoon dogs, Egyptian fruit bats, Golden Syrian Hamsters, and Macaques. SARS COV-2 infection is not contagious in poultry, but it is exceedingly contagious in pigs and cattle. Clinical sign in infected animal includes cough, nasal discharges, respiratory distress. Currently there is no specific treatment and no vaccine for viral disease in animal are available so further studies and research are needed for treatment and vaccine development in animal.

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