REVIEW ARTICLE

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COVID-19 PANDEMIC

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Abstract

In December 2019, a mysterious outbreak of pneumonia emerged in Wuhan, China, with initial cases linked to a local seafood market. Subsequent investigations identified a novel coronavirus—later named SARS-CoV-2—through genomic analysis of respiratory samples cultured in human airway epithelial cells. The virus, distinguished by its crown-like protein spikes called peplomers, belongs to the beta-coronavirus group within the Sarbecovirus subgenus. This study explores various aspects of COVID-19, including its structure, mutation patterns, transmission mechanisms, methods of discovery, and the challenges it poses to global health in terms of morbidity, mortality, and public health preparedness.

Keywords: SARS-CoV-2, COVID-19, Mutation patterns, Transmission mechanisms, Public health impact, Coronavirus structure.

INTRODUCTION

The term "coronaviruses" was officially adopted in 1971, and by 2009, the group was categorized hooked onquatern genera: Beta, Alpha, Delta, and Gamma. By 2020, 45 species were recognized within the Orthocoronavirinae subfamily. These diseases interact with the ACE2 receptor in human cells, a key factor in how the disease progresses. There are differing views among researchers on whether lowering or increasing ACE2 activity might reduce the severity of infection-though both theories require further clinical testing. The severity of infection often correlates with ACE2 levels in tissues, and serious complications, especially among people with heart conditions, can include respiratory and cardiac issues. The virus likely originated in animals, with human-to-human transmission becoming widespread by January 2020 following the initial outbreak in Wuhan [1-6]

EPIDEMIOLOGY

Worldwide, there take been over 704 squillion confirmed COVID-19 cases. Among these, approximately 7 mountaindeceases and done 675 truckload recoveries taken placetestified. This leaves an estimated 22.1 million active cases still ongoing worldwide. More detailed or country-specific statistics are available if required [7].

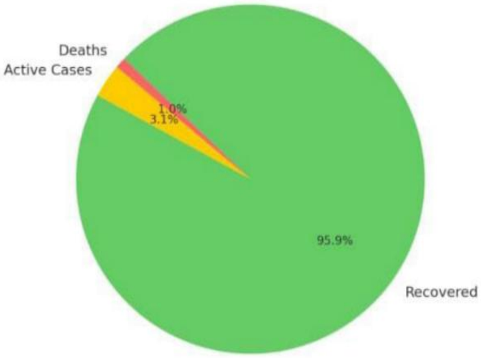


Figure: 01 Global Corona virusSuitcases Distribution

The Corona virusepidemic began trendy late 2019 within the food wholesale sector, with 41 confirmed cases reported by mid-January 2020 and early signs of human-to-human transmission. The second phase started on January 13, marked by rapid spread through hospitals and households. The first international case was identified in Thailand from a traveler coming from Wuhan. By January 19, the virus had reached multiple regions in China, and by January 23, infections had surged to 846 cases across 29 provinces and six countries. Wuhan implemented a lockdown, but it came after over 5 million residents had already traveled for the upcoming Chinese New Year, complicating containment efforts.[8]

Figure: 02 Countries with the most covid-19 Cases

By early 2021, the United States of America had the more no.of confirmed Corona cases, while 27 million reported. Other countries with high case counts included Republic of India, South American, the United kingdom, Cheremiss , Spain, France, Italian, Germany& Asia minor. These numbers reflect total cases, not current infections. The virus has been shown to impact men more severely, influenced by biological, occupational, and social factors. Older adults, especially those over 60, are also at greater risk of developing serious illness [9-10].

STUCTURE

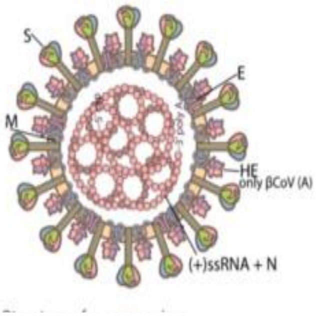


Figure: 03 Covid-19 Structure

Coronaviruses are generally spherical in shape and feature unique surface spikes. Their size ranges from 50 to 200 nanometers, with an average between 80 and 120 nm, and they have a molecular mass of about 40,000 kilodaltons. These viruses are enclosed in a lipid bilayer that houses essential operational poly peptides-namely the crust (M), wrapper (E), and spike (S) proteins. Along with the Virion, this envelope helps protect the virus outside the host.

In coronaviruses, the Wrapper (E), spike (S), and crust (M) proteins are present popular a molar ratio of roughly 1:20:300. The E and M proteins, together with the lipid bilayer, help determine the virus's shape and size. The spike (S) protein usually enables the virus to bind to host cells. However, in the human coronavirus NL63, this function is carried out by the M protein. The viral envelope has an average diameter of 85 nanometers and appears as a dense, double-layered structure under electron microscopy [11-14]

The Crust (M) polypeptide is the foremostorganizational element that coronavirus cover, crucial for maintaining its shape. It is a category3sheath protein made up regarding about 218 near 263 biomolecule and methods a sheet about '7.8' nanometers thick. The M protein has three key regions: a short N-Extreme ectodomain, a Spectrin region per3 spans, in addition a C-Extreme endodomain. It plays vital roles in the germ's life cycle, including envelope formation, assemblage, Shoot &pathogenesis [15-17].

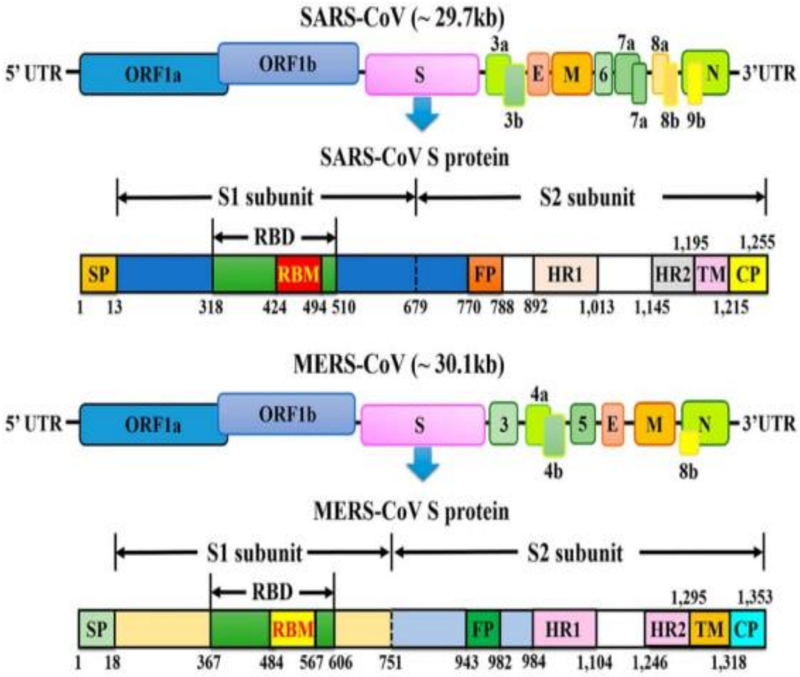


Figure: 04 Genome Organization and spike protein Structure of SARSr-CoV

The covering (E) polypeptide is a small but important structural component of the coronavirus, varying across different species. Each virus contains about 20 E protein molecules, which are 76 to 109 amino acids long and weigh between 8.4 and 12 kilodaltons. These integral membrane proteins consist of a spectrinkingdom and a C-terminal extra membrane kingdom. Structurally, they mostly spiral and form pentameric ion channels within the germ shell. The E polypeptide is complex in germ assembly, intracellular transport & Shoot.

Spike (S) proteins are the most distinctive feature of corona viruses, giving them their crown-like appearance. Each virus particle carries about 74 spikes, each around 20 nanometers long, formed by trimers of S proteins. These polypeptides are made up of of 2parts: S1, which comprises the stretch receptor-unbreakable province & fixnearswarm cells, & S2, which anchors this spike to the viral envelope and facilitates membrane fusion after activation by host enzymes [18-22].

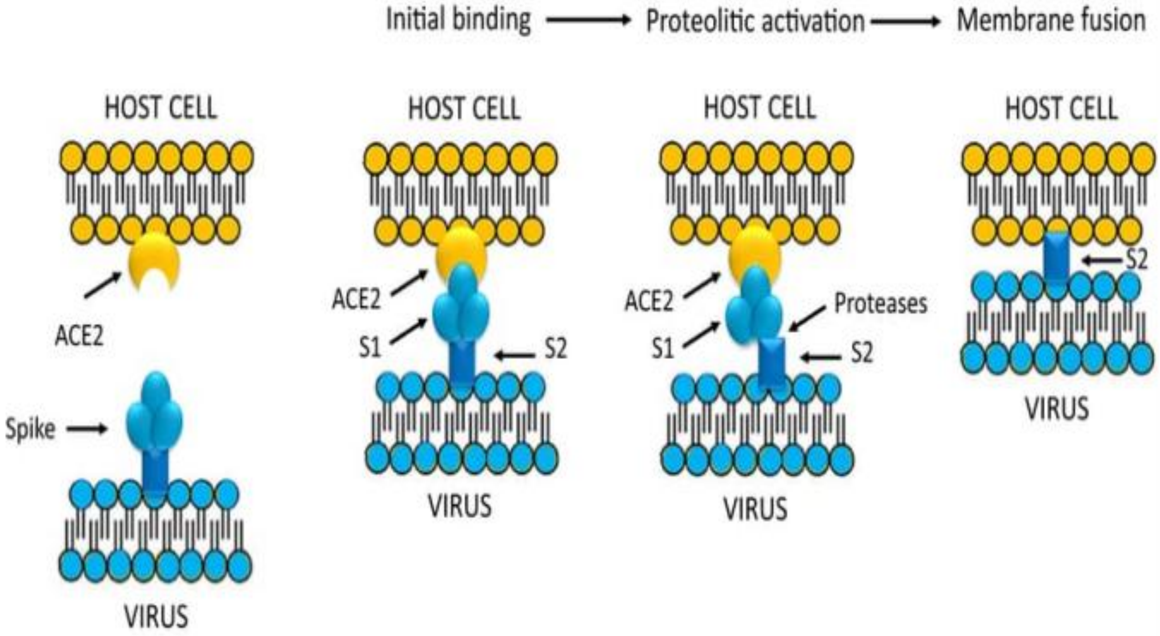


Figure: 05 Role of spike proteins

The spike (S) protein acts even a class 1mixture polypeptide, enabling the virus to enter host cells by binding receptors and fusing viral and cellular membranes. The active spike contains S1 and 2 S2 parts, linked until activated by host proteinases like TMPRSS2 or Lysosomal proteases. The S1 subunit is crucial for infection and host specificity, featuring two main domains: the N-deadlykingdom, which regularlydilemmas to sweeties on host cells, and the C-fatalkingdom (, which interacts with protein receptors such as ACE2, APN, and DPP4. In mouse hepatitis virus, the N- deadly kingdom binds to a protein receptor instead. Additionally, some beta coronaviruses possess hemagglutinin esterase (HE) proteins-small surface projections that assist in viral attachment and detachment from host cells [23-28].

The Virion protein is a phosphorylated weighing between 43 and 50 kilodaltons. It contains three conserved domains: the first two domains are rich in completelyelectricbiomolecule like arginine and lysine, while the third domain, located at the Aliphatic-terminal conclusion, carries a adversecustody due to a higher number of sharp amino acids [28-30].

SARSR-COV-2 VARIANTS

SARS**r**-CoV-2 has advanced thousands of variations, which are gatheredhooked ongrade or family by different organizations to aid in tracking and identification. GISAID, Nextstrain, and Pango each use distinct naming systems. For easier public communication, the WHO adopted Greek letters like Beta, Delta, Gamma &Alpha to label key alternatives. Nextstrain categorizes variants into clades such as 19a, 19b, 20a, 20b, and 20c, GISAID uses clades like L, O, V, S, G, GH, and GR, while to fix classifies them into lineages, many of which fall under the B.1 group.[31-33]

The Cluster 5 variant, which appeared among minks and workers on Danish mink farms, was eliminated from the human population in Denmark by February 2021 following strict control measures, including the culling of all minks. By December 2021, five major SARSr-CoV-2 variants-Delta (India), Gamma (Brazil), Alpha(UK),Bets(South Africa)and Omicron-were circulating worldwide, with Omicron detected in 57 countries. On December 19, 2023, the WHO designated a new variant, JN.1, as a "variant of interest." Despite expected increases in cases during winter months, the WHO assessed the overall health risk as low [34-35].

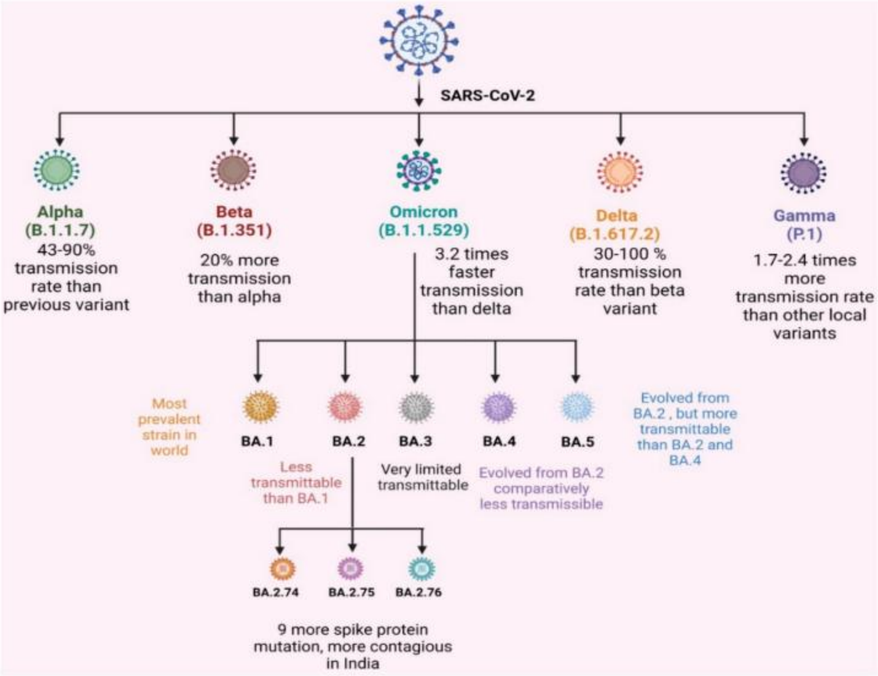


Figure: 06 Five Dominant Variants

TRANSMISSION:

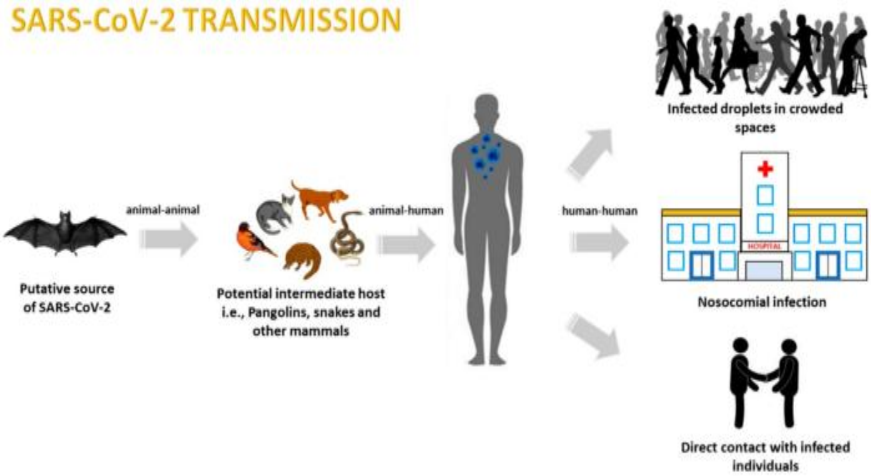


Figure: 07 SARS-CoV-2 Transmissions

ZOONOTIC ORIGIN

SARSr-CoV-2 possibleinitiated in willows& may takeacceptedtowardspeoplefinished one or more in between animal hosts. The virus's ability to infect specific tissues and species depends on how its spike protein binds to receptors on host cells. Coronaviruses generally infect epithelial cells, targeting the respiratory tract in humans and the digestive tract in animals. Transmission methods vary by species and include aerosols, contaminated surfaces, and fecal-oral routes. For example, SARS-CoV infects human lung cells via the ACE2 receptor through aerosols, while the TGEV strain in pigs infects intestinal cells using the APN receptor through fecal-oral transmission [36-39].

METHODOLOGY

At the Begin of the COVID-19 prevalent, numerous manufacturers rapidly developed diagnostic tests, though many awaited full clinical validations. These tests played a critical role during the initial global outbreak. Currently, FDA-approved commercial trailaimed at detecting SARSr-CoV-2 comprise nucleic acid amplification tests like Antibody (serology) tests, RT- PCR and antigen tests [40-4].

1. RT- PCR

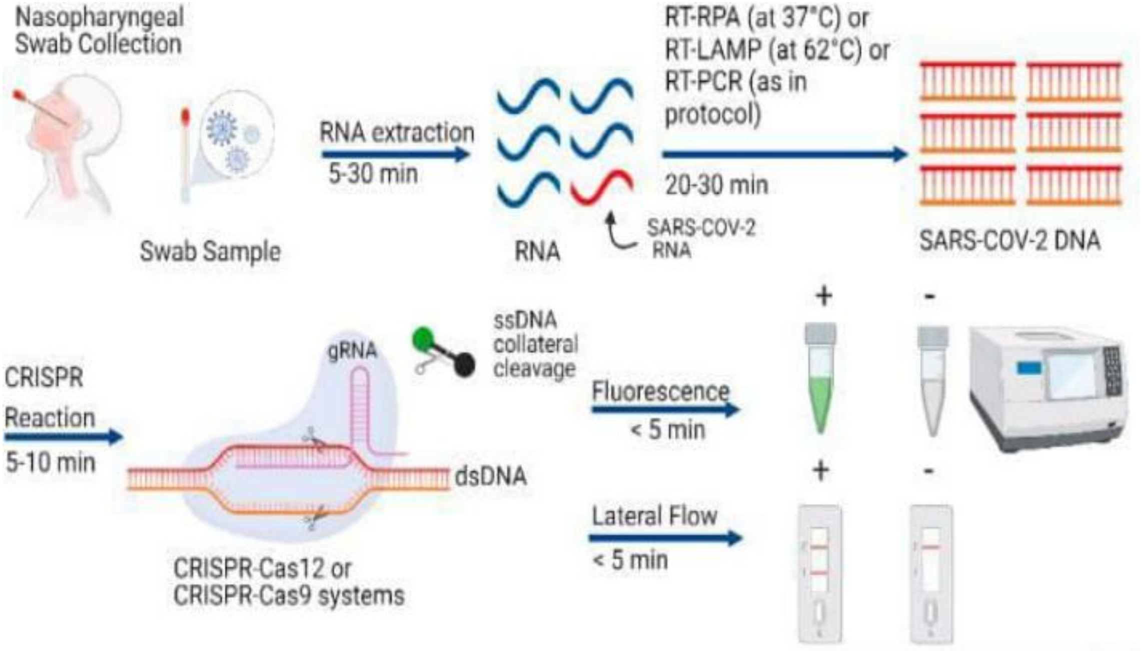


Figure: 08 RT-PCR Detection Test

Understanding cycle threshold (Ct) values and the factors affecting them is crucial for evaluating viral load and COVID-19 severity. Although clinical studies have investigated the link between Ct values and disease outcomes, results have been inconsistent. To clarify these relationships, a narrative review was conducted using literature up to April 2021 from sources like PubMed and Scopus. The review explores how Ct values relate to mortality, severity, and infectivity, while also examining factors such as sample collection and swab types that can influence Ct measurements [41-44].

ANTI BODY TESTIG

The Coronaepidemic has had widespread propertieshappening society, the economy, & healthcare universal. As nations plan to reopen, antibody testing has been proposed to aid gradual economic recovery by identifying IgM, IgG &IgA antibodies generated in response to SARS-CoV-2 infection [45-48]. There were 4 main kinds of antibody tests: rapid diagnostic tests, ELISAs, neutralization analyses, and chemi-luminescent Radio immunosorbent. No universal averageaimed at these tests exists, and their accuracy can vary, especially during early infection when sensitivity is low. Specificity improves after the first week, but many tests face challenges like high false-negative rates and design biases. This review examines current antibody testing methods, assesses their accuracy, and identifies gaps in knowledge [49-50].

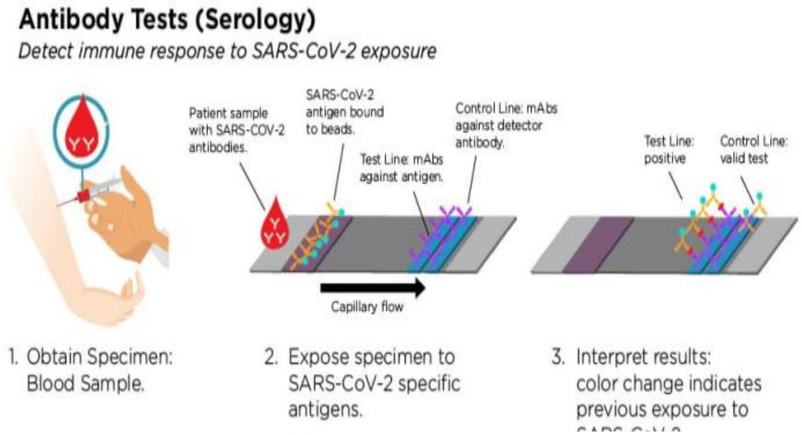


Figure: 09 Antibody testing Process

ANTIGEN DETECTION TEST

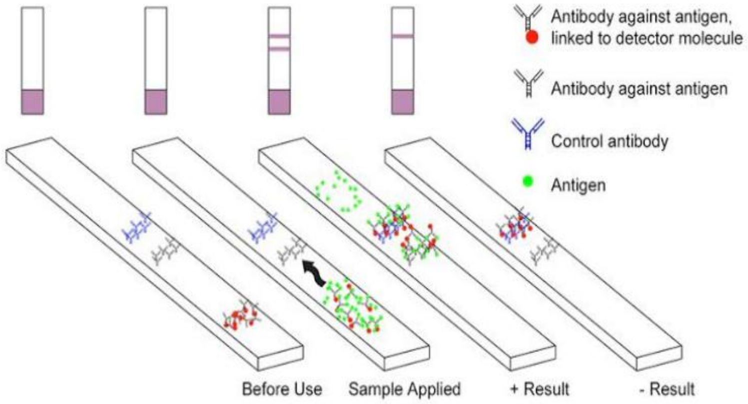


Figure: 10 Antigen detection Testing

Antigen-based immunoassays are important tools for diagnosing and managing infectious diseases. Advances have enhanced their sensitivity, specificity, and user-friendliness. They are particularly useful for detecting pathogens that are difficult or dangerous to culture and are commonly used for rapid diagnosis in healthcare settings. Some tests provide results in as little as 15 minutes, supporting fast and effective clinical decisions.[51][52]

TREATMENT

Initial treatment for COVID-19 typically includes medications to reduce fever, relieve pain, and suppress coughing [53.]

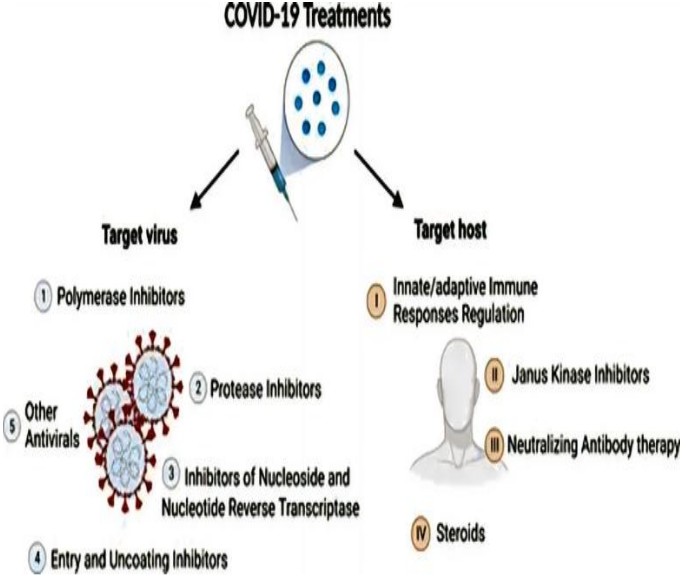
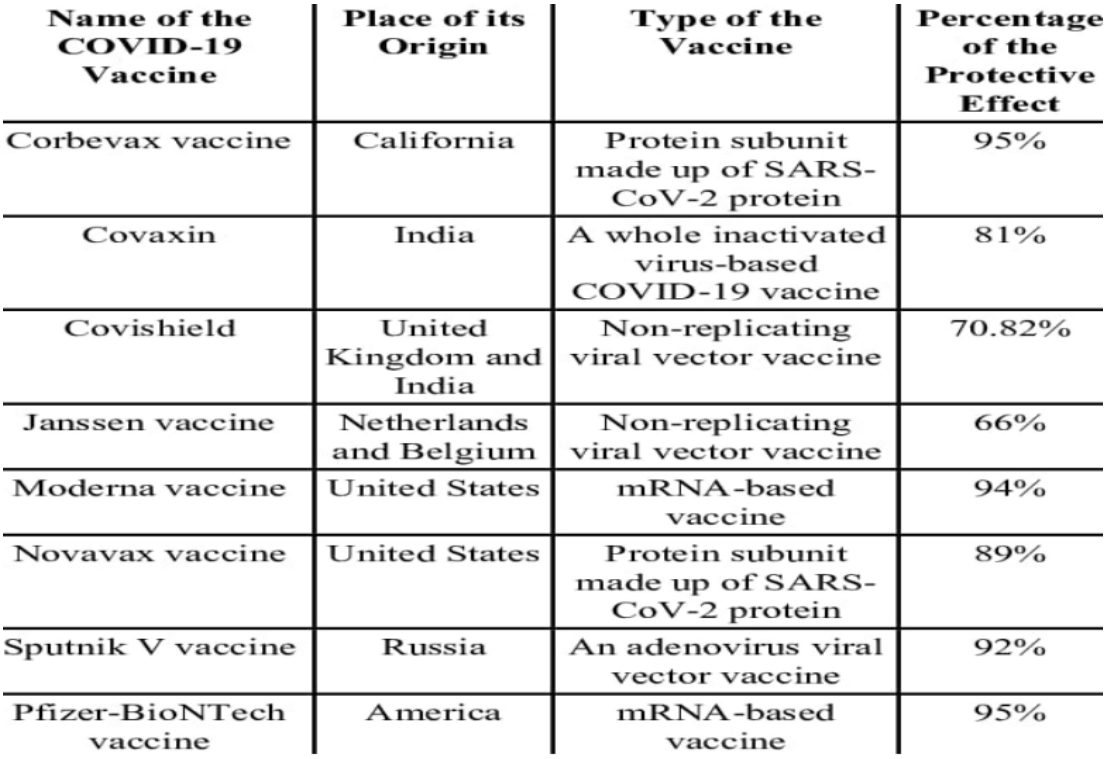


Figure: 11 Treatments for COVID-19

VACCINES



Name of the COVID-19 Vaccine	Place of its Origin	Type of the Vaccine	Percentage of the Protective Effect
Corbevax vaccine	California	Protein subunit made up of SARS-CoV-2 protein	95%
Covaxin	India	A whole inactivated virus-based COVID-19 vaccine	81%
Covishield	United Kingdom and India	Non-replicating viral vector vaccine	70.82%
Janssen vaccine	Netherlands and Belgium	Non-replicating viral vector vaccine	66%
Moderna vaccine	United States	mRNA-based vaccine	94%
Novavax vaccine	United States	Protein subunit made up of SARS-CoV-2 protein	89%
Sputnik V vaccine	Russia	An adenovirus viral vector vaccine	92%
Pfizer-BioNTech vaccine	America	mRNA-based vaccine	95%

CONCLUSION

The global response to COVID-19 showcased remarkable scientific collaboration and innovation, leading to the rapid development of vaccines using diverse technologies, including traditional inactivated viruses and advanced mRNA and protein subunit methods. Immunizations such as Pfizer-BioNTech (BNT 162b2), Corbevax, and m RNA vaccine (Moderna) take proven highly effective, playing a key role in lowering severe cases and deaths worldwide.

AUTHOR CONTRIBUTIONS

All authors are contributed equally

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DECLARATION OF COMPETING INTEREST

The Authors have no Conflicts of Interest to Declare.

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None

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