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ICARASET - 2021 PROCEEDINGS

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About the Conference:

6th International Conference on Advanced Research in Arts, Science, Engineering & Technology (ICARASET-2021) is a prestigious event organized with a motivation to provide an excellent international platform for the academicians, researchers, engineers, industrial participants and budding students around the world to share their research findings with the global experts. ICARASET-2021 will be held in Perambalur, India on 27th June 2021. The key intention of ICARASET-2021 is to provide opportunity for the global participants to share their ideas and experience in person with their peers expected to join from different

parts on the world. In addition this gathering will help the delegates to establish research or business relations as well as to find international linkage for future collaborations in their career path. We hope that ICARASET-2021 outcome will lead to significant contributions to the knowledge base in these up-to-date scientific fields in scope. The conference would offer a large number of invited lectures from renowned speakers all over the country. The Best paper awards will be given for the papers judged to make the most significant contribution to the conference.

Objective of the Conference:

To encourage regional and international communication and collaboration; promote professional interaction and lifelong learning; recognize outstanding contributions of individuals and organizations. To promote scientific and educational activities towards the advancement of the theory and practice of all engineering and technology fields and related arts and sciences. To foster and conduct collaborative multidisciplinary research in state of the art methodologies and technologies within its areas of expertise.

Conference Theme:

New and Expanding Horizons in Research Pursuits in Our Current Social and Scientific Scenario Worldwide

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CONTENTS

DISEASE-X: CROWN VIRUSES TRANSFORMED LIVESINTO CORONA FACTORIES AND DANCE OF THE PANDEMIC COVID-19

Dr. Ishan Y. Pandya*, Dr. Navneet Joshi & Dr. Amarnath Mishra*****
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Abstract:

Coronaviruses mainly infectsAves and mammals including humans.Earlier attacks of coronaviruses cause SARS, and MERS in humans. Structurally, the coronavirus is group of retroviruses (+SS-RNA) enclosed within lipid bilayer covered with spike proteins. Spike protein enables the virus to enter the pneunocytes. Within pneumocytes, viral multiplication increases that further starts infection cycle in host, and host with high viral load now serves as 'Corona-factory'.Current article, provides the description on molecular structure of coronaviruses, types or variants, infection cycle, and mode of transmission, symptoms of the disease CoViD-19, and diagnostic methods, possible treatments or vaccination. Intelligent Biochips will useful against 'disease-causing organisms' that can be detected prior to causing disease in the body and earlier treatment may prevent the progress of the disease at high-level.

Key Words: CoViD-19, Infection Cycle, Molecular Events, Symptoms, Diagnosis, Treatment, Biochip.

1. Introduction:

Like Bubonic plague, Cholera, Typhus, HIV-AIDS, now a microbial disease is spreading in 'all crowd' world.Pandemic CoViD-19 or Wuhan pneumoniae, its viral outbreak was first reported from the Wuhan, China. The word CoViD-19 could be decoded as "Co –corona, Vi – Virus, and D – Disease, December-Year-2019". TheCoViD-19 best fits in the examples of disease-X which is caused by any unknown pathogen called 'Pathogen-X' that has potential to create the epidemic or pandemic both situation to the world.[1]Scientific researches has proven that disease causing coronavirus naturally found in birds, and mammals. Coronaviruses zoonotically transmitted to humans from animals, and causes infection in nasopharyngeal or pulmonary tractand ~800millon alveoli of lungs. The reverse zoonosis possibly may cause infection to canines or other vertebrates, as infection of coronavirus was reported in India, recently. Nearly there 7 known human coronaviruses, these are HCoV-229E,HCoV-NL63,HCoV-OC43, Middle East respiratory syndrome–related coronavirus (MERS-CoV) or HCoV-EMC/2012), severe acute respiratory syndrome coronavirus (SARS-CoV-1), and severe acute respiratory syndrome coronavirus 2 (SARS-CoV-2). Currently, SARS-CoV-2has infected > 17Cr people and responsible forover38.1 lakhs deaths (up to June, 16-2021).

2. Mode of Transmission and Molecular Structure of Corona Virus:

Bats carry multiple coronaviruses and some are accessible by an intermediate animal source to human beings. Civet causes SARS-CoV, and camels MERS-CoV. Researchers are still trying to determine how animals are sapped into human beings by the new coronavirus. This is also interest of researchers and other policymakers that current virus is natural or genetically reengineered and CoViD-19 is pandemic or plan-demic or biological war? The 2019-nCoV shares nearly 70% nucleic acid sequence similarities to SARS-CoV. SARS zoonosis that first arose in China (2002), prior to expanding through a travel-oriented global epidemic in 2003, to 29 countries / regions, with 8k cases involving cases of fatality of 9.6%. It was believed that both nosocomial transmission SARS-CoV and MERS-CoV emerged in bats and those outbreaks were specifically spread to citizens from consumer civets and dromedary camels respectively [1]. The primary receptor of SARS-CoV1 is ACE-2, and hemagglutinin. MERS or Camelflu is a novel MERS-CoV-related, deadly zoonotic human infectious disorder of the Middle East countriesand people are expected to be infected by dermal contact with camels or camels by MERS-CoV at fatality rates of almost 35%, while nosocomial transmission is also an important characteristic [3]. DPP4 (CD26) are receptors for MERS coronaviruses.A significant amount of SARS-CoV and MERS-CoV study has contributed to the discovery of many coronaviruses such as SARS and MERS in bats. SARS-CoV2 bounds on Angiotensin converting enzyme -2 (hACE-2) receptors of pneumocytes of lungs. hACE participates in RAAS system, and is localized in various tissues viz. enterocytes of small intestine, Sertoli cells or Leydig cellsof seminiferous tubules, hepatocytes, pancreatic exocrine, cardiomyocytes, thyroid, and placenta. ACE2 Activity Assay and ACE Screening Assay for inhibitors may be performed to help promote scientific advancement in corona virus research area. Corona virus (CoVs) belongs to the order Nidovirales, the family Coronaviridae and the subfamily Coronavirinae are viruses enveloped with a positive single-stranded RNA genome. CoVs have the highest genomes among RNA viruses, with genetic material sizes ranging in length from 26-32 kb. CoVs are categorized into four genera based on genetic and antigenic criteria,

as described in table-1.Due to missense mutation there are many variants of coronaviruses are reports worldwide such as SARS-CoV-2 α variant, SARS-CoV-2 β variant, SARS-CoV-2 ϒ variant, SARS-CoV-2 δ variant, SARS-CoV-2 € variant, SARS-CoV-2 ζ variant, SARS-CoV-2 η variant, SARS-CoV-2 θ variant, SARS-CoV-2 ι variant, SARS-CoV-2 κvariant, Cluster 5- ΔFVI-spike etc. All variants shows certain amino acids position replacement in sequences.

Types	Species Infected	Strains of Coronavirus
α-CoVs	a. Humans	a. Human coronavirus NL63 (HCoV- NL63), Human coronavirus 229E (HCoV-229E)
	b. Porcine	b. Transmissible gastroenteritis coronavirus (TGEV),Porcine epidemic diarrhoea coronavirus (PEDV), Porcine respiratory coronavirus (PRCoV)
	c. Dogs	c. Canine Coronavirus (CCoV)
β-CoVs	a. Humans	a. Human coronavirus 4408 (HCoV-4408), Human coronavirus OC43 (HCoV-OC43), Human coronavirus HKU1 (HCoV-HKU1), severe acute respiratory syndrome coronavirus (SARS-CoV), Middle Eastern respiratory syndrome coronavirus (MERS-CoV).
	b. Bats,	b. Bat coronavirus (BCoV)
	c. Mouse	c. Murine hepatitis virus (MHV),
	d. Bovine	d. BCoV
	e. Porcine	e. Porcine hemagglutinating encephalomyelitis virus (HEV)
γ-CoVs	a. Birds	a. IBV (infectious bronchitis virus)
δ-CoVs	a. Porcine	a. PdCV (porcine deltacoronavirus)

3.1 Structure:

June and David first coined the word coronavirus. SARS-CoV-2 is 50-200nm in size and diameter is 85nm, containing lipid bilayer enveloped, (+) SS-RNA carrying retrovirus of genome size 27-32kbwith 4 main genes – S, E, M, N, and ORF segment. The genome has a 5′ methylated cap and a 3′ polyadenylated tail. Viral genome can synthesize ~9860 amino acids. The S, E, M, and N genes encode structural proteins, whereas ORF region encodes non-structural proteins viz. 3-chymotrypsinlike protease, papain-like protease, and RNA-dependent RNA polymerase (RDRP).TheA transcriptionregulatory sequence (TRS) motif is present at the 3' end of the leader sequence preceding most ORFs and thought to be important for a "copy-choice" mechanism that mediates theunique random template switching during RNA replication, resulting in a high frequency of homologousRNA recombination in coronaviruses. Coronavirus genome codes4 main types of structural proteins- the Spike protein(S) or peplomers, the Nucleocapsid (N), the Membrane (M), and the Envelope Protein (E), both essential for the formation of a structurally functional Viral Particle [6-8]. Virus assembly includes the membrane protein (M) and the envelope protein (E), whereas the spike protein (S) facilitates virus entry within host cells. On an average there are 74 spike proteins (each 20nm long) are present on coronavirus (according Kiss et al., 2006). Nonetheless, more recently it became apparent that some CoVs do not need a complete set of structural proteins to put together a coherent, contagious virion, which may be completely expendable to certain structural proteins or that these CoVs may express multiple proteins with conflicting compensatory mechanisms [7, 9-13].

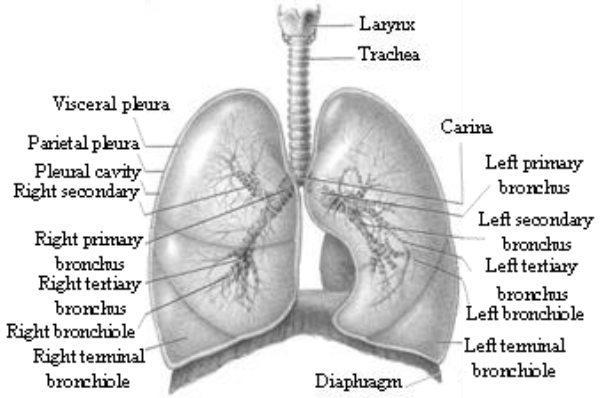


Fig: 1 Anterior View of human Pulmonary cavity and lungs

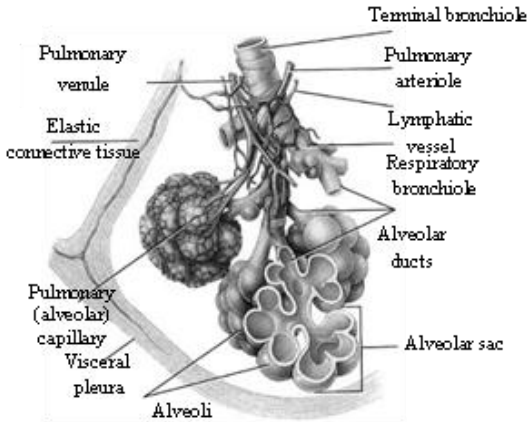
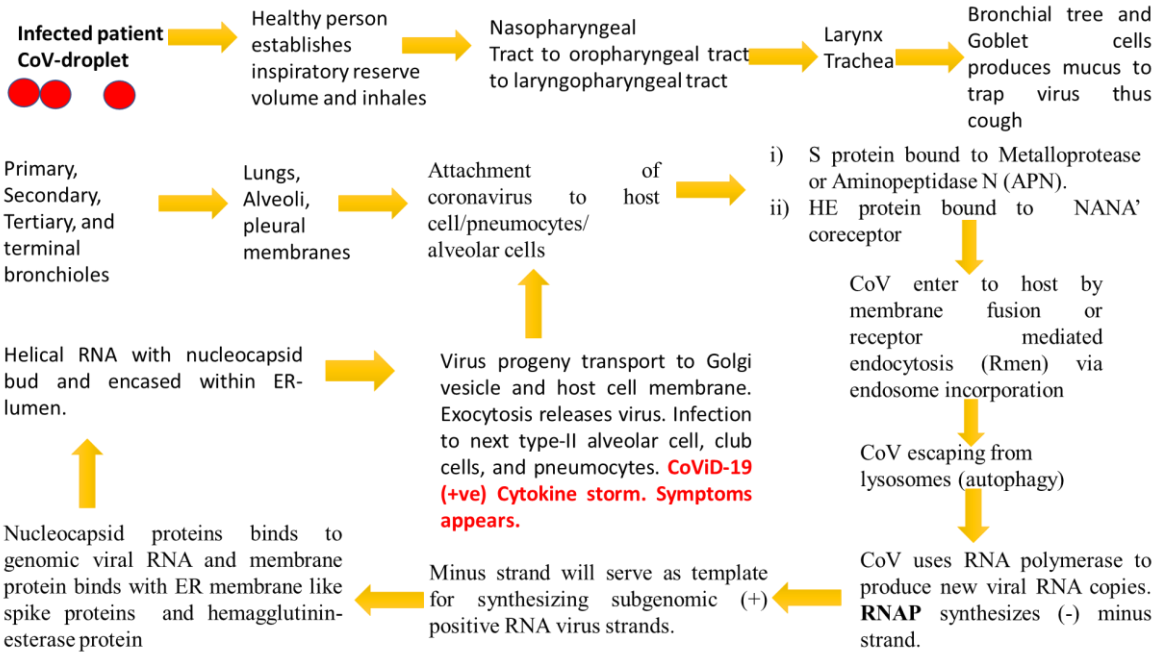


Fig: 2 Diagram of a portion of a lobule of the lung



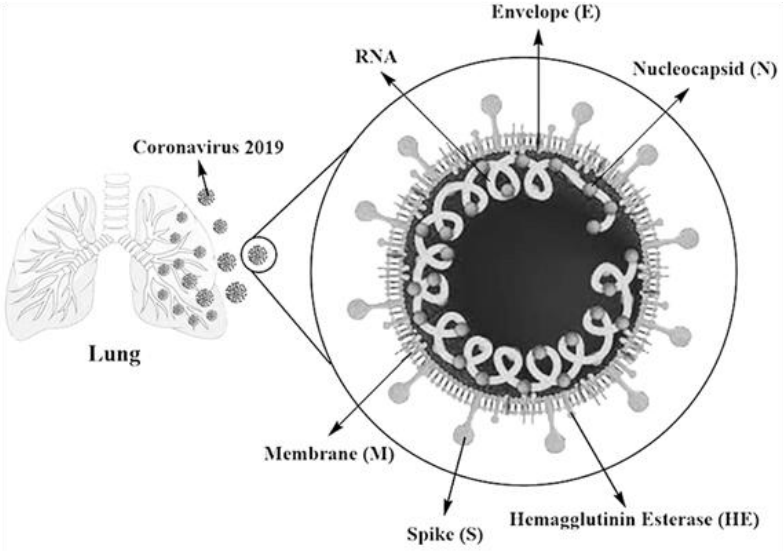
Flowchart 1: The infection and replication cycle of coronaviruses

E protein is integral protein 8.4-12kDa, and composed of 76-109 amino acids and responsible for intracellular trafficking and budding/morphogenesis. Independently, each protein performs mainly a task in the virus particle formation but is also active in other facets of the replication process. Many coronaviruses often contain the hemagglutinin-esterase protein (HE) associated with the envelope. The S protein is a fundamental determining factor of viral host selection and tissue tropism as well as a significant inducer of host immune responses, in addition to mediating virus entry. The coronavirus spike comprises three segments: a broad ectodomain, a transmembrane anchor with a single pass, and a small intracellular tail. The ectodomain consists of a subunit S1 receptor-binding, and a subunit S2 membrane-fusion. Analysis with electron microscopy found that the spike is a clove-shaped trimmer with three S1 heads and a trimeric S2 stalk [13-15]. Upon **virus** admittance, S1 attaches to a receptor for viral attachment on the host cell surface, and S2 fuses the viral membranes and host, enabling the entrance of viral genomes into host cells. Binding receptors and membrane fusion are the main and essential stages in the process of infection with coronavirus; they often act as the primary targets for human inventions. Some CoVs may also mediate single-cell fusion between infected and adjacent non-infected cells with S cell membrane development. Such a development of large, syncytia was suggested as an approach to allow the virus to propagate directly between cells, subverting antibodies to virus neutralization [16-21]. The only protein that attaches directly to the genome of the CoV RNA is Nucleocapsid protein N (~50kDa) contrary to the other major structural proteins [25]. While N is predominantly active in the viral genome and participates in the CoV replication process and the cell sensitivity of the host to a viral infection[26]. Role in assembly and budding was, interestingly, proposed to position N in the ER-Golgi Region [27, 28]. Nevertheless, the transient expression of N showed that the development of viral particles (VLPs) was significantly increased in some CoVs, suggesting that it might not be necessary to form envelopes but for the entire formation of the virus [12, 13, 29]. The most abundant protein is M, a type III transmembrane protein and specifies the structure of the viral envelope [30]. M consist of 218-263 amino acids. The principal leader of the CoV assembly is also regarded and communicates with all other essential structural coronaviral proteins [6]. M-protein homotypes are the main driving force behind the composition of the virion envelopes, but in themselves are not enough to shape the viruses [30-33]. For the retention and incorporation of S into new virions of the ER-Golgi intermediate compartment (ERGIC)/Golgi complex S and M is required [22, 34]. The attachment of M to N stabilizes the nucleocapside (N protein RNA complex) and inner core for virions and, in the end, facilitates viral assembly completion [22, 35, 36]. The viral envelope is formed by M and E together and is responsive enough for VLP production and distribution [7, 37, 38].

3.2 Envelope protein:

Coronaviruses display a complex receptor recognition pattern. A small, integral protein with 76-109 amino acids, the CoV E protein ranges from 8.4 and 12 kDa in size [39-41]. The E protein is the shortest, but also the most mysterious, of the major structural proteins. In both the main and the secondary structures, E has a small hydrophilic amino acid terminal, 7–12 amino acids followed by 25 amino acids, with a broad hydrophobic transmembrane domain (TMD), and a long hydrophilic carboxylic terminal, which is the majority of the protein [37, 42, 43]. At least one potential amphipathic α-helix in the hydrophobic area of TMD includes an ion

conducting pore that is oligomerized in membranes [44-46]. E is distributed extensively in the infected cell during the replication process, but the virion envelope only includes a small portion [47]. The bulk of the protein is located in the ER, Golgi and ERGIC (endoplasmic-reticulum–Golgi intermediate compartment) intracellular trafficking at which the enzyme is packaged and budded by CoVs. Recombinant CoVs lose E with significantly reduced viral titres, paralyzed viral maturity or ineffective progeny in output, which show the value of E in the development and maturation of the virus. [9-11, 48, 49].



3.3 Localisation:

The coronaviruses differentiate them from other well researched viruses, as they are enveloped in ERGIC from where the membrane envelope is extracted [89]. Once within the lumen of ERGIC, contagious virions are released from the infected cell via the host secretory pathway [50]. The protein E is therefore primarily found in the ER and Golgi complex, where the assembly, production and intra-cellular trafficking of the infectious viruses are concerned [32], [51], [41], [52]. The probability of epitope-tagged E proteins influencing their location has been expressed, however both FLAG-tagged and untagged forms of SARS-CoV E exhibit this pattern of distribution [53-55]. The sub-cellular location of the SARS-CoV E protein has also been studied using both cells and infected cells in Nieto-Torres, DeDiego [51], and it has been shown that the tag on E does not influence its position in both groups of cell E acquired with E-Golgi. The other viral architectural proteins certainly doesn't appear to have a considerable influence on E protein encoding, suggesting that SARS-CoV E localization happens at the ERGIC, mostly expressed spontaneously during an illness. While experiments examining the position of E have used only FLAG-tagged protein variants, the findings indicate that epitope tags do not seem to have any significance.It is important to establish which portion of the E protein contains data to target the ERGIC because it may relate to the way CoVs interact with other viral proteins and host proteins to facilitate the assembly of new infectious virus progenies. Nevertheless, there was little work into this aspect. Wu, Zhang [79] has focused on Signal P at the N-terminus of the SARS-CoV E protein, an expected signal-peptide site. Raamsman, Locker [41], however, did not report any variation in electrophoretic mobility during or after membrane integration of the A59 E Mouse Hepatitis Virus (MHV), suggesting that MHV E does not have a cleavable signaller sequence. The first to recognise the IBV E Protein C-terminus contained Golgi focused knowledge were Corse and Machamer [56]. They researched the existence of an N-terminus luminaire targeting signal, and used it to move the truncated terminal to the cell surface. In turn, the truncation from C-terminus and manufacturing of an E-complex chimeric were both retained at the complex of Golgi and the researchers concluded that perhaps the information on the Golgi targeting of IBV E protein was present in its C-terminus. The C-terminus was further cut down by a sequence of motifs between amino acid residues 44 and 72. The target information for the most part was cut down. This was the basis on which Cohen, Lin [54] also identified Complex Targeting Information in C-terminus for the Golgi SARS-CoV E protein. The researchers explicitly showed that that no highly conserved proline residue mutation residual mutation nor the β-strand disturbance that would stabilize the β-hairpin at either side was necessary to interrupt the binding of the SARS-CoV E protein to the Golgi complex.The researchers have explored Golgi targeting information in N-terminus E- protein using the chimeric N-terminus protein. It was interesting that N-terminus chimera was directed in the Golgi region and the researchers hypothesized that the SARS-CoV E protein N-terminus was provided with additional oriented details. The two N- and C-terminals were also used to clarify why the full-length E-protein with mutations alone in the C-terminus was not disrupted. It is clear from these analyses that knowledge of Golgi targeting is found primarily in the C-terminus of the CoV E, while additional targeting details does tend to be present in some CoV's, such as the SARS-CoV E, in the N-terminus.

3.4. Topology:

Several specific E protein topologies have been recognized and suggested for the various CoVs. Many studies have used simulation programs with conflicting forecasts among programming and some with analytical proofs. The IBV E C-terminus was found to be positioned in a cytoplasmic way while the N-terminus is in the lumen of the Golgi complex [37]. The MHV E terminal is found in cytoplasm, but no N terminal has been identified. The researchers proposed that it could be hidden in the lipid bilayer [41], based on the hydropathic plot of the protein. The C end of the cytoplasm was confirmed by the highly-hydrophobic N terminal and was hidden within the Golgi membrane [57]. For comparison, the TGEV E protein displays a C-terminus topology and an N-terminus cytoplasmic [58]. Nevertheless, to date the most attention has been paid to the topology of the SARS-CoV E protein. A SARS CoV E protein, Yuan and Liao[52] labelled with FLAG has been reported to have the cytoplasmic topology of the N and C-terminals. The algorithm prediction showed contradictory predictions of information and experimental evidence; TMHMM and MEMSAT predicted a C-terminus cytoplasmic N-terminus and a luminal C-terminus; HMMTop forecast a luminous N-term and a C-terminus cytoplasmic. In comparison, transfected, mutated and untagged SARS CoV E cells had a L-N terminus and a C-terminus cytoplasmic topology [51]. Because of the different topologies, there was also an inconclusive amount of TMDs for the CoV E enzyme. The prediction systems are likely to differ with their expected effects on the basis of the formulas used to measure an outcome in each experiment and/or in the window duration.It was proposed that the E protein may not show a typical membrane topology for various CoV groups, or that E orientation differs depending on the quantification of protein expression or oligomerisation [39]. The E protein may also determine its membrane topology depending on whether it functions as an ion channel, or whether the protein is present during assembly in a viral envelope [12].

3.5. Post-translational modifications in Coronavirus:

3.5.1 Palmitoylation:

Palmitoylation assists in subcellular protein transport through membrane compartments and can attenuate communication between protein and protein interactions (PPIs) [12, 59]. The hydrophobicity of palmitoylated proteins was increased and stated to support the membrane combination and also membrane anchoring functions[60, 61]. Palmitoylated viral proteins, including influenza virus proteins, envirus Envalves and filoviruses and F13 L of the vaccine virus, are well distributed in enveloped viruses [62]. The palmitoylation of the F13 L protein of the vaccine virus has demonstrated that it is essential for targeting proper membranes [63]. The nuclear core protein hepatitis C virus (HCV) connects ER membranes to the development of viral particles palmitoylation-dependent [64]. For CoV E proteins, palmitoylates were contained only in IBV, SARS-CoV and MHV [53, 56, 65]. Palmitoylation substrates are a variety of integral membrane proteins with the cysteine exist adjacent to the TMD which in turn is the target [66, 67]. Cysteine residues of the MHVA59 E protein are double or triple to alanine, and VLP formation reduces significantly [29, 67]. In fact, the three-mutated E proteins are unpredictable, degradable, and decrease the viral production of their respective recombinant MHV substantially, indicating that E palmitoylation plays a key role in the MH Viral assembly [65]. IBV E palmitoylation does not influence its localization in the environment of the Golgi system because of its distinct cysteine-mutated E proteins from their palmitoylated equivalents [56]. There has also been an interesting mutation with all three cysteine residues from the SARS-CoV E proteins in some hydrophobic TMD residues in the Golgi [53]. Although the researchers themselves did not show the role of the three-mutated E protein, the results show that SARS-CoV E protein does not even influence its site.Instead, the loss of both the TMD information for Golgi and the palmitoylated cysteine residues is possible as well as its association membrane losses [47]. Lopez, Riffle [65] indicated that the E protein palmitoylation can influence the interaction between the membrane and the protein. In contrast to the hydrophobic TMD, the positions of the palmitoylated cysteine residue probably increase the membrane sensitivity of the area to modify or regulate the protein-membrane connection.

3.5.2 Myristoylation:

The N-terminal of myristic acid (C14:0) is classified as N-terminal myristoylation, and is connected to a residue of glycine present in some virus, microbial, and bacterial proteins [68-71]. Other viral proteins include the polyovirus VP4 protein, SIV protein from Gag, the negative regulatory factor (NEF) universal immune virus (HIV) virus and the hepatitis B (HBV) protein from pre-S1 [72-75]. All these proteins have a preserved 1MGxxxS / T sequence, where ' x ' is an amino acid [76]. Coronavirus E proteins, like other Nidovirus order, have not apparently had a motif for myristoylation and are proposed only to be a unique feature in the order of Nidovirales to the Arteriviridae family [76]. Nonetheless, empirical evidence to support this does not appear to exist.

3.5.3 Ubiquitination:

Ubiquity and its counterpart, deubiquitination, are well-characterized post-translation adaptations, which help to maintain the homeostasis by regulating the level and functionality of cell proteins [77]. The virus may take advantage of this component or even encode its own deubiquitinating/ubiquitinating enzymes to drive the viral cycle of life [78]. So far, it has been reported that only SARS-CoV E is ubiquitined although its

relevance has not been established. The non-structural SARS-CoV (nsp) 3 protein co-locates with the E and its communicating with the nsp3 ubiquitin-like domain-1 through the N-terminal regulated. An ubiquitination study also revealed, separately, that E can be ubiquitised and its ubiquitisation coincides inversely with its consistency and half-life [78, 79]. Keng, Åkerström proposed that it could modulate viral development by downgrading output of e-components and thereby retain an optimum viral title, provided the late expression of the SARS-CoV accessory protein 8b. In the case of a natural infection though, this should be tested.

3.5.4 Glycosylation:

In N-related glycosylation, the moieties of oligosaccharides in the consensus series Asn-X-ser / Thr are bound to certain Asparagine residues. This assists cellular and viral proteins in the appropriate way through the successful recruitment of host chaperone proteins including calnexin and calreticulin. [80]. Glycosylation of CoV E and its function is very little accessible. In its luminal N-terminal, IBV E protein was proposed for containing a single glycosylation site while SARSCoV E is forecast to contain two potential glycosylation sites [81]. Corse and Machamer [37] suggested that asparagine residue 5 (N5) of the terminus should be glycosylated based on topology of IBV E. Yet, perhaps because of the relative proximity of the residue to the membrane, this was not observed. Residue N48 was also not glycosylated in SARS-CoV E, and for the same reasons was suggested to be non-functional [53]. On the other side, N66 has been shown to be glycosylated and, somewhat importantly, this residue mutation produced higher molecular weight forms comparable to the E protein dimers and trimers.This indicates that N66 glycosylation may work to reduce oligomerization of the E protein and potentially to facilitate a particular role of the E protein. Consequently, multimeric varieties of the E protein in N66 may not be glycosylated to increase the E functionality [82]. Westerbeck as well as Machamer [50] identified two types by using infected and transfected cells and, each of which had a specific function, of the IBV E protein.They indicated that the lower molecular weight, probably the monomeric type, works by distorting the host secretory pathway, while for virion assembly, the higher molecular weights are needed. Clearly, more research is needed to decide whether all CoV E-proteins are glycosylated, or are SARS-CoV-unique, which may offer them certain infective characteristics and an E-protein glycosylation property.

4.1 Symptoms, Diagnostic Methods, and Treatment of CoViD-19:

Symptoms of the disease vary from mild to chronic condition. The mild symptoms of SARS-CoV-2 are headache, hyposmia or smell blindness due to infection of sustentacular cells and olfactory nerves, hypogeusia, nasal congestion, Rhinorrhoea, cough/sputum, Myalgia, Sore throat, Pyrexia, Diarrhoea, which chronic symptoms cover all above symptoms along with Dyspnea or SOB, Anxiety, hypoxia, delirium, Amnesia, ICH, Psychosis, respiratory failure, pulmonary fibrosis, cardiac arrhythmias etc. Less common symptoms may include Hemoptysis and “CoViD-toes”. Infectedlungs possess higher load of coronaviruses thus patient body act as “Corona factory”. Those are on higher risk who have other complications such as IDDM, NIDDM, Diabetes insipidus, MODY, Cancer, HIV-positives, Mucormycosis Emphysema, Cystic fibrosis, or previously exposed by Chronic Obstructive Pulmonary Diseases-Bronchopulmopneumonoultramicroscopicsilicovolcanoconiosis, Long CoViD etc. The CoViD-19 is diagnosed using nasopharyngeal swab technique and further confirmation is carried by Reverse transcription polymerase chain reaction (RT-PCR), D-dimer test, CRISPR, NAT, dPCR, Microarray analysis, NGS-technology, Antigen test-ELISA, IgM-IgG antibody testing, Rapid diagnostic testing RDTs, NAb test, Breath test, biomarkers level diagnosis for CoViD-19 testing viz. lymphocyte, platelets, D-dimer, lactatedehydrogenase (LDH), C reactive protein (CRP),aspartate aminotransferase (AST) orserum glutamic-oxaloacetic transaminase [SGOT], alanineaminotransferase (ALT), creatinine, procalcitonin(PCT) and creatine kinase (CK), TNF-α and IL-6 are used. X-ray and CT-Scan, and MRI are used for organ condition examination. LDH and CRP level increases in CoViD patients and indicate lung tissue damage with CHD. CoViD patients under chronic stages may suffer liver tissue damage and have elevated levels of SGOT.TNF-α is present in blood and disease tissues of patients with COVID-19.During mild symptoms paracetamol use relieves against myalgia and fever, fluid therapy minimizes the risk of dehydration, and proning increases ability to respire too. In those with low oxygen levels, use of the glucocorticoid dexamethasone is strongly recommended, as it can reduce the risk of death. IgG1-mAb LY-CoV555 prevents the virus admittance in host cells by blocking to spike protein attachment, and inhibit the growth of disease. Drug Remdesivir blocks the RNA polymerase activity and inhibits viral replication or life cycle of coronavirus. Amphotericin-B is useful in co-fungal infection in patients. Casirivimab and imdevimabmAb’s commonly called “antibody cocktails” for SARS-CoV-2. Currently, Viral Vector Vaccines (This vaccine uses an viral vector cloned with SARS-CoV-2 genetic material. Such recombinant viral vaccine delivers the virus genetic material to host, that further synthesizes SARS-CoV-2 specific proteins that triggers immune cascade response), Genetic Vaccines (It contain a segment ofSARS-CoV-2 virus geneticmaterial that codes for aspecific protein. It can be DNAor RNA. After vaccination, our cells use the geneticmaterial to make theSARS-CoV-2 protein, which isrecognised by the immunesystem to trigger a response.This response builds immunememory, so your body canfight off SARS-CoV-2 infuture.), Inactivated Vaccines (It contain killed SARS-CoV-2 virus.The killed virus is recognised bythe immune system to trigger aresponse without causing illness), Attenuated Vaccines (Contain weakened SARS-CoV-2virus which is recognisedby the immune system to trigger aresponse without causing illness) and Protein Vaccines (which

contain proteins from the SARS-CoV-2 virus,which are recognised by the immune systemto trigger a response. This vaccine can be whole proteins, protein fragments, ormany protein molecules packed intonanoparticles)for CoViD-19 are under clinical trials, and few have been approved for community level use. This vaccination will protect the people from transmitting the coronavirus and reduces mortality rate.

4.2 Future Invention for Next Disease-X Pandemics:

There are 10^{31} viruses, 5 x 10^{30} bacteria, 5.1 million fungi on our planet. ~380 trillion viruses living inside our body, this virus figure is 10 times larger than number of cells (37 trillion) in human body. Yet, we have collected a very very less information about organisms and their behaviour. These organisms could be beneficial or harmful or engineeredas harmful to human and other species as well. From the learning lessons of current pandemic, it is necessary to study disease causing organisms in more depth and prepare the world technologically advance. The fusion of artificial intelligence technologies with genetic technologies, we can promote the invention of the Biochip technologies. Intelligent microbial (protozoan, fungal, bacterial, or viral) detection biochip with insertion of organism specific genetic information will be a promising research. Intelligent smart biochip with its rice-grain size inserted below dermis-interstitium in human body. This biochip will activate and detect the pathogen-X or any pathogen entry in body, and so the disease will be diagnosed earlier and possible treatment or medications may arrange, as well threat transmission will be prevented. Like, Praneem / Pranim Polyherbal tablets has antimicrobial antiviral properties, such herbal drugs development will useful in future pandemics.Herbalextracts from plants such as *Azadirachta indica, Ocimumtenuiflorum, Eucalyptus glabrata, Citrus sp., Syzygiumaromaticum, Cinnamomum verum, Sapindusemarginatus, Curcuma longa, Emblica officinalis, Momordica charantia*, *Piper longum*have higher medicinal nutritional values, these could be developed as herbal vaccines for immunizing the health and worn-out the pathogens.

Conflict: There is no conflict of interest.

9. References:

1. Cui, J., F. Li, and Z.-L. Shi, Origin and evolution of pathogenic coronaviruses. Nature reviews Microbiology, 2019. 17(3): p. 181-192.
2. Aloufi, A.D., et al., Trends of reported human cases of brucellosis, Kingdom of Saudi Arabia, 2004–2012. Journal of epidemiology and global health, 2016. 6(1): p. 11-18.
3. Azhar, E.I., et al., The Middle East Respiratory Syndrome (MERS). Infectious Disease Clinics, 2019. 33(4): p. 891-905.
4. Ge, X.-Y., et al., Isolation and characterization of a bat SARS-like coronavirus that uses the ACE2 receptor. Nature, 2013. 503(7477): p. 535-538.
5. Wang, M. and Z. Hu, Bats as animal reservoirs for the SARS coronavirus: hypothesis proved after 10 years of virus hunting. Virologica Sinica, 2013. 28(6): p. 315-317.
6. Masters, P.S., The molecular biology of coronaviruses. Advances in virus research, 2006. 66: p. 193-292.
7. Mortola, E. and P. Roy, Efficient assembly and release of SARS coronavirus-like particles by a heterologous expression system. FEBS letters, 2004. 576(1-2): p. 174-178.
8. Wang, C., et al., MERS-CoV virus-like particles produced in insect cells induce specific humoural and cellular imminity in rhesus macaques. Oncotarget, 2017. 8(8): p. 12686.
9. DeDiego, M.L., et al., A severe acute respiratory syndrome coronavirus that lacks the E gene is attenuated in vitro and in vivo. Journal of virology, 2007. 81(4): p. 1701-1713.
10. Kuo, L. and P.S. Masters, The small envelope protein E is not essential for murine coronavirus replication. Journal of virology, 2003. 77(8): p. 4597-4608.
11. Ortego, J., et al., Absence of E protein arrests transmissible gastroenteritis coronavirus maturation in the secretory pathway. Virology, 2007. 368(2): p. 296-308.
12. Ruch, T.R. and C.E. Machamer, The coronavirus E protein: assembly and beyond. Viruses, 2012. 4(3): p. 363-382.
13. Siu, Y., et al., The M, E, and N structural proteins of the severe acute respiratory syndrome coronavirus are required for efficient assembly, trafficking, and release of virus-like particles. Journal of virology, 2008. 82(22): p. 11318-11330.
14. Kirchdoerfer, R.N., et al., Pre-fusion structure of a human coronavirus spike protein. Nature, 2016. 531(7592): p. 118-121.
15. Song, H.C., et al., Synthesis and characterization of a native, oligomeric form of recombinant severe acute respiratory syndrome coronavirus spike glycoprotein. Journal of virology, 2004. 78(19): p. 10328-10335.
16. Kim, K.Y., et al., Human coronavirus in the 2014 winter season as a cause of lower respiratory tract infection. Yonsei medical journal, 2017. 58(1): p. 174-179.
17. Dominguez, S.R., C.C. Robinson, and K.V. Holmes, Detection of four human coronaviruses in respiratory infections in children: A one-year study in Colorado. Journal of medical virology, 2009. 81(9): p. 1597-1604.

18. Jimenez-Guardeno, J.M., et al., The PDZ-binding motif of severe acute respiratory syndrome coronavirus envelope protein is a determinant of viral pathogenesis. PLoS pathogens, 2014. 10(8).
19. Lau, S.K., et al., Severe acute respiratory syndrome coronavirus-like virus in Chinese horseshoe bats. Proceedings of the National Academy of Sciences, 2005. 102(39): p. 14040-14045.
20. Rest, J.S. and D.P. Mindell, SARS associated coronavirus has a recombinant polymerase and coronaviruses have a history of host-shifting. Infection, Genetics and Evolution, 2003. 3(3): p. 219-225.
21. Lu, G., Q. Wang, and G.F. Gao, Bat-to-human: spike features determining 'host jump'of coronaviruses SARS-CoV, MERS-CoV, and beyond. Trends in microbiology, 2015. 23(8): p. 468-478.
22. Fehr, A.R. and S. Perlman, Coronaviruses: an overview of their replication and pathogenesis, in Coronaviruses. 2015, Springer. p. 1-23.
23. Glowacka, I., et al., Evidence that TMPRSS2 activates the severe acute respiratory syndrome coronavirus spike protein for membrane fusion and reduces viral control by the humoral immune response. Journal of virology, 2011. 85(9): p. 4122-4134.
24. Qian, Z., S.R. Dominguez, and K.V. Holmes, Role of the spike glycoprotein of human Middle East respiratory syndrome coronavirus (MERS-CoV) in virus entry and syncytia formation. PloS one, 2013. 8(10).
25. de Haan, C.A. and P.J. Rottier, Molecular interactions in the assembly of coronaviruses. Advances in virus research, 2005. 64: p. 165-230.
26. McBride, R., M. Van Zyl, and B.C. Fielding, The coronavirus nucleocapsid is a multifunctional protein. Viruses, 2014. 6(8): p. 2991-3018.
27. Tooze, J., S. Tooze, and G. Warren, Replication of coronavirus MHV-A59 in sac-cells: determination of the first site of budding of progeny virions. European journal of cell biology, 1984. 33(2): p. 281-293.
28. Klumperman, J., et al., Coronavirus M proteins accumulate in the Golgi complex beyond the site of virion budding. Journal of virology, 1994. 68(10): p. 6523-6534.
29. Boscarino, J.A., et al., Envelope protein palmitoylations are crucial for murine coronavirus assembly. Journal of virology, 2008. 82(6): p. 2989-2999.
30. Neuman, B.W., et al., A structural analysis of M protein in coronavirus assembly and morphology. Journal of structural biology, 2011. 174(1): p. 11-22.
31. De Haan, C.A., H. Vennema, and P.J. Rottier, Assembly of the coronavirus envelope: homotypic interactions between the M proteins. Journal of virology, 2000. 74(11): p. 4967-4978.
32. Lim, K. and D. Liu, The missing link in coronavirus assembly retention of the avian coronavirus infectious bronchitis virus envelope protein in the pre-Golgi compartments and physical interaction between the envelope and membrane proteins. Journal of Biological Chemistry, 2001. 276(20): p. 17515-17523.
33. Ujike, M. and F. Taguchi, Incorporation of spike and membrane glycoproteins into coronavirus virions. Viruses, 2015. 7(4): p. 1700-1725.
34. Opstelten, D.J., et al., Envelope glycoprotein interactions in coronavirus assembly. The Journal of cell biology, 1995. 131(2): p. 339-349.
35. Escors, D., et al., The membrane M protein carboxy terminus binds to transmissible gastroenteritis coronavirus core and contributes to core stability. Journal of virology, 2001. 75(3): p. 1312-1324.
36. Narayanan, K., et al., Characterization of the coronavirus M protein and nucleocapsid interaction in infected cells. Journal of virology, 2000. 74(17): p. 8127-8134.
37. Corse, E. and C.E. Machamer, Infectious bronchitis virus E protein is targeted to the Golgi complex and directs release of virus-like particles. Journal of virology, 2000. 74(9): p. 4319-4326.
38. Baudoux, P., et al., Coronavirus pseudoparticles formed with recombinant M and E proteins induce alpha interferon synthesis by leukocytes. Journal of virology, 1998. 72(11): p. 8636-8643.
39. Kuo, L., K.R. Hurst, and P.S. Masters, Exceptional flexibility in the sequence requirements for coronavirus small envelope protein function. Journal of virology, 2007. 81(5): p. 2249-2262.
40. Arbely, E., et al., A highly unusual palindromic transmembrane helical hairpin formed by SARS coronavirus E protein. Journal of molecular biology, 2004. 341(3): p. 769-779.
41. Raamsman, M.J., et al., Characterization of the coronavirus mouse hepatitis virus strain A59 small membrane protein E. Journal of virology, 2000. 74(5): p. 2333-2342.
42. Li, Y., et al., Structure of a conserved Golgi complex-targeting signal in coronavirus envelope proteins. Journal of Biological Chemistry, 2014. 289(18): p. 12535-12549.
43. Torres, J., et al., Conductance and amantadine binding of a pore formed by a lysine-flanked transmembrane domain of SARS coronavirus envelope protein. Protein science, 2007. 16(9): p. 2065-2071.

44. Verdiá-Báguena, C., et al., Coronavirus E protein forms ion channels with functionally and structurally-involved membrane lipids. Virology, 2012. 432(2): p. 485-494.
45. Nieto-Torres, J.L., et al., Severe acute respiratory syndrome coronavirus envelope protein ion channel activity promotes virus fitness and pathogenesis. PLoS pathogens, 2014. 10(5).
46. Verdiá-Báguena, C., et al., Analysis of SARS-CoV E protein ion channel activity by tuning the protein and lipid charge. Biochimica et Biophysica Acta (BBA)-Biomembranes, 2013. 1828(9): p. 2026-2031.
47. Venkatagopalan, P., et al., Coronavirus envelope (E) protein remains at the site of assembly. Virology, 2015. 478: p. 75-85.
48. Curtis, K.M., B. Yount, and R.S. Baric, Heterologous gene expression from transmissible gastroenteritis virus replicon particles. Journal of virology, 2002. 76(3): p. 1422-1434.
49. Ortego, J., et al., Generation of a replication-competent, propagation-deficient virus vector based on the transmissible gastroenteritis coronavirus genome. Journal of virology, 2002. 76(22): p. 11518-11529.
50. Westerbeck, J.W. and C.E. Machamer, A coronavirus E protein is present in two distinct pools with different effects on assembly and the secretory pathway. Journal of virology, 2015. 89(18): p. 9313-9323.
51. Nieto-Torres, J.L., et al., Subcellular location and topology of severe acute respiratory syndrome coronavirus envelope protein. Virology, 2011. 415(2): p. 69-82.
52. Yuan, Q., et al., Biochemical evidence for the presence of mixed membrane topologies of the severe acute respiratory syndrome coronavirus envelope protein expressed in mammalian cells. FEBS letters, 2006. 580(13): p. 3192-3200.
53. Liao, Y., et al., Biochemical and functional characterization of the membrane association and membrane permeabilizing activity of the severe acute respiratory syndrome coronavirus envelope protein. Virology, 2006. 349(2): p. 264-275.
54. Schoeman, D. and B.C. Fielding, Coronavirus envelope protein: current knowledge. Virology journal, 2019. 16(1): p. 69.
55. Nal, B., et al., Differential maturation and subcellular localization of severe acute respiratory syndrome coronavirus surface proteins S, M and E. Journal of general virology, 2005. 86(5): p. 1423-1434.
56. Corse, E. and C.E. Machamer, The cytoplasmic tail of infectious bronchitis virus E protein directs Golgi targeting. Journal of virology, 2002. 76(3): p. 1273-1284.
57. Maeda, J., et al., Membrane topology of coronavirus E protein. Virology, 2001. 281(2): p. 163-169.
58. Godet, M., et al., TGEV corona virus ORF4 encodes a membrane protein that is incorporated into virions. Virology, 1992. 188(2): p. 666-675.
59. Basu, J., Protein palmitoylation and dynamic modulation of protein function. Current Science-Bangalore-, 2004. 87: p. 212-217.
60. Salaun, C., J. Greaves, and L.H. Chamberlain, The intracellular dynamic of protein palmitoylation. Journal of Cell Biology, 2010. 191(7): p. 1229-1238.
61. Fujiwara, Y., et al., Structural basis for the membrane association of ankyrinG via palmitoylation. Scientific reports, 2016. 6(1): p. 1-11.
62. Sobocińska, J., et al., Protein palmitoylation and its role in bacterial and viral infections. Frontiers in immunology, 2018. 8: p. 2003.
63. Grosenbach, D.W., D.O. Ulaeto, and D.E. Hruby, Palmitylation of the vaccinia virus 37-kDa major envelope antigen Identification of a conserved acceptor motif and biological relevance. Journal of Biological Chemistry, 1997. 272(3): p. 1956-1964.
64. Majeau, N., et al., Palmitoylation of hepatitis C virus core protein is important for virion production. Journal of Biological Chemistry, 2009. 284(49): p. 33915-33925.
65. Lopez, L.A., et al., Importance of conserved cysteine residues in the coronavirus envelope protein. Journal of virology, 2008. 82(6): p. 3000-3010.
66. Resh, M.D., Fatty acylation of proteins: new insights into membrane targeting of myristoylated and palmitoylated proteins. Biochimica et Biophysica Acta (BBA)-Molecular Cell Research, 1999. 1451(1): p. 1-16.
67. He, M., P. Jenkins, and V. Bennett, Cysteine 70 of ankyrin-G is S-palmitoylated and is required for function of ankyrin-G in membrane domain assembly. Journal of Biological Chemistry, 2012. 287(52): p. 43995-44005.
68. Wilcox, C., J.-S. Hu, and E.N. Olson, Acylation of proteins with myristic acid occurs cotranslationally. Science, 1987. 238(4831): p. 1275-1278.
69. James, G. and E.N. Olson, Fatty acylated proteins as components of intracellular signaling pathways. Biochemistry, 1990. 29(11): p. 2623-2634.
70. Boutin, J.A., Myristoylation. Cellular signalling, 1997. 9(1): p. 15-35.

71. Nimchuk, Z., et al., Eukaryotic fatty acylation drives plasma membrane targeting and enhances function of several type III effector proteins from Pseudomonas syringae. Cell, 2000. 101(4): p. 353-363.
72. Chow, M., et al., Myristylation of picornavirus capsid protein VP4 and its structural significance. Nature, 1987. 327(6122): p. 482-486.
73. Henderson, L., et al., Molecular characterization of gag proteins from simian immunodeficiency virus (SIVMne). Journal of Virology, 1988. 62(8): p. 2587-2595.
74. Harris, M., et al., In vivo derived HIV-1 nef gene products are heterogeneous and lack detectable nucleotide binding activity. AIDS research and human retroviruses, 1992. 8(5): p. 537-543.
75. Persing, D.H., H. Varmus, and D. Ganem, The preS1 protein of hepatitis B virus is acylated at its amino terminus with myristic acid. Journal of virology, 1987. 61(5): p. 1672-1677.
76. Du, Y., F.A. Zuckermann, and D. Yoo, Myristoylation of the small envelope protein of porcine reproductive and respiratory syndrome virus is non-essential for virus infectivity but promotes its growth. Virus research, 2010. 147(2): p. 294-299.
77. Álvarez, E., et al., The envelope protein of severe acute respiratory syndrome coronavirus interacts with the non-structural protein 3 and is ubiquitinated. Virology, 2010. 402(2): p. 281-291.
78. Isaacson, M.K. and H.L. Ploegh, Ubiquitination, ubiquitin-like modifiers, and deubiquitination in viral infection. Cell host & microbe, 2009. 5(6): p. 559-570.
79. Keng, C.-T., et al., SARS coronavirus 8b reduces viral replication by down-regulating E via an ubiquitin-independent proteasome pathway. Microbes and infection, 2011. 13(2): p. 179-188.
80. Vigerust, D.J. and V.L. Shepherd, Virus glycosylation: role in virulence and immune interactions. Trends in microbiology, 2007. 15(5): p. 211-218.
81. Fung, T.S. and D.X. Liu, Post-translational modifications of coronavirus proteins: roles and function. Future Virology, 2018. 13(6): p. 405-430.
82. Wang, B., et al., Mechanistic understanding of N-glycosylation in Ebola virus glycoprotein maturation and function. Journal of Biological Chemistry, 2017. 292(14): p. 5860-5870.
83. Sawhney G., Sharma M. Molecular structure of coronavirus and transmission. A complete study of structure and function of envelope, spikes, and post-translational modifications exhinited by coronavirus. (2021) Basics of Medical microbiology and Virology. Vol.1., ISBN-978-93-90847-58-7.
84. Patrick C. Y. Woo, Yi Huang, Susanna K. P. Lau, Kwok-Yung Yuen. Coronavirus Genomics and Bioinformatics Analysis.Viruses 2010, 2, 1804-1820; doi:10.3390/v2081803
85. Jing-Bao Nie. In the Shadow of BiologicalWarfare: Conspiracy Theorieson the Origins of COVID-19 and Enhancing GlobalGovernance of Biosafety as a Matter of UrgencyBioethical Inquiry. 2020. https://doi.org/10.1007/s11673-020-10025-8
86. Yuan Huang, Chan Yang, Xin-feng Xu, Wei Xu and Shu-wen Liu,. Structural and functional properties of SARS-CoV-2 spike protein: potential antivirus drug development for COVID-19. Acta Pharmacologica Sinica (2020) 41:1141–1149; https://doi.org/10.1038/s41401-020-0485-
87. Khurshid SJ (2020) Novel Coronavirus (nCoV-2019): Is it a Bioweapon?. J Bioterror Biodef 11: 166.
88. Shmona Simpson, Michael C Kaufmann, Vitaly Glozman, Ajoy Chakrabarti. Disease X: accelerating the development of medicalcountermeasures for the next pandemic. Lancet Infect Dis 2020;20: e108–15.

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