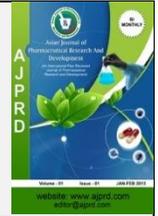


Available online on 15.10.2020 at <http://ajprd.com>

Asian Journal of Pharmaceutical Research and Development

Open Access to Pharmaceutical and Medical Research

© 2013-20, publisher and licensee AJPRD, This is an Open Access article which permits unrestricted non-commercial use, provided the original work is properly cited

Open  Access

Review Article

A review articles of Clinical outcomes, and the origin, transmission, Immunologic aspects of characteristics and public health response to novel corona virus (COVID19)

Prangya P Acharya¹, Prasant Kumar Panda², Deepthi Kiran³, Ajay Kumar Sahu*⁴

¹Department of Microbiology, Sambalpur University, Odisha

²Department of Clinical Microbiology, Sum Ultimate Bhubaneswar

³Department of Microbiology, Bangalore University, Bangalore

⁴Department of Microbiology, Bangalore University, Bangalore

ABSTRACT

An acute respiratory disease caused by a novel corona virus SARS-Co-2, also known as covid-19, the corona virus diseased 2019 has spread throughout china and received worldwide attention, on 30th January 2020. World health organization officially declared the covid19 epidemic as a public health emergency of international concern. In December 2019, cases of unidentified pneumonia with a history of exposure in the human sea food market were reported in wuhan, a novel corona virus was identified to be accountable for this disease, by world health organization confirmed that this disease can spread through human to human through droplet of sneezing, and its spread rapidly around the country and the world, as of 18th February 2020 the number of confirmed cases of covid19 had reached 75, 198 with 2009 fatalities. Serve acute respiratory syndrome and middle east respiratory syndrome, among the symptom composition of the 45 fatality cases has collected, several independent research groups have indentified that SARAS – CoV-2 belongs to the beta corona virus with highly angiotensin converting enzyme as that for SARAS – CoV-2, Corona viruses (CoVs), incorporated positive-sense RNA diseases, are depicted by the club-like spikes that adventure from their surface, an abnormally huge RNA genome, and a specific replication technique. CoVs cause a selection of diseases in mammals and birds ranging from enteritis in cows and pigs and upper respiratory sickness in chickens too possibly deadly human respiratory diseases. Here, we provide a quick presentation to CoVs talking.

Key words- corona virus, positive sense RNA infection, transmission, clinical outcomes, characteristics of covid19, public health response

ARTICLE INFO: Received 02 July 2020; Review Completed 15 Sept. 2020; Accepted 07 Oct. 2020; Available online 15 Oct. 2020



Cite this article as:

Acharya PP, PK, Deepthi Kiran, Sahu AK, A review articles of Clinical outcomes, and the origin, transmission, Immunologic aspects of characteristics and public health response to novel corona virus (COVID19), Asian Journal of Pharmaceutical Research and Development. 2020; 8(5):129-137. DOI: <http://dx.doi.org/10.22270/ajprd.v8i5.793>

*Address for Correspondence:

Ajay K Sahu- Microbiologist, Black Diamond College, jharsuguda Deepthi Kiran- Lecture at Bangalore City College, Bangalore

INTRODUCTION-

Corona viruses (CoVs) were first recognized during the 1960s; however, we do not have the foggiest idea where they originate from. A CoV may be a kind of regular infection that causes a disease in your nose,

sinuses, or upper throat ¹. Most CoVs are not perilous. They get their name from their crown like shape. Here and there, however not frequently, a CoVs can taint the two creatures and people ². Most CoVs spread a uniform way other cold-causing infections do: Through contaminated individuals hacking and wheezing, by contacting a tainted individual's

hand or face, or by contacting things, as an example, door handles that tainted individuals have contacted³. The side effects of most CoVs are such as other upper respiratory contamination, including runny nose, hacking, pharyngitis, and here and there a fever. Much of the time, you will not know whether you've got a coronavirus or an alternate cold-causing infection, for instance, rhinovirus. Including nose and throat swabs and blood work, to ascertain if your virus was caused by a CoV, yet there is no motivation to. The test outcomes would not change how you treat your side effects, which commonly leave during few days⁴. Be that because it may, if a coronavirus contamination spreads to the lower tract (your windpipe and your lungs), it can cause pneumonia, particularly. In additional seasoned individuals, individuals with coronary,

Symptom of corona virus

Fever-

Fever is the point at which a human internal heat level goes over the ordinary scope of 36–37°C (98–100° Fahrenheit). It is a typical restorative sign. Different expressions for a fever incorporate precise and controlled hyperthermia⁵. As the internal heat level goes up the individual may feel common cold and basically cold in asymptomatic in nature,

Chest pain-

Heart or vein issues that can cause chest torment: Angina or a respiratory failure. The most well-known manifestation is chest torment that may feel such as snugness, substantial weight, pressing, or pulverizing torment⁶. Expanding (irritation) in the sac that encompass the heart causes torment in the middle pieces of chest.

Rapid heart beat-

There is no particular antibody for corona virus to help forestall a corona virus disease, do very similar things to maintain a strategic distance from the normal virus⁷.

Breathing problems-

There are numerous reasons for breathing issues. These regular breathing issues incorporate constant sinusitis, hypersensitivities, and asthma. These issues can cause a large group of side effects, for example, nasal blockage, runny nose, irritated or watery eyes, chest clog and working relax⁸⁻¹¹.

Pneumonia-

Pneumonia is a disease of the lungs with a scope of potential causes. It tends to be a genuine and dangerous

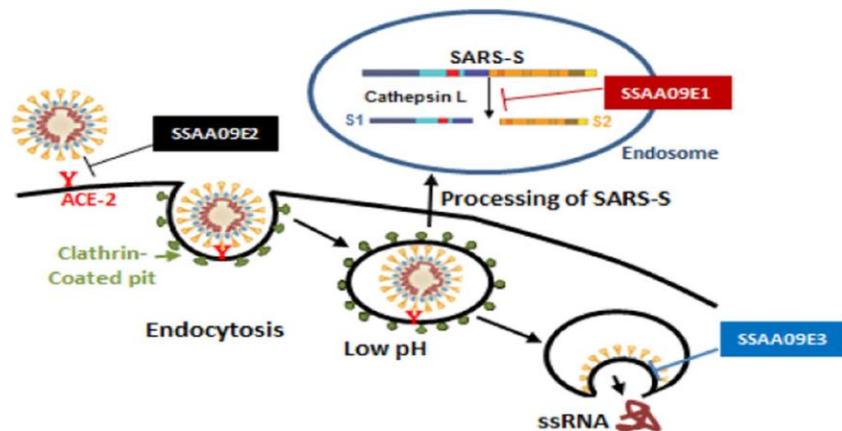
illness. It ordinarily begins with a bacterial, viral, or parasitic disease. The lungs become aroused, and the small air sacs, or alveoli, inside the lungs top off with liquid¹²⁻¹⁸. There is no antibody for corona virus. To help forestall a corona virus disease, do very similar things you do to maintain a strategic distance from the normal virus¹⁹⁻²¹

- Wash your hands completely with cleanser and warm water or with liquor based hand sanitizer
- Keep your hands and fingers from your eyes, nose and mouth
- Avoid close contact with individuals who are contaminated
- You treat a corona virus contamination a similar way you treat a virus:
 - Get a lot of rest
 - Drink liquids
- Take over-the-counter medication for an irritated throat and fever. However, do not offer headache medicine to youngsters or teenagers more youthful than use ibuprofen or acetaminophen
- A humidifier or hot shower can likewise help facilitate a sore and scratchy throat
- Even when a corona virus causes Middle Eastern respiratory syndrome (MERS) or severe acute respiratory syndrome (SARS) in different nations, the sort of corona virus contamination normal in the U.S. is certifiably not a genuine risk for a generally sound grown-up. In the event that you become ill, treat your side effects and contact a specialist²²⁻²⁵.

Genomic organization

CoVss contain a non-divided, positive-sense RNA genome of ~30 KB. The genome contains a 5' end structure along with a 3' poly (A) tail, permitting it to go about as a marina for interpretation of the replicase poly proteins. The replicase quality encoding the non structural proteins (nsp) possesses 66% of the genome, around 20 KB, instead of the basic and extra proteins²⁶⁻²⁸, which makeup just around 10 KB of the viral genome. The 5' end of the genome contains a pioneer succession and un translated locale (un translated region [UTR]) that contains different stem circle structures required for RNA replication and translation. Moreover, toward the start of each basic or frill quality is transcriptional administrative arrangements (TRSs) that are required for articulation of each of these qualities²⁶⁻³⁰. The 3' UTR too contains RNA structures required for replication and amalgamation of viral RNA. The association of the corona virus genome is 5'-pioneer UTR-replicase-S (Spike)- E (Envelope) - M (Membrane) - N (Nucleocapsid) - 3' UTR poly (A) tail with embellishment qualities mixed inside the auxiliary qualities at the 3' end of the genome. The embellishment proteins are

only superfluous for replication in tissue culture; in any case.



Virion structure

CoV versions are round with measurements of roughly 125 NM as portrayed in late examinations by cryo-electron tomography what is more, cryo-electron microscopy. The most conspicuous component of CoVs is the club-formed spike projections exuding from the outside of the brain. These spikes are a definite highlight of the vision and give them the presence of a sunlight based crown, inciting the name, CoVs. Inside the envelope of the brain is the nucleocapsid. CoVs have helically even nucleocapsids, which are extraordinary among positive-sense RNA infections, however unmistakably increasingly regular for negative-sense RNA infections³¹⁻³². The E protein (~8– 12 kDa) is found in little amounts in the brain. The corona virus E proteins, however profoundly disparate, have a typical design. The layer topology of E protein is not totally settled yet most information recommends that it is a transmembrane protein. The E protein has a N-terminal ectodomain and a C-terminal endodomain and has particle channel action. Rather than other basic proteins, recombinant infections coming up short on the E protein are not constantly deadly, despite the fact that this is an infection type subordinate. The E protein encourages get together and arrival of the infection yet in addition has different capacities. In case, the particle direct action of SARS-CoV E protein is not required for viral replication, however, is required for pathogenesis. The N protein establishes the main protein present in the nucleocapsid. It is made out of two separate areas, an N-terminal domain (NTD) and C-terminal domains (CTD), both equipped for restricting RNA in vitro, yet every space utilizes extraordinary systems to tie RNA. It has been recommended that ideal RNA restricting requires commitments from the two areas. N protein is likewise intensely phosphorylated, and phosphorylation has been proposed to trigger a basic change, upgrading the affinity for viral versus non-viral RNA. N protein ties the viral

genome in a dabs on-a-string type compliance³³⁻³⁴. Two specific RNA substrates have been identified Ed for N protein; the TRSs what is more, the genomic bundling signal.

Pathogenesis-

Human CoVs Preceding the SARS-CoV flare-up, CoVs were just idealistic to cause gentle, self-constraining respiratory diseases in people. Two of these human CoVs are α -CoVs, HCoV-229E what is more, HCoV-NL63, while the other two are β -CoVs, HCoV OC43, and HCoV-HKU1. HCoV-229E and HCoV-OC43 were separated about 50 years back, While HCoVNL63 and HCoV-HKU1 has as of late been identified follow the SARS-CoV episode. These infections are endemic in the human populaces, causing 15–30% of respiratory tract diseases every year. They cause increasingly serious illness in neonates, the older, also, in people with basic ailments, with a more prominent occurrence of the lower respiratory tract contamination in these populaces. HCoV-NL63 is additionally connected with intense laryngotracheitis (croup). One intriguing part of these infections is their disparities in resistance to hereditary changeability. HCoV-229E detaches from around the world have just insignificant succession disparity, while HCoVOC43 separates from a similar area yet detached in various years show signify cannot hereditary fluctuation. This imaginable clarifies the failure of HCoV-229E to cross the species obstruction to taint mice while HCoV-OC43 and the firm related ox-like corona virus³⁵⁻³⁷,

Innate and adaptive immunity

Three components are crucial for SARS-CoV induced diseases: 1) the role of CD8+ T cells in defense against the virus, which causes apoptosis in the infected cells, 2) interactions of the virus with macrophages and dendritic cells, which initiate the early innate and subsequent. Adaptive immune responses and 3) type I interferon (IFN)

system, an innate response against viral infections, which can inhibit virus replication in the early phase. Firstly, the central part of the body's anti-viral immunity is based on the interaction between antigen and antigen Presentation cells (APC) when the virus enters the cells. The infected cells are recognized by virus-specific cytotoxic T lymphocytes (CTLs) via viral peptides as the antigen presented by major histocompatibility complex (MHC). The antigen presentation of virus mostly depends On MHC I molecules, but MHC II also has its contribution in some cases. The MHC I molecules display pieces of virus proteins on the surface of infected cells, which creates a signal to activate nearby CD8+ T cells to induce apoptosis in the infected cells. There are Many reports on the relationship between various MHC polymorphisms and the susceptibility to SARS-CoV, but little is known about this association in COVID-19. Such information could provide beneficial aspects of personalized medicine for treatment or prevention Of COVID-19

Innate and adaptive immunity

Three components are crucial for SARS-CoV induced diseases: the role of CD8+ T cells in defense against the virus, which causes apoptosis in the infected cells, interactions of the virus with macrophages and dendritic cells, which initiate the early innate and subsequent Adaptive immune responses and 3) type I interferon (IFN) system, an innate response against viral infections, which can inhibit virus replication in the early phase. Firstly, the central part of the body's anti-viral immunity is based on the interaction between antigen and antigen Presentation cells (APC) when the virus enters the cells. The infected cells are recognized by virus-specific cytotoxic T lymphocytes (CTLs) via viral peptides as the antigen presented by major histocompatibility complex (MHC). The antigen presentation of virus mostly depends on MHC I molecules, but MHC II also has its contribution in some cases. The MHC I molecules display pieces of virus proteins on the surface of infected cells, which creates a signal to activate nearby CD8+ T cells to induce apoptosis in the infected cells. There are Many reports on the relationship between various MHC polymorphisms and the susceptibility to SARS-CoV, but little is known about this association in COVID-19. Such information could provide beneficial aspects of personalized medicine for treatment or prevention of COVID-19.

MERS-CoV

In addition to the airway epithelial cells, MERS-CoV can also replicate in human monocytes, macrophages, dendritic

cells, and activated T cells. The typical lung pathological change Caused by MERS-CoV is diffuse alveolar damage. In addition, pleural and pericardial effusions associated with generalized congestion and consolidation of lungs have been noted, and the severity of lung lesions were noted to be correlated with extensive infiltration of neutrophils and macrophages. Similar to SARS-CoV, MERS-CoV can induce high levels of proinflammatory cytokines and chemokines in human monocyte-derived macrophages and dendritic cells. MERS-CoV infection was also reported to induce increased concentrations of proinflammatory cytokines (IFN- γ , TNF- α , IL15, and IL17). The high serum cytokine and chemokine levels in MERS patients were correlated with increased infiltration of neutrophil and monocytes along with severe tissue damage in the lung. Thus, the pathological change in the lungs is similar between SARS-CoV and MERS-CoV. Whereas, the higher mortality rate in MERS-CoV-infected patients may be due to the higher incidence of pericarditis in infected patients.

SARS-CoV-2

The first autopsy of COVID-19 victims along with immune histological staining revealed the presence of SARS-CoV-2 in the airway epithelia and macrophages, suggesting that the virus can infect both epithelial cells and macrophages. The majority of infiltrating cells are macrophages and monocytes with moderate amounts of multinucleated giant cells and neutrophils.

Vaccination for prevention of COVID-19

As with many vaccine-preventable viral diseases like measles and chicken pox, the newly emerged SARSCoV-2 infection assumes an epidemiological characteristic capable of evading containment measures and facilitating pandemic potential. Thus, a high proportion of Undetected infections with mild or no symptoms can efficiently sustain viral transmission. While containment and lockdown can serve as temporary control measures, effective vaccines or therapeutic agents are much needed for the ultimate control of the disease. The vaccine research and development thus far have progressed at an unprecedented speed; the first dose of RNA-based SARS-CoV-2 vaccine was administered to test its safety in humans on March 16, 2020, only 2 months after the new virus was first identified. Such Rapid progress was facilitated by a combination of multiple factors, including advances in vaccine research on SARS and MERS, as recently reviewed, progress in a number of vaccine technology platforms to the early stage of human trial, and readily available support from the well-orchestrated international collective effort of the Coalition for Epidemic Preparedness Innovations (CEPI).

CEPI Coordinated COVID-19 Vaccine Projects

Jan 23	University Queensland – molecular clamp Inovio Pharm – DNA Moderna Inc - RNA (NIH and others for further studies)
Jan 31	CureVac - RNA Printer™ lipid nanoparticle (LNP)
Feb 3	GSK - adjuvant
Feb 4	CSIRO – Animal study; scale up Production
Mar 3	DynaVax technology - CpG adjuvant
Mar 10	Hong Kong University – Modified nasal spray NovaVax – Protein-coupled nanoparticles
Mar 16	Moderna vaccine trial begins
Mar 18	Oxford - ChAdOx1 vector vaccine

1. CEPI coordinated COVID-19 vaccine projects.

Immunological approaches to treatment of COVID-19

The disease spectrum of COVID-19 can be divided into mild infection, pneumonia, ARDS, and even multiple organ failure. After a decade of research on coronavirus, unfortunately, still there are no licensed vaccines, effective specific antivirals, nor drug combinations supported by high-level evidence to treat the infection, especially for newly emerging strains such as SARS-COV-2. Several strategies are being considered for the treatment of COVID-19, including the use of antimicrobial agents, immunotherapy with virus-specific antibodies in convalescent plasma, monoclonal and polyclonal antibodies produced in vitro or genetically modified antibodies, and interferons. Here we focus on immune based therapies, but for the sake of completeness, we also include therapies using antimicrobial agents as 7supplementary information

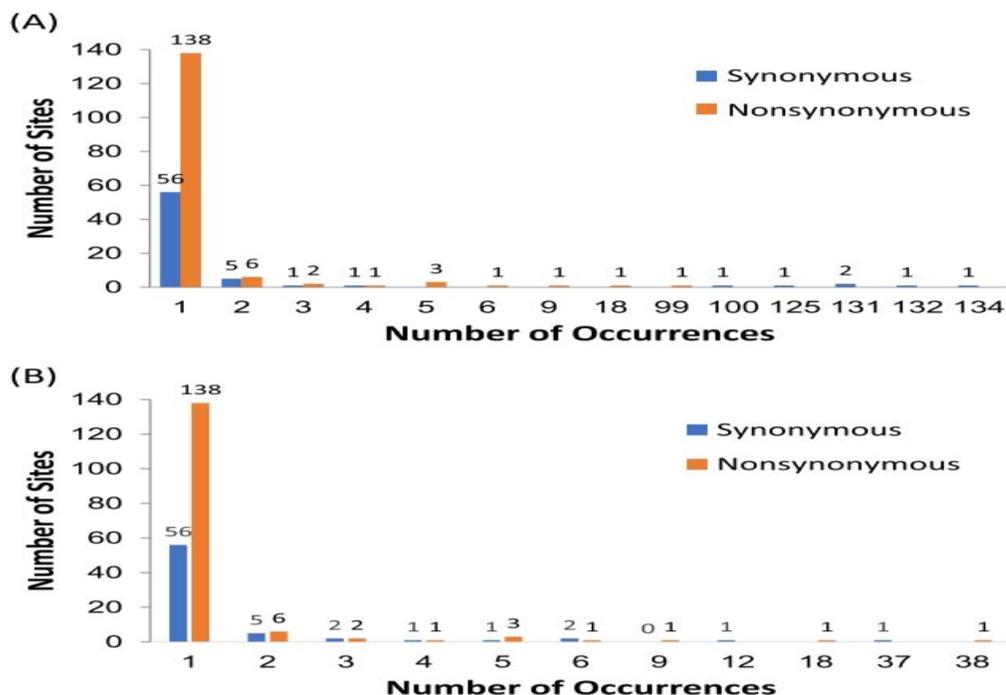
Table: 1 comparison of non synonymous and synonymous divergence between SARS COV-2, RaTG13 and Pangolin 2019

Gene	Length	SARS cov2 VS RaTG13	SARS COV-2 VS Pangolin 2019	RaTG13 VS Pangolin 2019
All	9555	0.042	0.051	0.054
Orf1a	4330	0.048	0.051	0.049
Orf1b	2692	0.024	0.016	0.019
Spike	1219	0.041	0.104	0.107
Orf3	274	0.060	0.066	0.072
Envelope	75	0.018	0.037	0.018
Matrix	221	0.021	0.033	0.019
Orf6	60	0.099	0.026	0.040
Orf7	121	0.061	0.066	0.088
Orf8	121	0.150	0.069	0.420

Table: 2 Non singleton detected across the sampled SARS- cov-2 genome

Gene position	Gene	RaTG13	Pangolin 2017	Pangolin 2019	Major allele	Minor allele	Amount of charge	Sequence
614	Or1ab	G	G	G	G	A	1	H116q
1190	Or1ab	C	C	C	C	T	2	P308s
5084	Or1ab	A	A	A	A	G	3	A1606t
9438	Or1ab	C	C	C	C	T	2	T30581
21707	S	C	C	C	C	T	5	V366f
26144	Orf3	G	G	G	G	T	18	G215v
28077	Orf8	G	G	G	G	C	99	L845
28854	N	C	C	C	C	T	5	S194l
29019	N	A	A	A	A	T	2	D249h
29303	N	C	C	C	C	T	2	K3431
65844	H	G	G	G	G	T	6	K5287l
65972	S	T	T	T	C	T	5	K234m
54211	S	G	A	A	A	T	5	H451q
32658	N	A	A	A	G	T	6	Hi584q
326145	Orf6	T	T	T	G	A	2	G876na
625	Orlab3	G	G	G	T	C	5	Gij5586

652	N	C	C	C	C	C	3	Mi698a
-----	---	---	---	---	---	---	---	--------



Graph no- 3 synonymous and non synonymous occurrences

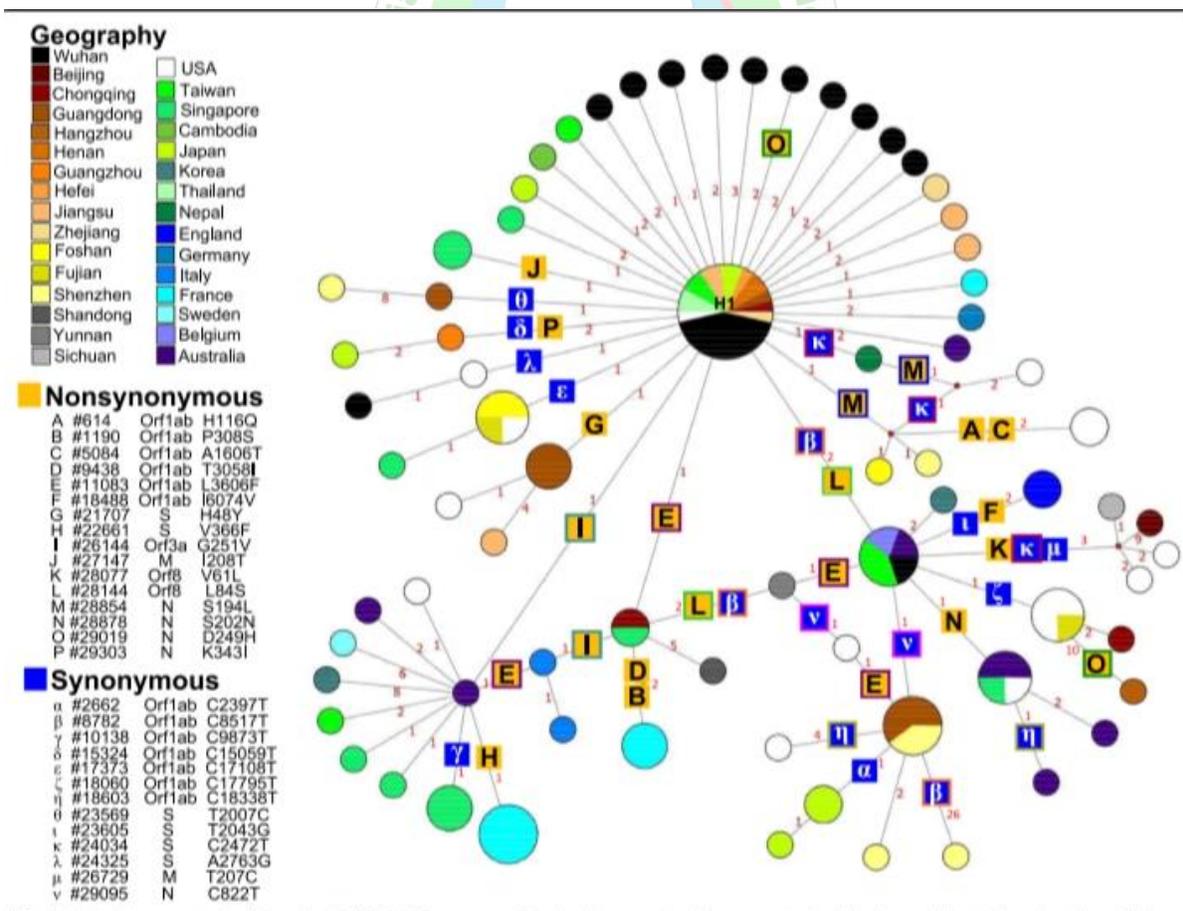
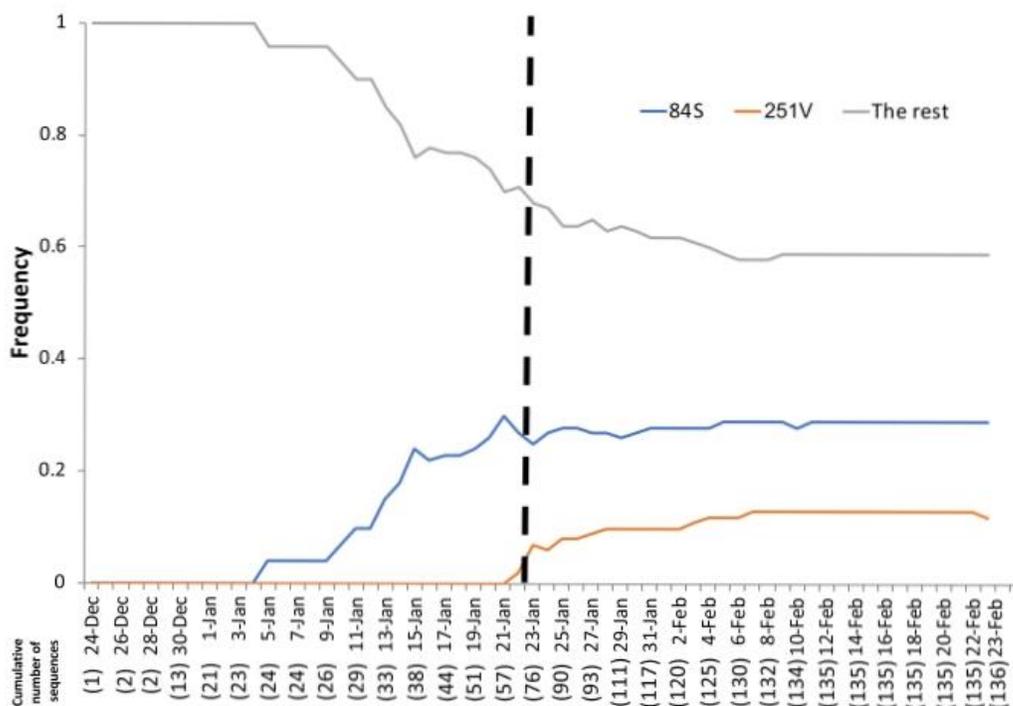
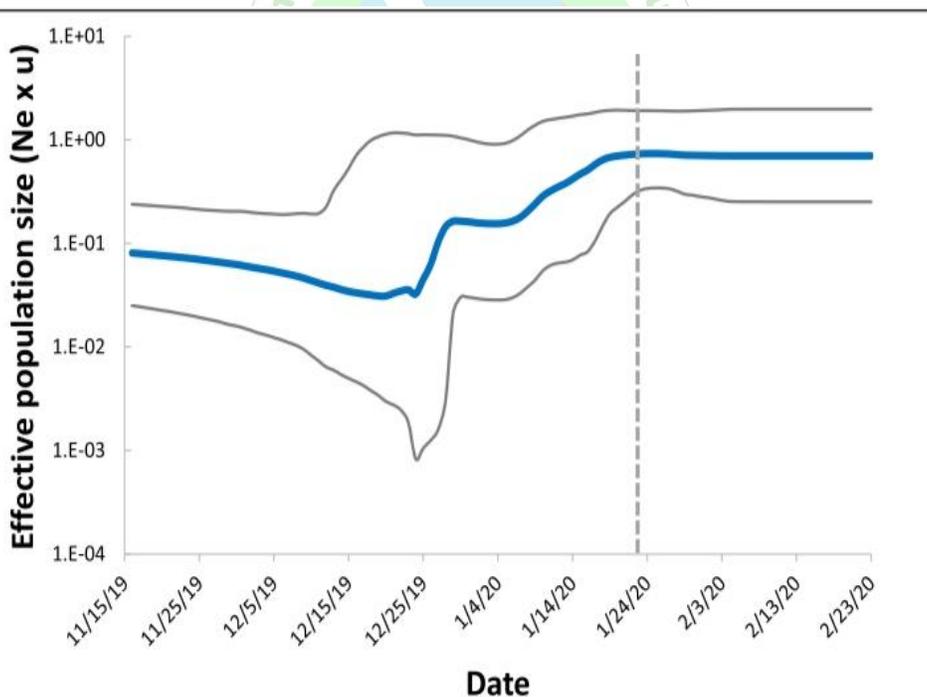


Figure: 4 Genomic arrangement of SARS- CoV-2



Graph: – 5 statistical characteristic and sequence of mutation



Graph:- 6 effective of population sequence

Determination, prevention and treatment-

The Middle East where MERSCoV keeps on following, The identification of cases will manage the advancement of general well-being measures to control episodes. It is additionally imperative to analyze instances of serious veterinary CoV-induced sickness, for example, porcine epidemic diarrhea virus (PEDV) and infectious bronchitis

virus (IBV), to control these pathogens and secure nourishment supplies. Reverse transcription polymerase chain reaction (RT-PCR) has become the strategy of decision for the determination of human CoV, as multiplex continuous RT-PCR examines have been created, can identify every one of the four respiratory HCoVs and could be additionally adjusted to novel CoVs. Serologic examines are significant in situations where RNA is difficult religion

to disengage or is never again present, and four epidemiological examines. Until this point in time, there are no antiviral therapeutics that specifically target human CoVs, so medications are just strong. In vitro, interferons (IFNs) are just somewhat successful against CoVs. IFNs in the mix with ribavirin may have expanded movement in vitro when contrasted with IFNs alone against some CoVs; nonetheless, the viability of this mix in five requires further assessment. The SARS and MERS episodes have invigorated research on these infections and this explore has identified countless appropriate antiviral targets, for example, viral proteases, polymerases, and section proteins. Signify cannot work remains, be that as it may, to create drugs that focus on these procedures furthermore, can repress viral replication. Just constrained choices are accessible to forestall carnivorous diseases. Immunizations have just been endorsed for IBV, transmissible gastroenteritis virus (TGEV), and Canine CoV, however, these immunizations are not constantly utilized in light of the fact that they are either not extremely powerful, or now and again have been accounted for to be associated with the determination of novel pathogenic curves by means of recombination of flowing strains. Antibodies to veterinary pathogens, for example, PEDV, might be valuable in such situations where the spread of the infection to another area could prompt serious misfortunes of veterinary creatures. On account SARS-CoV, few potential antibodies have been grown yet none is yet endorsed for use. These immunizations incorporate recombinant constricted infections, live infection vectors, or individual viral proteins communicated from DNA plasmids. Helpful SARS-CoV killing antibodies have been created and could be recovered and utilized again in case of another SARS-CoV flare-up. Such antibodies would be generally valuable for ensuring human services laborers. When all is said in done, it is imagined that live lessened antibodies would be the most efficacious in focusing on CoVs. This was outlined account of TGEV, where constricted variation, porcine respiratory corona virus (PRCV), showed up in Europe during the 1980s. This variation just caused gentle infection and totally shielded swine from TGEV.

Acknowledgement-

The authors thank to Dr. P.K Panda, P.P Acharya and co-authors Deepthi Kiran for his/her assistance in the preparation of manuscript.

Authors Contribution-

Dr. Panda has the main contribution that to guide us to write the manuscript as well help to give the source of material and P.P Acharya has collected all data regarding corona virus and their clinical aspect, D kiran help to assistance the preparation of manuscript.

Funding – Not applicable

Ethics approval and consent to participate- Not applicable

Consent of publication- Not applicable

Competing- The author declare that they have no competing interest.

REFERENCE –

1. Channappanavar R, Perlman S. Pathogenic human coronavirus infections: causes and consequences of cytokine storm and immunopathology. *Semin Immunopathol.* 2017; 39(5):529–39.
2. Walls AC, Park YJ, Tortorici MA, Wall A, McGuire AT, Veesler D. Structure, function, and antigenicity of the SARS-CoV-2 spike glycoprotein. *Cell.* 2020; 181(2):281–92.
3. Zhou P, Yang XL, Wang XG, Hu B, Zhang L, Zhang W, Si HR, Zhu Y, Li B, Huang CL, Chen HD, Chen J, Luo Y, Guo H, Jiang RD, Liu MQ, Chen Y, Shen XR, Wang X, Zheng XS, Zhao K, Chen QJ, Deng F, Liu LL, Yan B, Zhan FX, Wang YY, Xiao GF, Shi ZL. A pneumonia outbreak associated with a new coronavirus of probable bat origin. *Nature.* 2020; 579(7798):270–3.
4. Guillon P, Clement M, Seville V, Rivain JG, Chou CF, Ruvoen-Clouet N, Le Pendu J. Inhibition of the interaction between the SARS-CoV spike protein and its cellular receptor by anti-histo-blood group antibodies. *Glycobiology.* 2008; 18(12):1085–93.
5. Yan R, Zhang Y, Li Y, Xia L, Guo Y, Zhou Q. Structural basis for the recognition of the SARS-CoV-2 by full-length human ACE2. *Science.* 2020; 367(6485):1444–8.
6. Meyer B, Drosten C, Muller MA. Serological assays for emerging coronaviruses: challenges and pitfalls. *Virus Res.* 2014; 194:175–83.
7. WHO. Update 49 - SARS case fatality ratio, incubation period. <https://www.who.int/csr/sars/archive/2003_05_07a/en/>. Accessed 29 March 2020.
8. WHO. Middle East respiratory syndrome coronavirus (MERS-CoV). <<https://www.who.int/emergencies/mers-cov/en/>>. Accessed 29 March 2020.
9. Chan JF, Yuan S, Kok KH, To K.K, Chu H, Yang J, Xing F, Liu J, Yip CC, Poon RW, Tsoi HW, Lo SK, Chan KH, Poon VK, Chan WM, Ip JD, Cai JP, Cheng VC, Chen H, Hui CK, Yuen KY. A familial cluster of pneumonia associated with the 2019 novel coronavirus indicating person-to-person transmission: a study of a family cluster. *Lancet.* 2020; 395(10223):514–23.
10. Zhu N, Zhang D, Wang W, Li X, Yang B, Song J, Zhao X, Huang B, Shi W, Lu R, Niu P, Zhan F, Ma X, Wang D, Xu W, Wu G, Gao GF, Tan W. China Novel Coronavirus I. and Research T. A Novel Coronavirus from Patients with Pneumonia in China, 2019. *N Engl J Med.* 2020; 382(8):727–33.
11. Wu JT, Leung K, Bushman M, Kishore N, Niehus R, de Salazar PM, Cowling BJ, Lipsitch M, Leung GM. Estimating clinical severity of COVID-19 from the transmission dynamics in Wuhan. *China Nature Medicine.* 2020; 26:506–10.
12. Wu Z, McGoogan JM. Characteristics of and important lessons from the coronavirus disease 2019 (COVID-19) outbreak in China: summary of a report of 72314 cases from the Chinese Center for Disease Control and Prevention. *JAMA.* 2020.
13. Wang SF, Chen KH, Chen M, Li WY, Chen YJ, Tsao CH, Yen MY, Huang JC, Chen YM. Human-leukocyte antigen class I Cw 1502 and class II DR 0301 genotypes are associated with resistance to severe acute respiratory syndrome (SARS) infection. *Viral Immunol.* 2011; 24(5):421–6.
14. Keicho N, Itoyama S, Kashiwase K, Phi NC, Long HT, Ha LD, Ban VV, Hoa BK, Hang NT, Hijikata M, Sakurada S, Satake M, Tokunaga K, Sasazuki T, Quy T. Association of human leukocyte antigen class II alleles with severe acute respiratory syndrome in the Vietnamese population. *Hum Immunol.* 2009; 70(7):527–31.

15. Hajeer AH, Balkhy H, Johani S, Yousef MZ, Arabi Y. Association of human leukocyte antigen class II alleles with severe Middle East respiratory syndrome-coronavirus infection. *Ann Thoracic Med.* 2016; 11(3):211–3.
16. Ito T, Wang YH, Liu YJ. Plasmacytoid dendritic cell precursors/type I interferon-producing cells sense viral infection by toll-like receptor (TLR) 7 and TLR9. *Springer Semin Immunopathol.* 2005; 26(3):221–9.
17. Akira S, Hemmi H. Recognition of pathogen-associated molecular patterns by TLR family. *Immunol Lett.* 2003; 85(2):85–95.
18. Huang LR, Chiu CM, Yeh SH, Huang WH, Hsueh PR, Yang WZ, Yang JY, Su IJ, Chang SC, Chen PJ. Evaluation of antibody responses against SARS coronavirus nucleocapsid or spike proteins by immunoblotting or ELISA. *J Med Virol.* 2004; 73(3):338–46.
19. Murphy BR, Whitehead SS. Immune response to dengue virus and prospects for a vaccine. *Annu Rev Immunol.* 2011; 29:587–619.
20. Casadevall A, Pirofski LA. The convalescent sera option for containing COVID-19. *J Clin Invest.* 2020; 30(4):1545–8.
21. Wan Y, Shang J, Sun S, Tai W, Chen J, Geng Q, He L, Chen Y, Wu J, Shi Z, Zhou Y, Du L, Li F. Molecular Mechanism for Antibody-Dependent Enhancement of Coronavirus Entry. *J Virol.* 2020; 94:5.
22. Halstead SB. Pathogenesis of dengue: challenges to molecular biology. *Science.* 1988;239(4839):476–81.
23. Mair-Jenkins J, Saavedra-Campos M, Baillie JK, Cleary P, Khaw FM, Lim WS, Makki S, Rooney KD, Nguyen-Van-Tam JS, Beck CR, Convalescent Plasma Study G. The effectiveness of convalescent plasma and hyperimmune immunoglobulin for the treatment of severe acute respiratory infections of viral etiology: a systematic review and exploratory meta-analysis. *J Infect Dis.* 2015; 211(1):80–90.
24. Xinhua. China puts 245 COVID-19 patients on convalescent plasma therapy. <http://www.xinhuanet.com/english/2020-02/28/c_138828177.htm>. Accessed 29 March 2020.
25. McFadden G, Mohamed MR, Rahman MM, Bartee E. Cytokine determinants of viral tropism. *Nat Rev Immunol.* 2009;9(9):645–55.
26. Drosten C, Gunther S, Preiser W, van der Werf S, Brodt HR, Becker S, Rabenau H, Panning M, Kolesnikova L, Fouchier RA, Berger A, Burguiere AM, Cinatl J, Eickmann M, Escriou N, Grywna K, Kramme S, Manuguerra JC, Muller S, Rickerts V, Sturmer M, Vieth S, Klenk HD, Osterhaus AD, Schmitz H, Doerr HW. Identification of a novel coronavirus in patients with severe acute respiratory syndrome. *N Engl J Med.* 2003; 348(20):1967–76.
27. Kuiken T, Fouchier RA, Schutten M, Rimmelzwaan GF, van Amerongen G, van Riel D, Laman JD, de Jong T, van Doornum G, Lim W, Ling AE, Chan PK, Tam JS, Zambon MC, Gopal R, Drosten C, van der Werf S, Escriou N, Manuguerra JC, Stohr K, Peiris JS, Osterhaus AD. Newly discovered coronavirus as the primary cause of severe acute respiratory syndrome. *Lancet.* 2003; 362(9380):263–70.
28. Peiris JS, Lai ST, Poon LL, Guan Y, Yam LY, Lim W, Nicholls J, Yee WK, Yan WW, Cheung MT, Cheng VC, Chan KH, Tsang DN, China Lancet. 2020; 395(10223):497–506.
- Yung RW, Ng TK, Yuen KY, group S.s. Coronavirus as a possible cause of severe acute respiratory syndrome. *Lancet.* 2003; 361(9366):1319–25.
29. Cheung CY, Poon LL, Ng IH, Luk W, Sia SF, Wu MH, Chan KH, Yuen KY, Gordon S, Guan Y, Peiris JS. Cytokine responses in severe acute respiratory syndrome coronavirus-infected macrophages in vitro: possible relevance to pathogenesis. *J Virol.* 2005; 79(12):7819–26.
30. Law HK, Cheung CY, Ng HY, Sia SF, Chan YO, Luk W, Nicholls JM, Peiris JS, Lau YL. Chemokine up-regulation in SARS-coronavirus-infected, monocytiderived human dendritic cells. *Blood.* 2005; 106(7):2366–74.
31. Ziegler T, Matikainen S, Ronkko E, Osterlund P, Sillanpaa M, Siren J, Fagerlund R, Immonen M, Melen K, Julkunen I. Severe acute respiratory syndrome coronavirus fails to activate cytokine-mediated innate immune responses in cultured human monocyte-derived dendritic cells. *J Virol.* 2005; 79(21):13800–5.
32. Ng DL, Al Hosani F, Keating MK, Gerber SI, Jones TL, Metcalfe MG, Tong S, Tao Y, Alami NN, Haynes LM, Mutei MA, Abdel-Wareth L, Uyeki TM, Swerdlow DL, Barakat M, Zaki SR. Clinicopathologic, Immunohistochemical, and Ultrastructural Findings of a Fatal Case of Middle East Respiratory Syndrome Coronavirus Infection in the United Arab Emirates, April 2014. *Am J Pathol.* 2016;186(3):652–8.
33. Wong CK, Lam CW, Wu AK, Ip WK, Lee NL, Chan IH, Lit LC, Hui DS, Chan MH, Chung SS, Sung JJ. Plasma inflammatory cytokines and chemokines in severe acute respiratory syndrome. *Clin Exp Immunol.* 2004;136(1):95–103.
34. Kim ES, Choe PG, Park WB, Oh HS, Kim EJ, Nam EY, Na SH, Kim M, Song KH, Bang JH, Park SW, Kim HB, Kim NJ, Oh MD. Clinical progression and cytokine profiles of Middle East respiratory syndrome coronavirus infection. *J Korean Med Sci.* 2016; 31(11):1717–25.
35. Min CK, Cheon S, Ha NY, Sohn KM, Kim Y, Aigerim A, Shin HM, Choi JY, Inn KS, Kim JH, Moon JY, Choi MS, Cho NH, Kim YS. Comparative and kinetic analysis of viral shedding and immunological responses in MERS patients representing a broad spectrum of disease severity. *Sci Rep.* 2016; 6:25359.
36. Yao XH, Li TY, He ZC, Ping YF, Liu HW, Yu SC, Mou HM, Wang LH, Zhang HR, Fu WJ, Luo T, Liu F, Chen C, Xiao HL, Guo HT, Lin S, Xiang DF, Shi Y, Li QR, Huang X, Cui Y, Li XZ, Tang W, Pan PF, Huang XQ, Ding YQ, Bian XW. A pathological report of three COVID-19 cases by minimally invasive autopsies. *Zhonghua Bing Li Xue Za Zhi.* 2020; 49(0):E009.
37. Huang C, Wang Y, Li X, Ren L, Zhao J, Hu Y, Zhang L, Fan G, Xu J, Gu X, Cheng Z, Yu T, Xia J, Wei Y, Wu W, Xie X, Yin W, Li H, Liu M, Xiao Y, Gao H, Guo L, Xie J, Wang G, Jiang R, Gao Z, Jin Q, Wang J, Cao B. Clinical features of patients infected with 2019 novel coronavirus in Wuhan.