WOLKITE UNIVERSITY

COLLEGE OF NATURAL AND COMPUTATIONAL SCIENCES

DEPARTEMENT OF BIOTECHNOLOGY

Review on the Prospect of SARS-Cov-2 to Play Rhinovirus in the Current World

Prepared by: **ID**

1. **MELKAMU KERIE……..... NCSR/243/09**
2. **DEMISE DALE…… NCSR/095/09**
3. **IBSA TEMESGEN…… NCSR/195/09**
4. **YENEW NALIGN…… NCSR/357/09**
5. **ENKUAYE YASGAT……NCSR/119/09**
6. **ZEBNAY ABEBE……...……...NCSR/365/09**

Advisor: Admas Berhanu (Asst. Prof.)

Wolkite, Ethiopia

January, 2021

Table of Contents

Acknowledgement ii
Abbreviations iii
Abstract iv
1. INTRODUCTION 1
1.1. Problem Statement: 2
1.2. Objectives: 2
1.2.1. Specific Objective: 2
2. LITERATUR REVIEW 3
2.1. Historical Tradition of Common Cold and Corona 3
2.1.1. Origin and Evolution of Rhinovirus 3
2.1.2. Origin and Evolution of SARS-CoV-2 3
2.2. Biological Feature of Rhinovirus and SARS-CoV-2 3
2.2.1. Genome structure of Rhinovirus 3
2.2.2. Genome structure of sars-cov-2 3
2.3. The pattern of infection, mortality and morbidity of Rhinovirus and SARS-CoV-2 4
2.3.1. Transmission 4
2.3.1.1. Transmission of Rhinovirus 4
2.3.1.2. Transmission of SARS-CoV-2 5
2.3.2. Symptom 7
2.3.2.1. Rhinovirus Symptom 7
2.3.2.2. SARS-COV-2Symptom 8
2.4. The future of Rhinovirus and SARS-Cov-2 in prevention and cure 8
2.4.1. Vaccine approaches against rhinovirus 8
2.4.2. Humoral immunity to SARS-CoV-2 9
3. CONCLUSION 11
4. RECOMMENDATION 11
REFERENCES 12

Acknowledgement

First of all, we are grateful to thank the almighty God for his mercy and protection.

Secondly, we would like to express our special thanks to our advisor Admas Berhanu (Asst. Prof.) for his critical comments and guidance, with patience, throughout the work.

Thirdly, we would like to extend our acknowledgement to all faculty members of Biotechnology Department for their support during the review work and preparing this manuscript.

Finally, we would like to thank our parents for their unreserved financial and moral support to help us grow physically and academically throughout our journey towards achieving our BSc degree.

Abbreviations

ACE2	Angiotensin-Converting Enzyme 2
COVID 19	Corona Virus Disease 2019
HRV	Human Rhino Virus
RBD	Receptor-Binding Domain
RDRP	RNA Dependent RNA polymerase
SARS-COV-2	Severe Acute Respiratory Syndrome Corona Virus-2
URI	Upper Respiratory tract Infection
VP	Viral Protein
WHO	World Health Organization

Abstract

Severe acute respiratory syndrome coronavirus 2 (SARS-CoV-2) is a new emergent virus identified in late 2019 as the etiological agent behind a mysterious outbreak of pneumonia in Wuhan, China. The World Health Organization (WHO) later named the disease as coronavirus disease 19 (COVID-19) to account for the variety of clinical manifestations associated with SARS-CoV-2 infection. HRV is the most common cause of upper respiratory tract infection (URI); HRVs are now linked to exacerbations of chronic pulmonary disease, asthma development, and, more recently, severe bronchiolitis in infants and children as well as fatal pneumonia in elderly and immunocompromised adults. Since then, various countries have been following different approach to bank the disease, this includes stay at home declaration, avoiding public gathering, restricting public services and schooling, hence; the disease seems getting benign as a result the level of mortality and morbidity seems declining time to time. This gives an insight that the declining pathogenicity of the disease may be finally terminated as a benign communicable disease like common cold though the agent of the disease is different. These reviews entirely focus on predicting the role of Covid-19 in the current world as a public health concern vis-à-vis the traditional common cold.

Key word; covid-19, sars-cov-2

1. INTRODUCTION

Human rhinoviruses were first discovered in the 1950s in an effort to identify the etiology of the common cold. Worldwide and nearly year-round, HRV is the most common cause of URI, leading to considerable economic burdens in terms of medical visits and school and work absenteeism(Fendrick *et al*., 2003and Nichol *et al.* 2005).

However, while once thought to cause relatively benign upper respiratory tract illness, HRVs are now linked to exacerbations of chronic pulmonary disease, asthma development, and, more recently, severe bronchiolitis in infants and children as well as fatal pneumonia in elderly and immune compromised adults. Understanding of the spectrum of illness of HRVs draws largely from advances in molecular methods that have facilitated the detection and characterization of HRV groups and strains.

A novel coronavirus (SARS-CoV-2) that was first detected in December 2019, Wuhan City, Hubei Province, China, is posing a significant threat now by creating a pandemic situation of the COVID-19 (Yang Y. *et al,* 2020 and WHO, 2020). According to WHO (2020) presently above 22 million confirmed cases have been identified. The disease terrorized over 210 countries/territories/areas.

The origin of SARS-CoV-2 was postulated to be from bats, considering them the natural reservoirs of the virus (Chan *et al.,* 2020). The search for probable intermediate hosts is going on, keeping the main focus on animal species available for sale in the Huanan seafood market. Recently, a study suggested the pangolins to serve as a natural reservoir host of SARS-CoV-2-like corona viruses (Pangolin-CoV) based on 91.02% sequence similarities at the whole-genome level between pangolin-CoV and SARS-CoV-2. Additionally, the S1 protein of pangolin coronavirus was reported to be closer to SARS-CoV-2 than bat coronavirus (RaTG13) (Zhang T. and Wu Q, 2020).

Moreover, the association of the extended survival and reach of Rhinovirus to all age groups and all countries in the world, and the extension of SARS-Cov-2 in various strains and in varying level of pathogenicity from season to season, gives a trajectory of its continual existence in the population. But, may be subject to a decrease in the level of infection and/or severity, as common cold does in the pre-covid world and of course till date. Hence, this study will critically review if SARS-CoV-2 end up being a second type of common cold with

a potential to contracted by every one in every part of the world; but, may be with a less potential to result irreversible damage.

1.1. Problem Statement:

Covid-19 has been a global pandemic since March 2020 declared by the world health organization. Since then, various countries have been following different approach to bank the disease, this includes stay at home declaration, avoiding public gathering, restricting public services and schooling etc.

Tough, we are in the pandemic still now; the level of severity is varying across continents and countries. Particularly, in Africa though the rate of new infection increases from time to time, the disease seems getting benign as a result the level of mortality and morbidity seems declining time to time. This gives an insight that the declining pathogenicity of the disease may be finally terminated as a benign communicable disease like common cold though the agent of the disease is different. Hence, this work tries to compare and contrast the nature of the two viruses from the historical, biological and public health concerns, and their associated diseases if they are going to have a similar impact in the current world in the near future.

1.2. Objectives:

- To predict the role of Covid-19 in the current world as a public health concern vis-à-vis the traditional common cold.

1.2.1. Specific Objective:

- To compare and contrast the historical tradition of common cold and Corona;
- To compare and contrast the biological features of Rhinovirus and SARS-CoV-2;
- To examine the pattern of infection, the mortality and morbidity across countries;
- To deduce the fate of corona in concomitant with common cold;

2. LITERATUR REVIEW

2.1. Historical Tradition of Common Cold and Corona

2.1.1. Origin and Evolution of Rhinovirus

Further comparative molecular genetic analysis of common cold viruses in bats, humans and dromedaries suggests that this common cold virus was actually transmitted from camels to humans. Common cold virus evolution could provide a scenario for MERS emergence Drosten and his team isolated live camel common cold viruses and discovered that these could principally also enter human cells -- via the same receptor used by the common cold virus "HCoV-229E." However, the human immune system is able to defend itself against the camel viruses, just as it can against common cold viruses (*www.scincedaily.com).*

2.1.2. Origin and Evolution of SARS-CoV-2

The association of initially confirmed SARS-CoV-2 cases with Huanan Seafood market suggested that the market place has played a role in the early spreading (Li Q, Guan X, Wu P.*et al.,* 2020); Huang C, Wang Y. *et al.* (2020), however, whether it is the origin of the outbreak and what is the native host(s) of SARS-CoV-2 remain uncertain. In fact, the firstly documented patient was not linked to Huanan Seafood market (Huang C, Wang Y. *et al.* (2020).

2.2. Biological Feature of Rhinovirus and SARS-CoV-2

2.2.1. Genome structure of Rhinovirus

Human rhinovirus is a non-enveloped virus with a positive sense single-stranded RNA (CssRNA) of approximately 7.2 kb that encodes 11 proteins (Palmenberg *et al.,* 2009, 2010; Palmenberg and Gern, 2015). The viral capsid of HRV is comprised of four viral proteins: VP1, VP2, VP3, and VP4. The remaining viral proteins are responsible for viral replication and subsequent assembly. Antigenic variation among HRV types is derived from variations in the exposed surface of VP1, VP2, and VP3, while embedded VP4 is responsible for RNA packaging during assembly.

2.2.2. Genome structure of sars-cov-2

The genome of SARS-CoV-2 is comprised of a single-stranded positive-sense RNA (Wu, S.*et al.* 2020). The newly sequenced genome of the SARS-CoV-2was submitted in the NCBI genome database (NC_045512.2) ~29.9 Kb in size (Lu, X. *et al.*, 2020). The genetic makeup of SARS-CoV-2 is composed of 13–15 (12 functional) open reading frames (ORFs) containing ~30,000 nucleotides. The genome contains 38% of the GC content and 11 protein coding genes, with 12 expressed proteins. The genetic arrangement of ORFs highly resembles the SARS-CoV and MERS-CoV (Lu, Y. *et al.* (2015). The ORFs are arranged as replicase and protease (1a–1b) and major S, E, M, and N proteins, which follow a typical 5′-3′ order of appearance, and are considered as major drug/vaccine targets. These gene products play important roles in viral entry, fusion, and survival in host cells (Tong, T.R., 2009).

The genomic organization of the SARS-CoV-2 is sharing about 89% sequence identity with other CoVs. The translated sequences of SARS-CoV-2 proteins were retrieved from the GenBank (Accession ID: NC_045512.2). The whole genome of SARS-CoV-2 encodes about 7096 residues long polyprotein which consists of many structural and non-structural proteins (NSPs). The nucleotide content of the viral genome is held mainly by two non-structural proteins ORF1a and ORF1ab followed by structural proteins. Polyproteins pp1a and pp1ab are encoded by ORFs 1a and 1b, where polyprotein pp1ab is encoded by the ribosomal frame shift mechanism of the gene 1b. These polyproteins are further processed by virally encoded pretenses and produce 16 proteins, which are well conserved in all CoVs belonging to the same family. MERS-CoV is closely related to the SARS-CoV-2 as it carries a larger genome with ~30,119 nucleotides.

2.3. The pattern of infection, mortality and morbidity of Rhinovirus and SARS-CoV-2

2.3.1. Transmission

2.3.1.1. Transmission of Rhinovirus

HRVs are transmitted from person to person via contact (either direct or through a fomite) or aerosol (small or large particle) (Hendley JO. and Gwaltney JM. (1988), Jennings LC. And Dick EC. (1987). HRV infection is efficiently initiated by intranasal and conjunctival inoculation but not by the oral route. In studies of natural and experimental HRV infection, the virus is regularly deposited onto the hands and introduced into the environment. HRV is detected in 40% of naturally infected volunteers' hands and 6% of objects in the home (Gwaltney JM.*et al.* (1987). In a study of 24 married couples with one experimentally infected partner, the transmission of HRV infection occurred in 9 couples during contact

periods ranging from 63 to 149 h (Alessio D. (1987). Under experimental conditions, HRV will survive in an indoor environment for hours to days at an ambient temperature and on undisturbed skin for 2 h (Hendley J *.et al.* (1973). The frequency and duration of HRV shedding in aerosols are not well understood. In one study, HRV was transmitted via an aerosolized route to 56% of 18 volunteers who played cards for 12 h with experimentally infected subjects (Dick EC, *.et al.* (1987).

2.3.1.2. Transmission of SARS-CoV-2

It is clear now that SARS-CoV-2 can be transmitted by human-to-human despite the majority of the early cases had contact history with the Huanan Seafood market (Guan X.*et al.* (2020). Analysis of 425 patients with confirmed COVID-19 showed that the incubation period is 3 to 7 days. The mean was 5.2 days (95% CI: 4.1 to 7.0), and the 95th percentile of the distribution is 12.5 days (95% CI: 9.2 to 18) (Guan X.*et al.* (2020). Notably, it was reported that the incubation period could be as long as 24 days in a rare case (Guan WJ.*et al*. (2020). The basic reproductive number (R_0) up to the period of 4 Jan 2020 was estimated based on the study of 425 patients to be 2.2 (meaning that one patient has been spreading infection to 2.2 other people) (Guan X.*et al.* (2020), slightly smaller than the value of 2.68 by a modeling in another (Leung K. (2020). The R_0 of SARS-CoV-2 from both of these two studies is smaller than that of SRAS, which are 3 before public health measures were implemented (Bauch CT.*et al*. (2005)]. However, subsequent investigation based on the analysis of high-resolution real-time human travel and infection data estimated that the R_0 is much larger, ranging from 4.7 to 6.6 before the control measures (Sanche S.*et al*. (2020), implying that SARS-CoV-2 is highly contagious and more infectious than initially estimated. This conclusion is consistent with the wide spread of SARS-CoV-2 within a short period time and was also echoed by the finding that SARS-CoV-2 Spike (S) protein had 10- to 20-fold higher affinity to human angiotensin-converting enzyme 2 (ACE2) receptor than that of SARS-CoV based on the Cryo-EM structure analysis of S proteins (Wrapp D.*et al.(*2020). Similar to SARS-CoV, the entry of SARS-CoV-2 into host cells depends on the recognition and binding of S protein to ACE2 receptor of the host cells (Hoffmann M.et al. (2020). The high affinity of S protein to ACE2 receptor likely contributes to the quick spreading of virus. The finding of ACE2 as the receptor of SARS-CoV-2 also indicates that human organs with high ACE2 expression level, such as lung alveolar epithelial cells and enterocytes of the small intestine, are potentially the target of SARS-CoV-2(Zou X.*et al*. (2020).

As a new coronavirus, it is not known yet about how SARS-CoV-2 spreads. Current knowledge for SARS-CoV-2 transmission is largely based on what is known from the similar corona viruses, particularly SARS-CoV and MERS-CoV, in which human-to-human transmission occurs through droplets, contact and fomites. SARS-CoV is predominantly transmitted through indirect or direct contact with mucous membranes in the mouth, eyes, or nose. It has been shown that unprotected eyes and exposed mucous membranes are vulnerable to SARS-CoV transmission (Belser JA.*et al.* (2013). A member of the national expert panel on pneumonia was infected by SARS-CoV-2 after the inspection in Wuhan (Cheng-wei.*et al.* (2020). As he wore a N95 mask but not any eye protector, and experienced eye redness before the onset of pneumonia, it was thus suspected that unprotected exposure of the eyes to SARS-CoV-2 might be another transmission pathway (Cheng-wei.*et al. (*2020). However, SARS-CoV-2 was not detected from the conjunctival swab sample in a confirmed COVID-19 patent with conjunctivitis (Zhou Y.*et al.* (2020), suggesting that more evidences are needed before concluding the conjunctival route as the transmission pathway of SARS-CoV-2. The mode of transmission by MERS-CoV is not well understood but is believed to spread largely via the respiratory close contact route (Zumla A.*et al.* (2015), Hijawi B.*et al*. (2013).

Based on the transmission mode of SARS-CoV and MERS-CoV, a serial of preventive measures have been recommended, including avoiding close contact with people suffering from acute respiratory infections and frequent hand-washing(WHO.(2020). The viruses of SARS-CoV-2 were also detected in the stool samples in some patients but not all (Chan JF.*et al*. (2020), (Holshue ML.*et al*. (2020) suggesting that a possible fecal-oral transmission occurs (Kaushal S.*et al.* (2020). A systematic study showed that viruses could be detected in oral swabs, anal swabs and blood samples of the patients, and the anal swabs and blood could test positive when oral swab tested negative(Zhang W.*et al*.(2020). Furthermore, a trend of shift from more oral positive in the collected samples during the early period of patient infection to more anal positive during later period of infection was also found (Zhang W.*et al*.(2020). Therefore, a multiple shedding routes of SARS-CoV-2 might exist.

One of the challenges for preventive control of SARS-CoV-2 spreading is that the viruses are likely transmitted by asymptomatic contact. A German business man was found infected by SARS-CoV-2 after attending a conference together with a colleague, who had no signs or symptoms of infection but had become ill due to the SARS-CoV-2 infection later (Rothe C.*et al*. (2020). This observation suggests that infected patients likely start to shed viruses before

the onset of any symptom, which undoubtedly will bring great challenge to the current practice of preventive control by measuring body temperature. Despite the claim of the transmission by asymptomatic contact has been challenged (Kupferschmidt K. (2020), other asymptomatic carriers were also observed to transmit the viruses of SARS-CoV-2(Bai Y.*et al.* (2020), Hoehl S.*et al. (*2020). Consistently, a study found that an asymptomatic patient had a similar vial loads in the samples of nasal and throat swabs to that of the symptomatic patients (Zou L.*et al*. (2020).

2.3.2. Symptom

2.3.2.1. Rhinovirus Symptom

With the increasing use of molecular methods of viral detection, asymptomatic HRV infection has been noted to be relatively common, particularly in children. The frequent detection of HRV in asymptomatic individuals may also reflect one of several states: prolonged virus shedding after a symptomatic respiratory illness has resolved; mild, unrecognized symptoms; or the incubation period prior to the onset of symptoms. In children less than 4 years old, rates of asymptomatic infection range from 12 to 32% (Singleton RJ.*et al.* (2010), Fry AM.*et al*.(2011) and tend to be higher in the youngest age groups (Fry AM.*et al.*(2011). A study conducted in Alaska's Yukon Kush kowkim Delta to characterize the etiology of lower respiratory tract-associated hospitalizations in children less than 3 years old selected controls from the community if they had no respiratory symptoms in the previous 2 weeks. Among 425 community control children, 33% tested positive for HRV by real time PCR of nasopharyngeal swab specimens (Singleton RJ.et al. (2010)87); this rate was not significantly different from that observed for children hospitalized with lower respiratory tract illness. In contrast, (Iwane et al. (2011) detected HRV in nasal and throat swab specimens from 12.5% of asymptomatic children less than 5 years old recruited at well-child primary care visits in three different regions of the United States (Rochester, NY; Nashville, TN; and Cincinnati, OH). This difference in observed rates of asymptomatic HRV infection may be attributed to the higher prevalence of HRV in the youngest age groups or to environmental factors in the Alaska Native community, including household crowding and a lack of running water, that predispose individuals to respiratory illnesses (Hennessy TW .*et al*.(2008).

2.3.2.2. SARS-COV-2Symptom

Symptoms of CoVID- 19 are non-specific and the disease presentation can range from no-symptoms (asymptomatic) to severe pneumonia and death. A study of 41 patients (Chaolin *et al*.,2020) who were initially diagnosed with the outbreak(the diagnosis date was up to 2 January) found that the most common symptoms were fever(98%), cough(76%), myalgia or fatigue(44%); and a typical symptoms included sputum(28%), headache(8%), hemoptysis (5%) and diarrhea(3%). About half of the patients had dyspnea (the median from onset to dyspnea was 8days). Lymphocytopenia was observed in 63% of patients. All patients had pneumonia. Complications included acute respiratory distress syndrome (29%), acute heart injury (12%), and secondary infections (10%); 32% of patients required treatment in the ICU. Analysis of 1099 confirmed cases (upto29January) conducted by Nan Shan Zhong' steam (Weijie *et al*., 2020) found that the most common symptoms were fever (87.9%), cough(67.7%), diarrhea(3.7%) and vomiting(5.0%). 25.2% of the patients had at least one underlying disease (such as hypertension, chronic obstructive pulmonary disease). Lymphocytopenia was observed in 82.1% of patients. On admission, 50% of the patients presented ground-glass shadow on chest CT. A retrospective study (Wang *et al*.2019) of 138 hospitalized patients from January 1 to 28 found that patients receiving treatment in the ICU were older, more likely to have underlying diseases, and more likely to have dyspnea, and the median length of stay was 10 days (Wang et al., 2019). Recent studies indicate that patient's ≥ 60 years of age are at higher risk than children who might be less likely to become infected or, if so, may show milder symptoms or even asymptomatic infection (Li *et al.,* 2020a). Epidemiology Working Group for NCIP Epidemic Response of the Chinese Center for Disease Control and Prevention (Working, 2020), with a total of 72,314 patients, reported that there were 44,672 (61.8%) confirmed cases, and 889 asymptomatic cases (1.2%) among the total number of patients. Among confirmed cases, most were age 30-79 years (86.6%), and considered mild/mildpneumoa (80.9%).

2.4. The future of Rhinovirus and SARS-Cov-2 in prevention and cure

2.4.1. Vaccine approaches against rhinovirus

For decades, vaccine development against RVs has been considered almost impossible (Barclay WS.*et al.* (1989). The large breadth of RV serotypes is a major obstacle in

developing therapy. Neutralizing humoral responses against RV infection are associated with protection; however, the mechanisms of their induction are poorly understood. Upon RV infection, IgG and IgA are observed in the serum and the airways, respectively (Papi A. (2011). High levels of serotype specific antibodies are associated with protection. Despite this, the main limiting factor with humoral responses against RV is that, owing to the high number of serotypes, little cross-reactivity is elicited by neutralizing antibodies (Glanville N. (2015). Recent advances in understanding RV serotypes and viral capsid structures provide promising vaccine targets. The amino acid identity within RV serotypes is at 70%, and VP1 and VP4/VP2 (VP0) capsid regions are the most conserved (Stobart CC. (2017). A recombinant VP0 vaccine in conjunction with an IFA/CpG adjuvant in mice elicited strong cross-reactive Th1 responses and, following virus challenge, enhanced neutralizing antibody responses within the serotype (Glanville N .*et al*. (2013). The usage of immunogens, such as VP0, in combination with Th1-promoting adjuvants provides a promising avenue for RV vaccine development [Glanville N.et al.(2015). The main limitation with vaccines against RV is increasing the breadth of the immune responses across other serotypes. For example, vaccination of rabbits with VP1/VP3 increases neutralizing antibodies only within a specific group of serotypes64. Taken together, these results highlight the difficultly for a single antigen providing protection across all RV serotypes (Schlingmann B.*et al.(*2018) Through the use of an adjuvanted polyvalent RV vaccine in macaques and mice, the induction of neutralizing antibodies across a diverse range of RV serotypes is feasible (Lee S.*et al.(*2016). The identification of conserved regions within the RV genome and production of an adjuvanted polyvalent RV vaccine provide exciting pathways for RV vaccine development. Overall, recent advances in understanding RV immunity increase hopes that a vaccine may be feasible after all.

2.4.2. Humoral immunity to SARS-CoV-2

Humoral immune responses to SARS-CoV-2 are mediated by antibodies that are directed to viral surface glycoprotein, mainly the spike glycoprotein and the nucleocapsid protein. Such antibodies neutralize viral infection of human cells and tissues expressing angiotensin-converting enzyme 2 (ACE2). The 180 kDa spike glycoprotein contains two subunits (i.e., N-terminal S1 and C-terminal S2) and is considered an important antigenic determinant capable of inducing a protective immune response (Ou X.*et al.* (2020).

The S1 subunit holds a receptor-binding domain (RBD; residues 331–524), which mediates viral binding to functional ACE2 receptors on susceptible cells and is the main target for SARS-CoV-2 neutralizing antibodies (Tai W.*et al. (*2020). The major role of neutralizing antibodies is antigen binding and interaction with cells bearing Fc γ-receptors to modulate subsequent immune responses. Considerable IgG responses against SARS-CoV-2 proteins (eg, nucleocapsid protein, S1, ORF9b, nsp5, and others; have been detected in convalescent serum samples from patients who have recovered from COVID-19 by use of SARS-CoV-2 proteome microarray technology[Jiang H. et al.(2020)]. Functional neutralizing antibodies specific to SARS-CoV-2 that are produced following infection, vaccination, or both (anti-spike glycoprotein and anti-RBD) are considered important for viral neutralization and viral clearance, and are quantified by use of in vitro neutralization assays. For these reasons, antibody titres might be good biomarkers for the protective efficacy of antibodies and successful humoral immune responses after SARS-CoV-2 exposure (Okba NMA.*et al*. (2020). Indeed, a strong correlation (*r* range 0·87–0·94) between neutralizing antibody responses against the spike glycoprotein, the nucleocapsid protein, and RBD proteins detected by the plaque reduction neutralization test and those detected by ELISAs has been reported in patients with PCR-confirmed COVID-19.(Okba NMA.*et al*.(2020). IgG, IgM, and IgA responses to the SARS-CoV-2 cysteine-like protease have also been reported in patients with COVID-19, and these responses correlate well with antibody titres to the nucleocapsid protein [Martinez. *et al*. (2020). High-quality studies that examine the duration of protection by functional neutralizing antibodies and the potential for reinfection are needed in large cohorts of patients with COVID-19 to further understand and characterize SARS-CoV-2-specific immunity. Most patients with COVID-19 or those who are convalescent have virus-specific IgM, IgA, and IgG responses in the days after infection, suggesting that antibodies mediate protective immunity to SARS-CoV-2(Padoan A.*et al*. (2020). The overall kinetics of the antibody response against SARS-CoV-2 are analogous to those for SARS-CoV-1, which are characterized by robust seroconversion (IgM and IgG) 7–14 days following symptom onset and antibody concentrations persisting for weeks to months after infection and viral clearance (Lou B. *et al*. (2020).A longitudinal study assessing the kinetics of spike glycoprotein-specific antibodies in patients with COVID-19 found that IgA antibodies were produced early (in the first week) and peaked in concentration at 20–22 days, whereas IgM antibodies reached high titres at 10–12 days that subsequently waned 18 days after the onset of symptoms (Padoan A . *et al*.(2020). A seroprevalence study that examined IgG responses to spike glycoprotein in 40 patients with COVID-19 after symptom onset reported that IgG

titres increased during the first 3 weeks and began to decrease by 8 weeks(Adams ER . *et al*.(2020).In individuals with mild COVID-19, a rapid decline of RBD-specific IgG titres within 2–4 months has been observed in several studies, suggesting that SARS-CoV-2-induced humoral immunity might not be long-lasting in individuals with mild disease(Ibarrondo. *et al*. (2020). Similar results have been reported with antibody responses specific to SARS-CoV-2 nucleocapsid protein (Liu T.*et al*. (2020).

3. CONCLUSION

Those viruses are characterized by a high mutation rate, up to a million times higher than that of their hosts. Virus mutagenic capability depends upon several factors, including the fidelity of viral enzymes that replicate nucleic acids, as SARS-CoV-2 RNA dependent RNA polymerase (RdRp).Those two viruses are single stranded positive RNA virus and transmitted through body contact from person to person. Most of the time both virus attack human respiratory system. But they differ protein encoding gene and their genome size, however they cause economic burden to the society by work absenteeism, school and home staying.

4. RECOMMENDATION

For the prevention of covid-19 spreading many countries construct different strategy like, staying at home, avoid public gathering and restrict public service and wearing mask but it is not enough in addition to these the country will focus on vaccine development to eliminate the transmission of sars-cov-2.

REFERENCES

Adams ER Ainsworth M an and R et al.2020. Antibody testing for COVID-19: a report from the National COVID Scientific Advisory Panel. *medRxiv*. (published online July 7.).

Alessio D, Peterson J, Dick C, Dick E.1976. Transmission of exper-imental rhinovirus colds in volunteer married couples. J. Infect. Dis.133:28–36.

Bai Y, Yao L, Wei T, Tian F, Jin DY, Chen L. et al.2020. Presumed Asymptomatic Carrier Transmission of COVID-19. JAMA.

Barclay WS, al-Nakib W, Higgins PG, et al.1989: The time course of the humoral immune response to rhinovirus infection. Epidemiol Infect. 103(3): 659–69.

Bauch CT, Lloyd-Smith JO, Coffee MP, Galvani AP.2005. Dynamically modeling SARS and other newly emerging respiratory illnesses: past, present, and future. Epidemiology. 16:791–801.

Belser JA, Rota PA, Tumpey TM.2013; Ocular tropism of respiratory viruses. Microbiol Mol Biol Rev.77:144–56.

Chan JF-W, Yuan S, Kok K-H, To KK-W, Chu H, Yang J, Xing F, Liu J, Yip CC-Y, Poon RW-S *et al*: 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):514-523.

Cheng-wei Lu X-fL, Zhi-fang Jia. 2019-nCoV transmission through the ocular surface must not be ignored. The Lancet. 2020;36:30313–5.

Cimerman S, Chebabo A, Cunha CAd, Rodríguez-Morales AJ.2020; Deep impact of COVID-19 in the healthcare of Latin America: the case of Brazil. Braz J Infect Dis.; 24(2):93–5.

Chaplin, Yeming W, Xing wang L,et al.2020.Clinicalfeaturesofpatientsinfected with 2019 novel corona virus in Wuhan, China. Lancet;(395):497–506.

Dick EC, Jennings LC, Mink KA, Wartgow CD, Inhorn SL.1987.Aerosol transmission of rhinovirus colds. J. Infect. Dis.156:442–448.

Fendrick AM, Monto AS, Nightengale B, Sarnes M. 2003. The economic burden of non-influenza-related viral respiratory tract infection in the United States. Arch. Intern. Med. 163:487–494.

Flahault A.2020. Has China faced only a herald wave of SARS-CoV-2? Lancet. 395(10228):947.

Fry AM, Lu X, Olsen SJ, Chittaganpitch M, Sawatwong P, Chantra S, Baggett HC, Erdman D.2011.Human rhinovirus infections in rural Thailand: epidemiological evidence for

rhinovirus as both pathogen and bystander. PLoS One6:e17780. doi:10.1371/joural.pone.0017780.

Germen center for infection research. Common cold virus originated in camels, science daily/2016; <www.sciencedaily.com /release /2016/08/160818093438.htm>

Gutiérrez AB, Rodríguez-Morales AJ, Narváez Mejía ÁJ, García Peña ÁA, Giraldo Montoya ÁM, Cortes Muñoz AJ, García AL, Ospina Serrano AV, Escobar BP, Acevedo Medina CA, et al.2020. Colombian consensus recommendations for diagnosis, management and treatment of the infection by SARS-COV-2/ COVID-19 in health care facilities - Recommendations from expert´s group based and informed on evidence. Infection. 24:1–102.

Guan Y, Zheng BJ, He YQ, Liu XL, Zhuang ZX, Cheung CL. et al.2003. Isolation and characterization of viruses related to the SARS coronavirus from animals in southern China. Science. 302:276–8.

Guan WJ, Ni ZY, Hu Y, Liang WH, Ou CQ, He JX. et al.2020. Clinical characteristics of coronavirus disease 2019 in China. N Engl J Med.

Glanville N, McLean GR, Guy B, et al.: Cross-serotype immunity induced by immunization with a conserved rhinovirus capsid protein. PLoS Pathog. 2013; 9(9): e1003669.

Gwaltney JM, Moskalski PB, Hendley JO.1978. Hand-to-hand trans-mission of rhinovirus colds. Ann. Intern. Med.88:463–467.

Hendley J, Wenzel R, Gwaltney JM, Jr.1973. Transmission of rhino-virus colds by self-inoculation. N. Engl. J. Med.288:1361–1364.

Hendley JO, Gwaltney JM.1988. Mechanisms of transmission of rhi-novirus infections. Epidemiol. Rev.10:243–258.

Hennessy TW, Ritter T, Holman RC, Bruden DL, Yorita KL, Bulkow L, Cheek JE, Singleton RJ, Smith J.2008. The relationship between in-home water service and the risk of respiratory tract, skin, and gastrointestinal tract infections among rural Alaska natives. Am. J. Public Health98:2072–2078.

Hijawi B, Abdallat M, Sayaydeh A, Alqasrawi S, Haddadin A, Jaarour N. et al. Novel coronavirus infections in Jordan, April 2012: epidemiological findings from a retrospective investigation. East Mediterr Health J. 2013;19(Suppl 1):S12–8. [PubMed] [Google Scholar].

Hoffmann M, Kleine-Weber H, Krüger N, Müller M, Drosten C, Pöhlmann S. The novel coronavirus 2019 (2019-nCoV) uses the SARS-coronavirus receptor ACE2 and the cellular protease TMPRSS2 for entry into target cells. bioRxiv. doi: https://doi.org/10.1101/2020.01.31.929042.

Hoehl S, Berger A, Kortenbusch M, Cinatl J, Bojkova D, Rabenau H. et al. Evidence of SARS-CoV-2 Infection in Returning Travelers from Wuhan, China. N Engl J Med. 2020 [Epub ahead of print] [PMC free article] [PubMed] [Google Scholar].

Huang C, Wang Y, Li X, Ren L, Zhao J, Hu Y. et al.2020. Clinical features of patients infected with 2019 novel coronavirus in Wuhan, China. Lancet. 395:497–506.

Hu B, Zeng LP, Yang XL, Ge XY, Zhang W, Li B. et al.2017. Discovery of a rich gene pool of bat SARS-related coronaviruses provides new insights into the origin of SARS coronavirus. PLoS Pat hog. 13:e1006698.

Ibarrondo FJ Fulcher JA Goodman-Meza D et al.2020. **Rapid decay of anti-SARS-CoV-2 antibodies in persons with mild COVID-19.***N Engl J Med.* **383**: 1085-1087.

Iwane MK, Prill MM, Lu X, Miller EK, Edwards KM, Hall CB, Griffin MR, Staat MA, Anderson LJ, Williams JV, Weinberg GA, Ali A, Szilagyi PG, Zhu Y, Erdman DD.2011. Human rhinovirus species associated with hospitalizations for acute respiratory illness in young US children. J. Infect. Dis.204:1702–1710.

Jacobs SE, Lamson DM, St George K, Walsh TJ.2013. Human rhinoviruses. Clin Microbiol Rev; 26 (1):135–162.

Jennings LC, Dick EC.1987. Transmission and control of rhinoviruscolds. Eur. J. Epidemiol.3:327–335.

Jiang H-w Li Y Zhang H-n et al.2020. Global profiling of SARS-CoV-2 specific IgG/IgM responses of convalescents using a proteome microarray. *medRxiv*.

Ji WWW, Zhao X, Zai J, Li X.2020. Homologous recombination within the spike glycoprotein of the newly identified coronavirus may boost cross-species transmission from snake to human. J Med Virol. 92(4):433–40.

Kupferschmidt K.2020. Study claiming new coronavirus can be transmitted by people without symptoms was flawed. Science.https://www.sciencemag.org/news/2020/02/paper-non-symptomatic-patient-transmitting-coronavirus-wrong.

Kuroda M, Niwa S, Sekizuka T, et al.2015. Molecular evolution of the VP1, VP2, and VP3 genes in human rhinovirus species C. Sci Rep;5:8185.

Lee S, Nguyen MT, Currier MG, et al.2016: A polyvalent inactivated rhinovirus vaccine is broadly immunogenic in rhesus macaques. Nat Commun. 7: 12838.

Li Q, Guan X, WuP, et al.2020a. Early transmission dynamics in Wuhan, China, of novels corona virus- infected pneumonia. NEnglJ Med Epub ahead of print.

Li Q, Guan X, Wu P, Wang X, Zhou L, Tong Y. et al.2020. Early Transmission Dynamics in Wuhan, China, of Novel Coronavirus-Infected Pneumonia. N Engl J Med.[Epub ahead of print] [PMC free article] [PubMed] [Google Scholar].

Li Z, Ge J, Yang M, Feng J, Qiao M, Jiang R, Bi J, Zhan G, Xu X, Wang L, et al.2020. Vicarious traumatization in the general public, members, and non-members of medical teams aiding in COVID-19 control. Brain Behav Immunity.

Lu, X. Zhao, J. Li, P. Niu, B. Yang, H. Wu, W. Wang, H. Song, B. Huang, N. Zhu,.2020. Genomic characterisation and epidemiology of 2019 novel coronavirus: implications for virus origins and receptor binding, Lancet 395; 565–574.

Lu, Y. Wang, W. Wang, K. Nie, Y. Zhao, J. Su, Y. Deng, W. Zhou, Y. Li, H. Wang,2015. Complete genome sequence of Middle East respiratory syndrome coronavirus (MERS-CoV) from the first imported MERS-CoV case in China, Genome Announc. 3;(e00818-00815).

Lou B Li T-D Zheng S-F et al.2020. Serology characteristics of SARS-CoV-2 infection since exposure and post symptom onset.*Eur Respir J.* (published online May 19.

Liu T Wu S Tao H et al.2020. Prevalence of IgG antibodies to SARS-CoV-2 in Wuhan—implications for the ability to produce long-lasting protective antibodies against SARS-CoV-2.*medRxiv.* (published online June 16.) (preprint).

Malik YS, Kumar N, Sircar S, Kaushik R, Bhat S, Dhama K, Gupta P, Goyal K, Singh MP, Ghoshal U, et al.2020. Coronavirus Disease Pandemic (COVID-19): challenges and a global perspective. Pathogens. 9:7.

Martinez-Fleta P Alfranca A González-Álvaro I et al.2020.SARS-Cov-2 cysteine-like protease (Mpro) is immunogenic and can be detected in serum and saliva of COVID-19-seropositiveindividuals.medRxiv. (publishedonlineJuly18.) (preprint)https://doi.org/10.1101/2020.07.16.20155853.

Millan-Oñate J, Rodríguez-Morales AJ, Camacho-Moreno G, Mendoza-Ramírez H, Rodríguez-Sabogal IA, Álvarez-Moreno C.2020. A new emerging zoonotic virus of concern: the 2019 novel Coronavirus (COVID-19). Infection. 24(3):187–92.

Nichol KL, D'Heilly S, Ehlinger E. 2005. Colds and influenza-like illnesses in university students: impact on health, academic and work performance, and health care use. Clin. Infect. Dis. 40:1263–1270.

Ou X Liu Y Lei X et al.2020.Characterization of spike glycoprotein of SARS-CoV-2 on virus entry and its immune cross-reactivity with SARS CoV.*Nat Commun.* 111620.

Okba NMA Müller MA Li W et al.2020. Severe acute respiratory syndrome coronavirus 2-specific antibody responses in coronavirus disease patients. *Emerg Infect Dis.* 26: 1478-1488.

Palmenberg AC, Spiro D, Kuzmickas R, et al. Sequencing and analyses of all known human rhinovirus genomes reveal structure and evolution. Science 2009;324 (5923):55–59.

Palmenberg, A. C., and Gern, J. E. (2015). Classification and evolution of human.

Pappas DE, Hendley JO, Hayden FG, Winther B. 2008. Symptom profile of common colds in school-aged children. Pediatr. Infect. Dis. J. 27:8 –11.

Palmenberg, A. C., Rathe, J. A., and Liggett, S. B. (2010). Analysis of the complete genome sequences of human rhinovirus. *J. Allergy Clin. Immunol.* 125, 1190–1199; quiz 1200–1191. doi: 10.1016/j.jaci.2010.04.010.

Papi A, Contoli M.2011. Rhinovirus vaccination: the case against. Eur Respir J. 37(1): 5–7.

Padoan A Sciacovelli L Basso D et al.2020. IgA-Ab response to spike glycoprotein of SARS-CoV-2 in patients with COVID-19: a longitudinal study.*Clin Chim Acta.* 507 : 164-166.

Redfield R.2020. Novel Coronavirus (2019-nCoV) Update: Uncoating the Virus. In: American Society for Microbiology.

Rothe C, Schunk M, Sothmann P, Bretzel G, Froeschl G, Wallrauch C. et al.2020. Transmission of 2019-nCoV Infection from an Asymptomatic Contact in Germany. N Engl J Med. [Epub ahead of print] [PMC free article] [PubMed] [Google Scholar].

Sanche S, Lin YT, Xu C, Romero-Severson E, Hengartner N, Ke R.2020. The Novel Coronavirus, 2019-nCoV, is Highly Contagious and More Infectious Than Initially Estimated. medRxiv. doi: https://doi.org/10.1101/2020.02.07.20021154.

Schlingmann B, Castiglia KR, Stobart CC, et al.2018: Polyvalent vaccines: High maintenance heroes. PLoS Pathog. 14(4): e1006904.

Shi Z, Hu Z.2008. A review of studies on animal reservoirs of the SARS coronavirus. Virus Res. 133 :74–87. [PMC free article] [PubMed] [Google Scholar].

Singleton RJ, Bulkow LR, Miernyk K, DeByle C, Pruitt L, Hummel KB, Bruden D, Englund JA, Anderson LJ, Lucher L, Holman RC,Hennessy TW.2010. Viral respiratory infections in hospitalized and community control children in Alaska. J. Med. Virol.82:1282–1290.

Stobart CC, Nosek JM, Moore ML.2017. Rhinovirus Biology, Antigenic Diversity, and Advancements in the Design of a Human Rhinovirus Vaccine. Front Microbiol. 8: 2412.

Song HD, Tu CC, Zhang GW, Wang SY, Zheng K, Lei LC. et al.2005. Cross-host evolution of severe acute respiratory syndrome coronavirus in palm civet and human. Proc Natl Acad Sci U S A. 102:2430–5. [PMC free article] [PubMed] [Google Scholar].

Tai W He L Zhang X et al.2020. Characterization of the receptor-binding domain (RBD) of 2019 novel coronavirus: implication for development of RBD protein as a viral attachment inhibitor and vaccine. *Cell Mol Immune.* 17: 613-620.

Tong, T.R. 2009. Drug targets in severe acute respiratory syndrome (SARS) virus and other coronavirus infections, Infectious Disorders–Drug Targets (Formerly Current Drug Targets-Infectious Disorders) 9 ;223–245.

Wang D, Hu B, Hu C,et al.2020.Clinical characteristics of 138 hospitalized patients with 2019 novel corona virus-infected pneumoniainWuhan,China.JAMA2019;Epuba head of print.

Wang M, Yan M, Xu H, Liang W, Kan B, Zheng B. et al.2005. SARS-CoV infection in a restaurant from palm civet. Emerg Infect Dis. 11:1860–5. [PMC free article] [PubMed] [Google Scholar].

WeijieG,ZhengyiN,YuH,etal.2020.Clinicalcharacteristicsof2019novelcoronavirusinfectionin ChinamedRxivpre print.

World Health O: 2020. Clinical management of severe acute respiratory infection when novel coronavirus; infection is suspected: interim guidance, 28 January 2020. Geneva: World Health Organization; vol. WHO/nCoV/Clinical/2020.3].

World Health Organization. 2020. Coronavirus disease 2019 (COVID-19) : situation report, 55. Geneva: World Health Organization.

Wrapp D, Wang N, Corbett KS, Goldsmith JA, Hsieh CL, Abiona O. et al.2020. Cryo-EM structure of the 2019-nCoV spike in the prefusion conformation. Science.[Epub ahead of print] [PMC free article] [PubMed] [Google Scholar].

Wu, S. Zhao, B. Yu, Y.M. Chen, W. Wang, Z.G. Song, Y. Hu, Z.W. Tao, J.H. Tian, Y.Y. Pei, M.L. Yuan, Y.L. Zhang, F.H. Dai, Y. Liu, Q.M. Wang, J.J. Zheng, L. Xu, E.C. Holmes, Y.Z. Zhang.(2020).A new coronavirus associated with human respiratory disease in China, Nature. **579**: 265–269.

Wu JT, Leung K, Leung GM.2020. Nowcasting and forecasting the potential domestic and international spread of the 2019-nCoV outbreak originating in Wuhan, China: a modelling study. Lancet. [Epub ahead of print] [PMC free article] [PubMed] [Google Scholar].

Xu X, Chen P, Wang J, Feng J, Zhou H, Li X. et al.2020. Evolution of the novel coronavirus from the ongoing Wuhan outbreak and modeling of its spike protein for risk of human transmission. Sci China Life Sci. [Epub ahead of print] [PMC free article] [PubMed] [Google Scholar].

Yang Y, Peng F, Wang R, Guan K, Jiang T, Xu G, Sun J, Chang C.(2020); The deadly coronaviruses: The 2003 SARS pandemic and the 2020 novel coronavirus epidemic in China. J Autoimmun. 109:102434–102434.

Yeo C, Kaushal S, Yeo D.2020. Enteric involvement of coronaviruses: is faecal-oral transmission of SARS-CoV-2 possible? Lancet Gastroenterol Hepatol. [Epub ahead of print] [PMC free article] [PubMed] [Google Scholar].

Zhang . T., Q. Wu, Z. Zhang. 2020. Probable pangolin origin of SARS-CoV-2 associated with the COVID-19 outbreak, Curr. Biol. 30;1578.

Zhang .Y.Z, E.C. Holmes,2020. A genomic perspective on the origin and emergence of SARS-CoV-2, Cell 181; 223–227.

Zhang T, Wu Q, Zhang Z.2020. Probable Pangolin Origin of SARS-CoV-2 Associated with the COVID-19 Outbreak. Curr Biol. 30(7):1346–51.

Zhang W, Du RH, Li B, Zheng XS, Yang XL, Hu B. et al.2020. Molecular and serological investigation of 2019-nCoV infected patients: implication of multiple shedding routes. Emerg Microbes Infect. 9:3869. [PMC free article] [PubMed] [Google Scholar].

Zumla A, Hui DS, Perlman S.2015. Middle East respiratory syndrome. Lancet. 386:995–1007.

Zou L, Ruan F, Huang M, Liang L, Huang H, Hong Z. et al.2020. SARS-CoV-2 Viral Load in Upper Respiratory Specimens of Infected Patients. N Engl J Med. [Epub ahead of print] [PMC free article] [PubMed] [Google Scholar].

Zhou P, Yang XL, Wang XG, Hu B, Zhang L, Zhang W. et al.2020. A pneumonia outbreak associated with a new coronavirus of probable bat origin. Nature. [Epub ahead of print] [PMC free article] [PubMed] [Google Scholar].

Zou X, Chen K, Zou J, Han P, Hao J, Z. H. 2020.The single-cell RNA-seq data analysis on the receptor ACE2 expression reveals the potential risk of different human organs vulnerable to Wuhan 2019-nCoV infection. Front Med. [Epub ahead of print] [PMC free article] [PubMed] [Google Scholar].