

An Overview on Nature Function in Relation with Spread of Omicron-Covid-19: Where Will the Next Pandemic Begin and Why the Amazon Forest Offers Troubling Clues

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Abstract: The effect of COVID-19 vaccination also depends on the population that accepts vaccines. Improving the COVID-19 vaccination methods will be tremendous to human health and the world economy. So, in this work, we use an interdisciplinary knowledge from climates, social sciences, geography, jungle, forestry and wood industry, genetic analysis, and computational biophysics, including artificial intelligence and docking simulation. The emergence of the omicron variant raises serious concerns because of the initial observation of a significant growth advantage compared to the Delta, lambda, beta, and gamma variants. Although the omicron variant preliminary observed in the EU/EEA and Asian countries depend on travel, several are now observed as parts of pandemic clustering in this zoon. Since, even if the severity of the disease is lower compared with other variants, particularly Delta, the fast transmissibility and resulting exponential growth of cases will soon outweigh any benefits of a potentially reduced severity. This research showed that though omicron covid-19 death cases are less severe than Delta, Omicron will be an important base for the emergence of new further variants through huge mutations in the future, which some are so dangerous. Due to the wet climate, the Amazon jungle is a suitable substrate for emerging any further corona variants.

Keywords: Omicron covid-19; Amazon forest; spike proteins; RNA mutation; equatorial climate.

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1. Introduction

1.1. Necessity to reimagine nature and environment.

Various human diseases take out mostly from various birds and monkeys: the flu and Ebola originated from birds and chimpanzees, respectively. Ecosystems in nature act the same as the human body: When strong and healthy, they are more resistant to disease and environmental effects. Although the ecosystem by itself has a variety of benefits to the environment humanity, when humans work the same as logging and mining extracting, these ecosystems have been destroyed. Therefore, wildlife and their habitats are changed towards abnormal biology and are more likely to be stressed or sick. In these situations, diseases between wildlife populations and humans will become more frequent due to destroying nature.

For instance, the COVID-19 strain likely passed from a bat and might be injected into other species before any ability to infect the world's people [1-10]. This exchange of wildlife is also a concern subject to nature because it decimates some strong animals, such as elephants and rhinos, which are critical to the stability of ecosystems [5-8]. In addition, deforestation rates have soared across the globe, driven extremely by agriculture and logging. This affects wildlife forests; it could accelerate climate change, consequently making an increase in the impact of the spread of disease [9-12]. From a human health point of view, the climate crisis causes a strong spreading of many diseases and complicates attempts to combat the other parts of the environment. Seasonality and weather are two main items that control the spreading of viruses, such as the flu. Although researchers have no idea how climate breakdown will impact the spread of COVID-19, they guess increasing the climate changes effects might increase the disease. Since we prevent humans from going into natural habitats and becoming exposed to animal viruses, wildlife habitats also must apply several projects to keep them as far from humans as possible [6, 7-9]. The negative effects of climate change should be mitigated and give nature the space to adapt naturally to the impacts. For many historical years, Natural ecosystems were strong and stable; therefore, humans thought they could do anything to nature. But nowadays, due to fast industrialization, we have reached an irreversible point. The global pandemic associated with the SARS-CoV-2 virus had fast and hard responses worldwide. Therefore to prevent the spread of the COVID-19, economic motilities have been increasingly limited in many centers. Recent research shows that 35% of tropical lands could help cut species extinction risk in half. We have to care the nature for caring for ourselves, and we must prevent zoonotic disease outbreaks by stopping the global wildlife trade [8, 9-13]. As a result, dramatic reductions in fossil fuels have occurred in many parts of the world. Therefore, emissions of anthropogenic pollutant gases have been decreased. This huge change in world cycles of greenhouse causes the possibility of 'real-time' research for scientists. The pandemic also affects forestry activities. Since many jungles have suffered drought largely, the timber industry is already locked due to Covid-19, while in the United States, hoarding of hygiene products increases demand for pulpwood.

Moreover, this pandemic has completely changed the importance of urban and forests due to decreasing the international travel limitation. In many urban places, the residents to avoid Covid-19 infection hot-spots are flooding into rural areas, consequently putting a lot of pressure on ecosystem services [14, 15]. Countries can use several suites of conservation tools to prevent this carbon from establishing or expanding protected areas, providing financial incentives for sustainable agriculture, and supporting community conservancies and indigenous peoples. Nowadays, countries and governments look locally for climate action to isolate the spread of Covid-19 via webinars and virtual meetings at both a local and national level [16-19]. Although technology has the powerful ability to connect people worldwide, it is difficult to match the pace of progress achieved through in-person negotiations. Countries are taking rapid action to curb the spread of Covid-19, from sheltering in place to issuing multi-trillion-dollar expenditures in some countries. The world's response to Covid-19 indicates that humanity needs to take fast action to stop climate change. Recent research on global emissions illustrates that changes in human behavior can show tangible results for climate action even at an individual level. If there is only one advantage that people can take from this pandemic, every single person has a role to play in ending global crises [11-19].

1.2. Forest animals' effect to increase the variants of Covid-19.

Tropics climate has been changed by Covid-19 and topicality. It is notable that capitalist and colonialist expansion and exploitation with factors of climate and disease paramount helped to arise empire while buttressing Western hegemony of dominance and superiorities. There are numerous items that show the relationship between meat consumption and the Covid-19 disease. For instance, the new coronavirus originates from a bowl of bat soup in China or meat processing in Brazil [12-20]. It also includes social injustices, precarious work, and environmental degradation. An important goal is not to allow animals, plants, and microbes to appear together with humans in the social composition. Various animals are known as natural reservoirs of pathogens that these pathogens can cross the species boundary and reach humans. The most severe infectious disease of the century that paralyzed the Asian continent (like Covid-19) was first transmitted by consuming some civet varieties. Contamination processes among humans and animals have complex ecologies and mechanics [21-29].

1.3. Classification of Omicron (B.1.1.529): SARS-CoV-2 Variant of Concern.

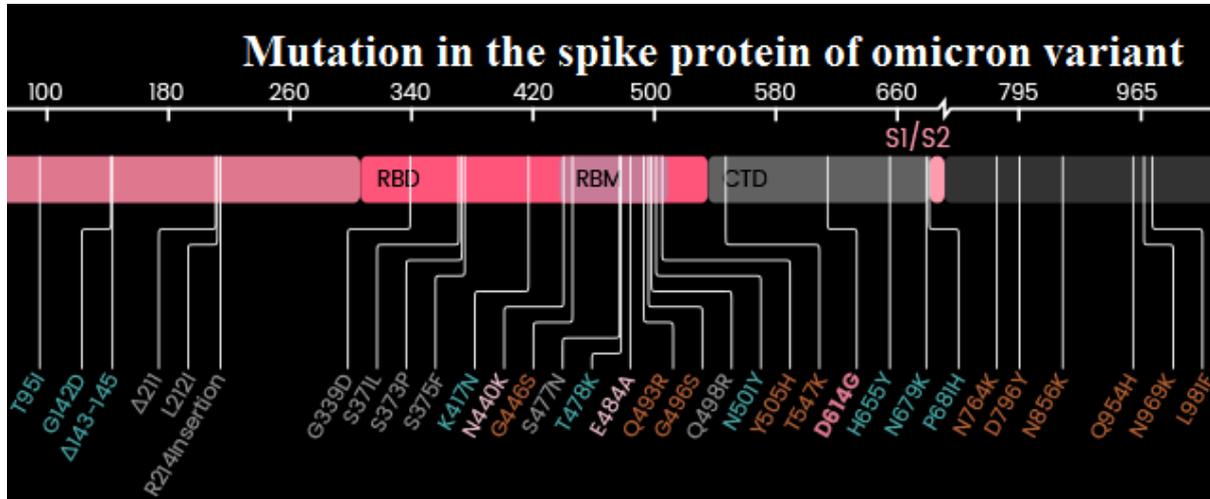
The B.1.1.529 variant of the coronavirus was first detected in South Africa in November 2021. Three separate peaks have specified the epidemiological condition that one of them belongs to the Delta variant. Recently, infections have increased significantly, coinciding with the B.1.1.529 variant. This variant consists of numerous mutations, much more than the other variants. Preliminary observation predicts a high risk of reinfection with this variant compared with other variants. Several cases of this variant appear to be increasing in many parts of South Africa. Some other labs have exhibited that for one widely used PCR test, one of the three target genes (S gene target failure) is not detected due to the sequencing confirmation of this variant. Some other testing shows this variant has a faster infection rate due to its growth advantage than the others. Omicron has a concern position due to dozens of mutations that can affect the way it behaves. Therefore, it needs to be further investigated for its potential impacts.

In contrast to omicron variants, current vaccines offer protection against severe disease and death from Covid-19 variants, including Delta [30-35]. At the same time, this variant has an emerging situation. Various mutations or combinations of them might change virus behavior. Omicron is of concern due to its several numbers of mutations that cause transmissibility and possible immune removal. In other words, humans got infected via it even if they have developed some natural immunity from previous Covid-19 infections. At the same time, we must not forget that preventing the transmission of Delta should remain our priority parallel with the omicron problem. All preventive measures suitable for the Delta variant continue to be effective against Omicron, based on data so far. Getting vaccinated with complete doses and taking all other preventive measures will decrease the risk of infection [35-40].

1.4. Variant coronavirus detection in the African jungle.

Although the observation of sequencing data in the African zones is generally low overall, the transmission of this variant cannot be excluded from other countries. Due to its fast spread across regions in South Africa, it also can be detected in other parts of African countries, or also some circulation in other countries is likely. The variant B.1.1.529 (Omicron) belongs to Pango lineage B.1.1.529, Nextstrain clade 21K, and is characterized by 30 amino acid

changes, three small deletions, and one small insertion in the spike protein. Those are including (A67V, Δ69-70, T95I, G142D, Δ143-145, Δ211, L212I, 214EPE, G339D, S371L, S373P, S375F, K417N, N440K, Q498R, N501Y, Y505H, T547K, D614G, H655Y, N679K, P681H, N764K, D796Y, G446S, S477N, T478K, E484A, Q493K, G496S, N856K, Q954H, N969K, L981F). Out of these changes, 15 are located in the receptor-binding domain (RBD) (residues 319-541).



Scheme 1. The spike protein of the Omicron Variant carries more than 30 mutations.

The variant also carries a number of changes and deletions in other genomic regions R203K, G204R, NSP3, NSP12, P323L, NSP14, I42V, V1069I, Δ1265, L1266I, A1892T, NSP4, NSP5, P132H, NSP6, A189V, Q19E, A63T (Scheme1 & Table 1) [38-43].

Table1. Antibody Pairs for the Detection of Omicron Nucleon capsid.

Antibody pairs	Capture Ab	Detection Ab
Pair 1	40143-MM08	40143-MM05
Pair 2	40143-MM08	40143-R004
Pair 3	40143-R004	40143-R004
Pair 4	40568-MM162	40588-RA84
Pair 5	40143-R004	40588-MM124
Pair 6	40143-MM05	40588-R001

The Omicron virus is the most divergent mutation that has been observed in huge numbers during the corona pandemic. Various exchanges in the codon of spike protein have been cleared with increased transmissibility, immune escapes, and other behaviors [32-39].

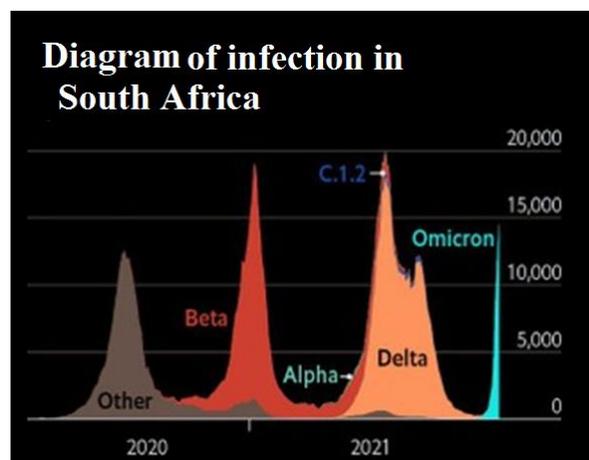


Figure 1. Omicron in South Africa.

Some variants previously described with related mutations in the spike proteins that were associated with vaccine sera. As Omicron has more S-gene mutations than other variants, large effects are expected. However, further biological investigations and vaccine effectiveness activities will have an index on vaccine effectiveness. The fast replacement of the Omicron by Delta in South Africa predicts that this virus is significantly more transmissible than the Delta variant in overall Covid-19 case numbers in South Africa (Figure 1) are currently is super spreading events by this variant. Moreover, the high detected growth rate might be because of immune escape. In addition, more information is needed to be able to provide a reliable estimate of the transmissibility of those variants. The past data from South African countries are shown unusual symptoms that have been associated with Omicron, and those are similar to other variants. Considering a lot of travel from the countries where cases have been reported, there is high probability of the further introduction of Omicron into the EU/EEA [38-42]. Although this variant has also been confirmed in travelers from Africa to Belgium, suggesting more widespread transmissions are already occurring. Given its immune escape potential and possible transmissibility advantage compared to other variants such as alpha, beta, and lambda, Omicron should have the capacity to spread faster once introduced to other countries, making the probability of spread high. If infections with the new variants are acquired, it is likely that at least a part of the population will experience severe disease [37-42]. Usual vaccines may also not be as effective for this new pandemic if partial or total immune escape from some vaccines. Also, there are insufficient data to assess whether existing treatment, such as monoclonal antibodies, will be effective in treatment. During RBD mutations in the spike protein of Omicron, immune escape potential from memory T cells is directed (Figure 2) [39-44].

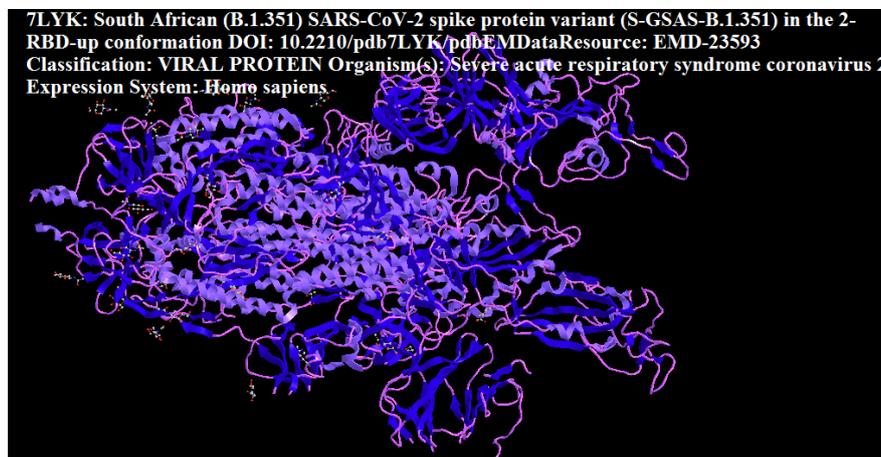


Figure 2. South African (B.1.351) SARS-CoV-2 spike protein variant.

Memory T cell might present a pathway to stable immunity that virus leads to spike protein mutations with escape pre-existing neutralizing antibodies. This phenomenon can be occurred either by offering more efficient activities from B cells responding to the CD4 T cells or via directly infected cells (CD8 T cells) (Figure 3) [45]. The present vaccines can be offered somewhat level of protection versus hospitalization and death, although *in vitro* activities evaluate both vaccines' neutralizing capacities. Public health responsibility should provide any urgent necessary to close immunity gaps in all adults and provide equitable coverage across countries and regions worldwide. National Immunization Technical Advisory centers in related countries should consider a booster dose for those 45 years of age and over, targeting the most vulnerable and the elderly first.

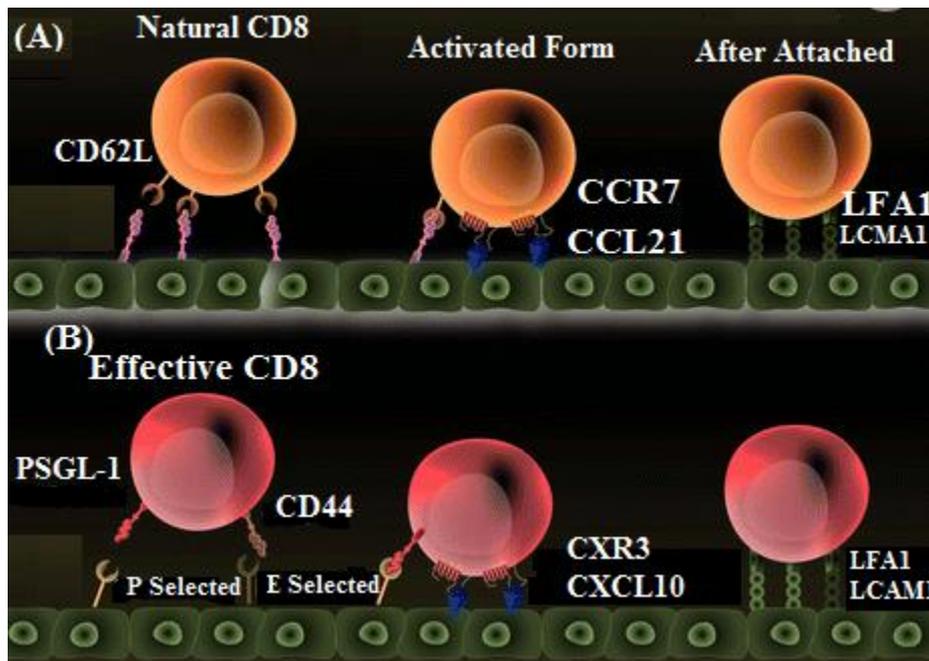


Figure 3. Natural and effector CD8-T-cells memory; (A) High endothelial; (B) Inflamed tissue.

Before the identification and emergence of Omicron, vaccinations were an important factor in reducing transmission, maintaining, or reintroducing pandemic events in countries with high risk [38]. The use of face masks, virtual working, and any modifications that reduce crowding on public transport can be helped to prevent the pandemic. It must be implemented immediately to increase protection against infection due to waning immunity, which could reduce transmission in the population and prevent additional hospitalizations and death.

2. Materials and Methods

2.1. Testing and sequencing.

Genomic surveillances are important to any fast detection of the presence and monitoring of epidemiological trends of this omicron variant. Providing important data to clear this new variant must include regular testing of representative samples and strengthening targeted sampling from persons coming from high-risk areas. African countries to rapidly antigen tests should be analyzed of the mutations in the nucleon capsid (N gene) of Omicron viruses, and sequencing of SARS-CoV-2 from wastewater (especially, analysis of wastewater from incoming flights) could be used as a complementary method.

There is evidence that the new omicron variant is transmitting in EU/EEA and Asian countries. Its global occurrence seems limited to a few countries (except south American countries due to the Amazon forest). Based on this evidence and several cases of this new pandemic in EU/EEA countries and some other Asian countries, strict travel restrictions are likely only to delay the impact of the novel variant in those countries. Limited terms may give the countries enough time to fight this new variant.

2.2. Prediction of any further dangerous mutations due to the Omicron variant.

Although Omicron Covid-19 death cases are less severe than Delta, Omicron will be an important base for the emergence of new further variants through huge mutations in the future; some of them are so dangerous. Using antibodies and vaccines is the last way to end the Covid-19 pandemic. However, potentially they provide a suitable substrate to over 6000

mutations, mostly on the spike (S) protein. It can be estimated that the number of coronavirus mutations is approximately around 300 000 genome isolates through genetic algorithms. To understand how mutations will impact vaccines and antibodies in development, the mechanism, frequency, and ratio of mutations on the S protein need to be defined. Moreover, a collection of 60 antibody structures have been analyzed to predict S protein's mutation-induced binding free energies through docking. Through genetic interactions, we exhibited that some mutations on the receptor-binding domain (RBD) are too stable, and others can break the binding of S protein and antibodies. We exhibited that most of the RBD mutations consist of those variants found in the South American and amazon zoon, South Africa, and equatorial districts. Their binding energies among the S proteins and ACE2 of the human angiotensin-converting enzyme have been evaluated, resulting in more infectious Covid-19 variants. Our results exhibit the urgent necessity to investigate the new mutation-resistant vaccines and antibodies and prepare for seasonal and Omicron vaccinations.

2.3. Mutations on the spike protein.

Mutagenesis is based on genetic information and serves as the main source for many types of genetic diseases. Generally, virus mutations are based on statistical selection and replication. Its mechanism for gene editing is under random genetic drift. Researchers' main goal is to understand how mutations can be able to change the corona structure and activities, therefore virulence and infectious is the main goal of researchers [45-50]. The quick spread of COVID-19 caused by the severe acute respiratory disease has led to 95,000,000 cases and 2,000,000 deaths. However, vaccines are of paramount importance and have a relatively more efficient and less time strategy to combat Covid-19 for their ongoing pandemic. The immune systems are a host defense center that prevents the human body from any microbes. As soon as the virus breaches the first cell layers, the immune system will be activated to identify pathogens via recognition receptors for macrophages [51-53]. Particularly, molecular patterns (PAMPs) located on pathogens introduce inflammatory reactions via various cytokines and chemokines. Another important way of defense is B or T lymphocytes (B cells or T cells) which are the main cellular pillars of the immune system [44]. These cells degrade unknown proteins through antigen mechanism; then, the peptide segments will be produced and destroyed by killer T cells. In Covid-19 patients, pathogens via binding to foreign antigens BCRs can help to recognize the antigens via antibodies to degrade whole peptides in B cells. T cells can recognize the signals and simulates more necessary signals to activate antibody-producing B cells.

Moreover, by entreating the antigen in human bodies, the T and B cells will be activated for changing the memory cells [54] as known memory T cells and memory B cells that quickly can be recognized and eliminate the foreigner antigen. Currently, several of the antibodies developed from patients' convalescent plasma for neutralizing SARS-CoV-2 and decreasing cytokine [55, 56]. Researchers aim is to produce an active production of antibodies based on the antigenic agent that resembles a disease-causing microorganism or genetic material. For coronavirus, the spike proteins are the main target that is based on three types of Covid-19 vaccine (Figure 4). From January 20, 2021, up to now, a total of 5000 unique mutations on the S protein have occurred. Among them, several mutations have occurred on the receptor, and it is notable that the RBD segment is the most interesting target for antibodies. Although among these vaccination methods, nucleic-acid vaccines are not dangerous compared to others, they have not been confirmed for any human use before by medical doctors. The big problem with

these kinds of vaccinations is the antibody characteristics, that the binding of a virus to unusual antibodies enhances its entry into cells [57].

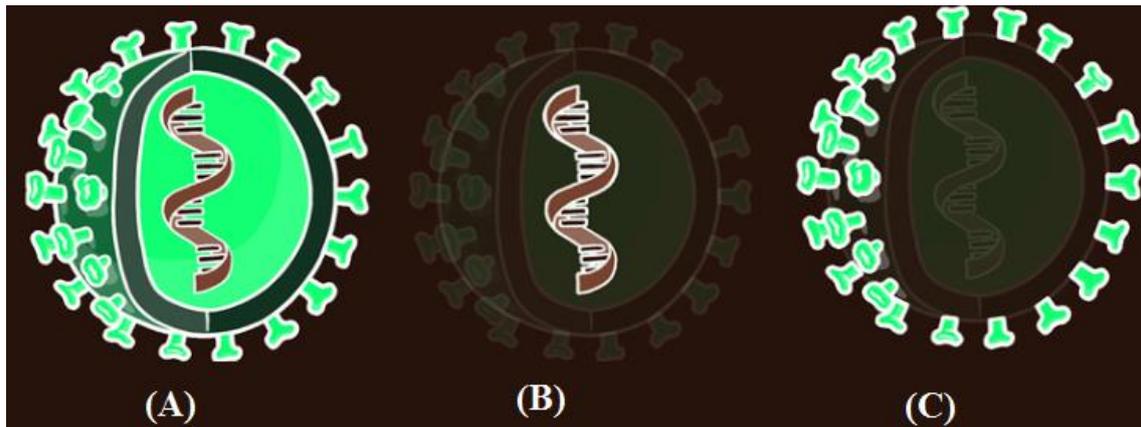


Figure 4. (A) using a whole virus; (B) Just the genetic material; (C): Parts that trigger the immune system.

The S protein of covid-19 has changed with many mutations, approximately 5000 mutations have been done, and 460 of them were detected on the RBD only [58, 59]. The effectiveness of any vaccine is related to several items, containing biological binding to the vaccine, mutations factors, dose and frequencies of vaccination, idiosyncratic response, and some human factors such as gender, genetic predisposition, and particularly climates. This also indicates a dangerous pandemic that will happen in the near future in equatorial countries such as Amazon and middle Africa based on omicron mutations. So, in this work, we use an interdisciplinary knowledge from the viewpoint of climates, social sciences, geography, jungle and wood industry, genetic analysis, and computational biophysics, including artificial intelligence and docking simulation.

2.4. Single Nucleotide Polymorphism (SNP).

In genetics, a single-nucleotide polymorphism (SNP) is replacing a single nucleotide base at a particular situation in the genome. SNPs in ACE-2 have been detected based on all related literature concerning genomic sequences "dbSNP" database in NCBI it has yielded more than 20,000 SNPs for the ACE2 gene. Then articles including information related to "COVID-19", based on geographies zoon 30 SNPs, were identified and rationally selected. Our work has shown the COVID-19 pandemic in viewpoint of SNP level that different allelic variants among geographic variation are associated with both case severity and allelic variation, especially in strains from Amazon and equatorial origins. Using a new alternative bioinformatics approach, we confirmed that the presence of the B.1.1.529 mutation correlates with increased case severity in a sample of 30 sequences from a shared geographic origin in the Amazon and equatorial regions [60].

Table 2. The distribution of 8 SNP types among many unique mutations and non-unique mutations on the S gene of SARS-CoV- 2 worldwide. N_U is the number of unique mutations, and R_{NU} indicates the ratios of these SNPs types among non-unique mutations (Reference [60] describes more details).

SNP type	Mutation type	N_U	R_{NU}
A > T	Transversion	454	1.12%
A > C	Transversion	341	0.55%
A > G	Transition	700	42.56%
T > A	Transversion	356	0.35%
T > C	Transition	779	4.13%
T > G	Transversion	277	0.41%

SNP type	Mutation type	N _U	R _{NU}
C > T	Transition	542	33.98%
C > A	Transversion	313	2.20%

Goyal *et al* [61], collected SARS-CoV-2 viral genome sequences using the Global Initiative on Sharing Avian Influenza Data (GISAID) database from 90,000 items and over 6400 cases containing patient status information [61]. Goyal *et al.* used BIONUMERICS SARS-CoV-2 plugin tool (bioMérieux, Applied Maths, Sint-Martens-Latem, Belgium) for processing and analyzing their genomic sequences. Next, each sequence was evaluated for SNPs discussion [61]. They exhibited that viral genome polymorphisms might affect case severity when other factors are controlled for. Still, it is important notable that this effect is swamped out by these other factors when comparing cases across different geographic regions [61]. Yong-Chan Kim *et al.* [62] extracted several cases of deaths of corona patients based on their ethnic groups. Detailed information on several countries' case fatality rates of COVID-19 was analyzed in Table 3 [62].

Table 3. Deaths of coronavirus disease in several ethnic groups [62].

Subject groups	Matching Groups in 1000 Genome Project	Case	Death	Case Fatality Rate (%)
African	African (AFR)	278815	5785	2.07
European	European (EUR)	2656437	196541	7.40
American	American (AMR)	4933972	241931	4.90
East Asian	East Asian (EAS)	104035	5620	5.40
South Asian	South Asian (SAS)	336933	5813	1.73

All statistical details were done by Yong-Chan Kim *et al.*, using SAS version 9.4 (SAS Institute Inc., Cary, NC, USA). Case fatality rates were accomplished as follows: case fatality rate (%) = (number of cases)/(number of deaths) × 100 [62]. They [62] evaluated corona's worldwide case fatality rates and genetic data on the IFITM3, ACE2, TMPRSS2, and IL6 genes. They accomplished log-linear regression analysis among those items and their allele frequencies of the IFITM3, ACE2, TMPRSS2, and IL6 genes in various ethnic groups. Several works have been done by Single-nucleotide polymorphism studies in different geographies, ages, and social conditions to find the relation between climates and corona diseases.

SNPs of ACE2 are a strong idea for finding the relation between disease and populations. ACE2 polymorphisms with severe acute respiratory syndrome resulted in important studies [63] other than recent reports on COVID-19. Via a software-based search, Chiu *et al.* [63] identified 103 SNPs in ACE2, which included 2 codings (rs4646116, rs4646179). Thus, no associations were detected between genetic variants and SARS susceptibility. The effect of novel coronavirus disease (COVID-19) varies significantly among different countries and continents, and so far, there has been no clear explanation for this observation, Anis Abobaker and coworkers said [64].

2.5. Evaluating expression of ACE2 Variants based on geography.

Severe acute respiratory syndrome Covid-19 follows host-cell angiotensin-converting ACE2 enzyme for cell entry. An accurate analysis of ACE2 can predict several single SNPs specific to different populations in equatorial zones and geographies. MD simulations have exhibited that several SNPs might be affected by interactions among enzymes- 2 (ACE2), so preparing an accurate definition for the regional differences observed in this infectivity is needed. Although the importance of specific ACE2 SNPs is unknown, there are no studies on in vitro validation, and accurate analysis of the various SNPs must be found in these specific

populations on receptor binding. The S1 subunit of spike protein recognizes the ACE2 receptors to facilitate viral binding to the cell, requiring S priming by cellular proteases. This mechanism permits the S2 to fusion event between the viral and cellular membrane to release the viral nucleoprotein complex [65]. However, mounting data shows that there are differences in the deaths among various countries [66-70].

This effect is due to host genetic differences affecting Covid-19 infectivity and mortality among different populations. To answer this subject, various geographies have investigated SNPs in the coding region of ACE2 to identify SNPs prevalent in particular populations to determine their ability to impact ACE2 binding of Covid-19. Calcagnile *et al.* reported "S19P" SNP common in African populations and "K26R" SNP common in European populations might change the attaching ability of ACE2 toward Covid-19 [71]. Li *et al.*, by MD calculation, exhibited surprising information concerning K26R and I468V that are SNP in East Asia, where decrease the binding affinity to ACE2[72].

So, studies for determining the contributions of population-specific SNPs of ACE2 are too important in geographies and ecologies or forest knowledge. They selected 3 more SNPs for more tests, including S19P, K26R, and N720D [71-73]; these 3 SNPs are usual in American and European zones. They used PCR-based mutagenesis to generate the plasmids expressing ACE2 types with a C-terminus.

3. Discussion

3.1. Comparing COVID-19 and deaths in East Asia with the USA and Europe.

The amazing low rate of COVID-19 deaths in East Asia compared with those in western countries are due to SNPs specific to East Asian people negatively affecting the ACE2-related pandemic with this disease.

Since the low COVID-19 morbidity in this area, the Genome database must be identified the related SNPs, causing amino acid changes at the spike protein [71, 72]. Therefore, Hashizume and coworkers looked at 5 SNPs from the East Asian or Japanese people who have a maximum dependent on related alleles frequencies of >0.1% or >0.001 (not in American or European) (Table 4). Consequently, 3 SNPs are not found in East Asian people [73].

Table 4. ACE2 SNPs in the different zone [73], Upper row, data from gnomAD; lower row, data from the 1000 Genomes database.

SNPs	Allele frequencies				
	East Asian	Japanese	American	European	African
V184a	-	0.0015	0	0	-
S257N	- 0.0013	-	0	0	0
I468V	0.0139 0.0026	0.0035	0	0	0
N638S	0.004 0.0026	-	0	0	0
L656X	- 0.0013	-	0	0	0
S19P	0	-	0	0	0.0031 0.003
K26R	0	-	0.0016 0	0.0056 0.0052	0.0009 0.002
N720D	0	-	0.0032 0.0038	0.0208 0.0183	0.0019 0

The S19P and K26R SNPs, affect ACE2 affinity toward SARS-2-S, and the third one, N720D is anticipated to have a small impact on SARS-2-S binding [71-73]. The amino acid situations are also important for binding to SARS-2-S, as shown in Figure 5, ACE2 variant with the L656X mutation [74, 75].

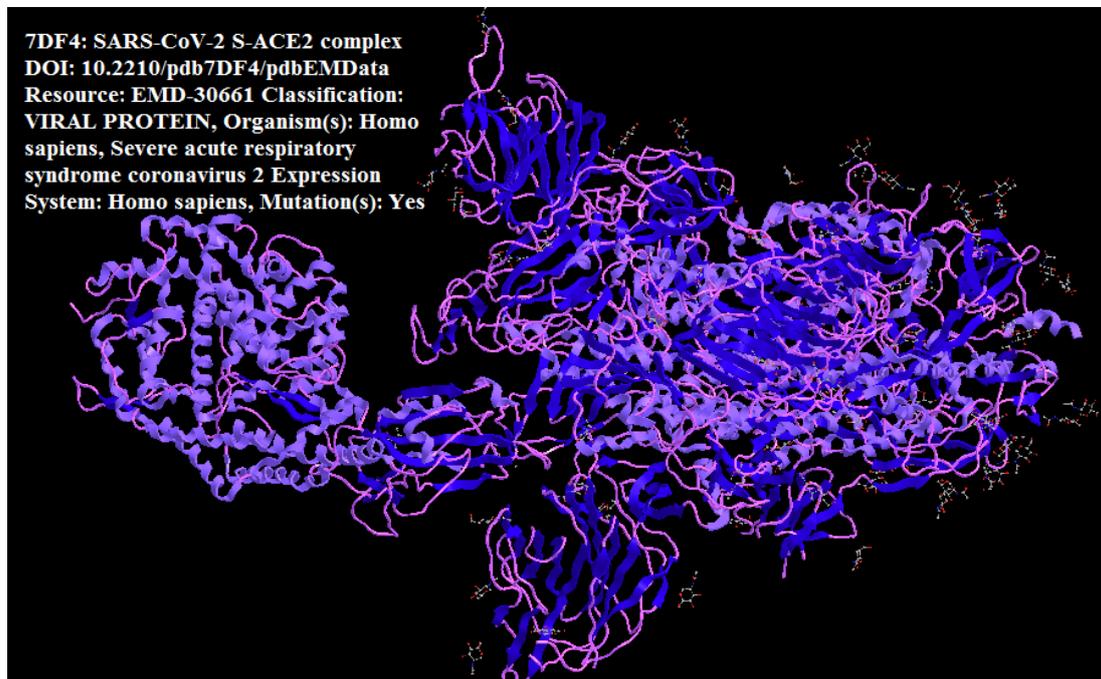


Figure 5. Conformational dynamics of SARS-CoV-2 trimeric spike glycoprotein in complex with receptor ACE2.

Although these SNPs are not in the amino acid residues critical, MD simulations have confirmed that some of those SNPs potentially affect the affinities of ACE2 toward Covid-19. The D614G mutation is currently found in most SARS-CoV-2 worldwide diseases and the cells expressing the ACE2 variants. Up to now, no D614G was observed with binding to the L656X expression plasmid [76].

Vaccination is the most effective and economical way of controlling pandemics. Around 250 vaccines in various medicinal centers have been applied up to now. This makes positive changes strengthen appear for binding. Generally, there are four versions of the Covid-19 vaccine worldwide consisting of (1)-virus vaccines, (2)- viral-vector vaccines, (3)- nucleic acid vaccines, and (4)- protein-based vaccines [77].

4. Conclusions

The coronavirus disease pandemic has gone out of control globally. There is no special medicine or effective treatment for this viral infection at present.

The emergence of the Omicron variant raises serious concerns because of the initial observation of a significant growth advantage and potential immune escape compared to the Delta, lambda, beta, and gamma variants. Therefore, interdisciplinary research, including in viewpoint of climates, social sciences, environmental sciences, geography, forestry and forest industry, genetic analysis, and computational biophysics, including artificial intelligence and docking simulation, is needed for any further activities.

In addition, deforestation rates have soared across the globe, driven extremely by agriculture and logging. This has effects on forest wildlife, but it could also accelerate climate change, consequently making an increase in the impact of the spread of Covid-19 disease.

Various animals are known as natural reservoirs of pathogens. Therefore, contamination processes among humans and animals have complex ecologies and mechanics. An important goal is not to allow animals, plants, insects, soils, and microbes to appear together with humans in the composition of the society.

Due to the wet climate, the Amazon jungle/forest is a suitable substrate for emerging any further corona variants. So, the researchers for fighting by corona must use interdisciplinary knowledge in viewpoints of climates, social sciences, environmental sciences, geography, forestry and forest industry, genetic analysis, and computational biophysics, including artificial intelligence and docking simulation.

Moreover, this pandemic has completely changed the importance of urban and forests due to decreasing the international travel restriction. In many urban places, the residents to avoid Covid-19 infection hot-spots are flooding into rural areas, consequently putting a lot of pressure on ecosystem services. Therefore, Wildlife parks and other centers such as Kilimanjaro National Park must be closed temporally (Scheme 1).

Using a new alternative bioinformatics approach, we confirmed that the presence of the B.1.1.529 mutation correlates with increased case severity in a sample of 30 sequences from a shared geographic origin in the Amazon and equatorial regions (Scheme 1).

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Conflicts of Interest

The authors declare no conflict of interest.

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