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Adaptive evolutionary analyses of the COVID-19 pandemic in twelve most affected countries

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Abstract

Viruses are detrimental to the population from time to time. Nevertheless, COVID-19 is the recent pandemic that affects almost all the countries of the world. September 2021, more than 4.5 million deaths are registered in the world as per latest report by the World Health Organization. The origin of coronavirus from animals has been discussed in this study. Twelve different SARSCoV-II genomes against five Middle East Respiratory Syndromes (MERS) genomes have been analyzed. In *silico* approaches have been utilized to analyze the phylogenetic history of SARS-CoV-II from different countries. The genomes of many countries are closely associated with the phylogenetic analysis. The results indicate twelve complete genome studies of representative SARS CoVs, MERS CoVs, and human SARS CoV-II, the genome was found to be the most comparable to the recent novel human SARS CoV-II genomes.

Introduction

A worldwide human disease includes exposures to viral airways [1]. The environment is considered as the most dangerous disease in most young, elderly, and established populations [2, 3]. In most communities, the factors of concern and life-saving are important [4]. In late 1930s, researchers discovered that viruses could cause airway infections [5]. A large variety of recent infections, in particular in neonates and infant respiratory tracts, were identified by modern, limited instruments at the beginning of the 20th century [6]. Multiple corona infections are the only genital diseases agent in growing forms of respiratory infections for humans and animals. The seventh coronavirus in COVID-19 including primates and dogs has been identified [7]. SARS and MERS are considered as the most dangerous viruses that affect the world. SARS also led to a significant number of deaths and inflamed human mortality in southern China, and MERS has suggested the change from the Middle East to Saudi Arabia [8, 9].

HCoV-229E (HCoV) [9] is a form of a bat and human coronavirus [10]. It is a strongly bound, strong, cohesive RNA virus that reaches to its host through APN receiver [11, 12]. A common HCoV-229E Cold Virus has moderate outcomes to significant morbidity, including pneumonia and bronchipelago. It also includes human coronavirus OC-43 (beta coronavirus genus). Nevertheless, these elevated morbidity findings are almost observed by the single-species pathogens co-infection. HCoV-NL63 belongs to class alpha coronavirus. The associated symptoms of coronaviruses include moderate to dramatically elevated respiratory tumors, respiratory tract contraction, croups, and bronchiolitis [12], elderly and immune-compromised patients frequently undergo acute respiratory exposure [13]. The coronavirus [10, 14] OC-43 is a member of the Original Coronavirus family, infecting humans and wildlife. An endogenous coronavirus is an enveloped RNA virus [13, 15, 16]. Human coronavirus HKU-1 (HCoV-HKU1) was described as a coronavirus of mice born. A respiratory illness takes place in people with signs of severe cold, tuberculosis, and bronchiolitis depression. It is a single-stranded RNA virus enveloped in the incredibly mild sensation by binding the host cell. The Middle East Air Respiratory Influenza, commonly identified as the MERS-CoV (MERS-CoV), is a Camel Flu [15, 17] having symptoms including diarrhea, cough, vomiting, and short-breath. The disease is usually more severe in individuals with serious health issues. MERS-CoV is the original conception of bats coronavirus.

Coronaviruses are massive, circular, and have cones. The width of corona viruses is about 85 mm and the thickness is around 20 nm [18]. The virus has a cover of thin shells [19, 20].

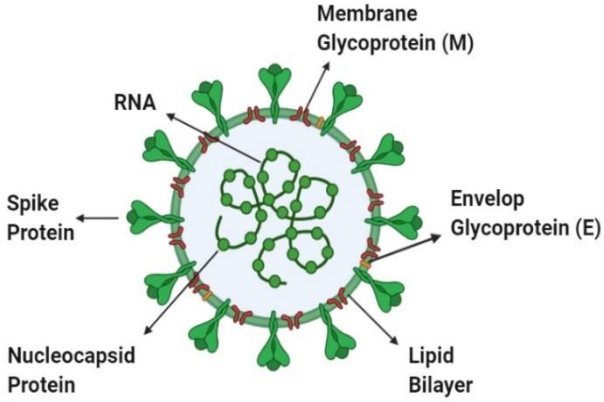

Fig. 1: Coronavirus Structure [20, 21]

The two-layered lipids include endogenous membrane (M), envelope (E), and Spike (S) [21] are present in the structure of coronavirus (**Fig. 1**). The primary pulse is RBD S1 (Receiver) and sub-unit S2 is the tree that connects the S in the viral envelope. E and M proteins are important for the development of the viral surroundings and the preservation of structural integrity [21].

The study of the evolutionary connection between animal host sources and SARS CoV-II has been a key focus in the majority of affected nations where SARS CoV-II has spread. Previous attempts to find the origins of SARS-CoV- II animal have used various strategies however could not explore completely. Before reporting the findings on the most affected countries, the first recent ecological changes in this region has been analyzed that favors the emergence of new zoonotic illnesses. Countries are focused on the containment and control of COVID-19 through developing specific legal frame work which has become necessary in the current circumstances [22]. Modern technologies i.e Artificial Intelligence and Big Data techniques are also increasingly being used to combat COVID-19 [23]. To emphasize the need of interdisciplinary collaboration in the battle against COVID-19, vaccination and social isolation were used. SARS and MERS are discussed in detail, including symptoms and biological characteristics such as COVID-19.

Materials and Methods

Sequence Retrieval

For the present study, twelve complete genomes of COVID-19 were retrieved from NCBI. For further analysis, five MERS-CoV sequences were retrieved from NCBI [8, 9]. The studies only looked at whole genome sequences with no nucleotide composition uncertainty [5].

Multiple Sequence Alignment

The Multiple Sequence Alignment (MSA) has been performed for the selected genome sequences by using Clustal Omega. Multiple sequence alignment was carried out on the whole genomes of 12 selected coronaviruses. In FASTA format, all sequences (nucleotides) are input into the MSA [13].

Mutations and Phylogenetic Analysis

A significant part of the genome is covered (>29 000 nt). NCBI database was used to find SARS-CoV-2 sequences were retrieved through NCBI [23]. A total of 12 sequences were utilized for future research and to assess the phylogeny and molecular epidemiology of the viral variants. 12 sequences were aligned by using Clustal Omega and phylogenetic tree was generated through MEGA X [10, 14].

Results and Discussion

The 12 complete genomes of COVID-19 from different countries were analyzed to reveal the similarities in the genomes of different regions.

The variations in the sequence of selected genomes were analyzed to explore the insignificance in the likelihood of several polymorphisms occurring in isolated mutations (**Table 1**). 12 genomes of COVID-19 were used to extract the nucleotides and 29000 locals were considered as the threshold. In such regions, the null hypothesis was that at each site, at a random point, the nucleotides are mutating in an individual consensus series and the mutation prevalence was determined by the fraction of the positions in the various genomes. The consensus sequences led to the conserved nucleotides in increasing position. A null theory was also evaluated and mutations occured at various sites were analyzed by distinct positions (**Fig. 2**). The vector norm was utilized to determine the substitution amount of data.

Using the Neighbor-Joining process, evolutionary history was inferred. The maximal tree will be seen with the branch length number of = 26.83493485. The proportion of repeated trees in which in the bootstrap test (500 replicates), the related taxa are grouped is shown next to the divisions. With branch lengths in the same units as those of the developmental distances used to conclude the phylogenetic tree, the tree is drawn to size (**Fig. 3**). The evolutionary distances have been determined using the Maximum Cumulative Probability process and are the number of base substitutions in units per position. This research discovered 16 nucleotide sequences. For each pair of sequences, all ambiguous locations have been deleted for (pairwise deletion option). There were a total of 29903 positions in the final dataset. Evolutionary tests were conducted in MEGA X. The genomes of India, Pakistan, Iran, and France have a close relationship and have the same origin as well.

The COVID-19 genome is intertwined with the genomes extracted from India (MT740436) and Saudi Arabia (MT740436). The genomes of COVID-19 from India, Iran, and Egypt, were observed similar. Furthermore, the genomes from Spain and Chile were also similar however the genome from Italy was similar to both the genomes. The COVID-19 genome is found in Italy to be closely linked to the COVID-19 genome in the US for further developmental analysis. Bangladesh, France, Italy, Spain, and China have strong connections to the United States (**Fig. 4**). The evolutionary relationship of of the selected 12 COVID-19 genomes were also analyzed against the 5 MERS genomes. According to this evolutionary analyses, it was observed that the MERS was strongly related to COVID-19 in the USA and UAE. It was also observed that the MERS genome has a clear connection with the COVID-19 genome.

Table 1: Detail of 12 genomes of COVID-19 with accession no. and country name as well as with sequence retrieved from NCBI and NCBI virus with respect to most effected countries

Genomes of COVID-19 retrieved from NCBI				
Sr #	**Accession No**	**Length**	**Location**	**Collection Date**
1	MT500122	29819	Pakistan: Karachi	3/16/2020
2	MT740436	29800	India: Gandhinagar	6/11/2020
3	MT447177	29793	Iran	3/26/2020
4	MT740381	29903	Bangladesh	6/18/2020
5	MT630421	29879	Saudi Arabia Jeddah	3/15/2020
6	MT624728	29846	Egypt	6/2/2020
7	MT709104	29782	Germany: Dusseldorf	3/20/2020
8	MT682732	29860	Italy	4/20/2020
9	MT709104	29838	France	5/14/2020
10	MT655131	29851	Spain	3/25/2020
11	MT739425	29889	USA: Virginia	1/03/2020
12	MT039874	29858	China	3/14/2020

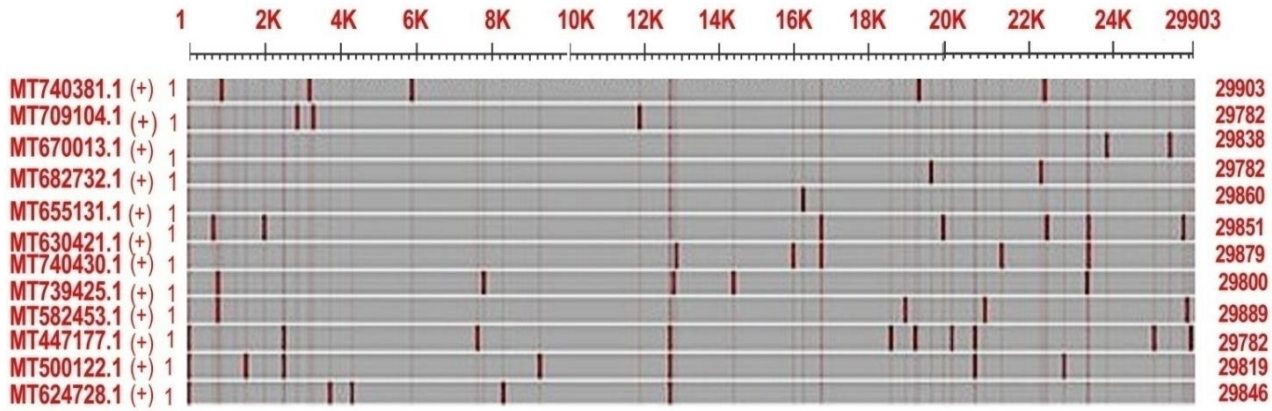

Fig. 2: Dark and light bands horizontally to show similarities and differences between the sequences of 12 genomes of COVID-19 retrieved from NCBI and NCBI virus.

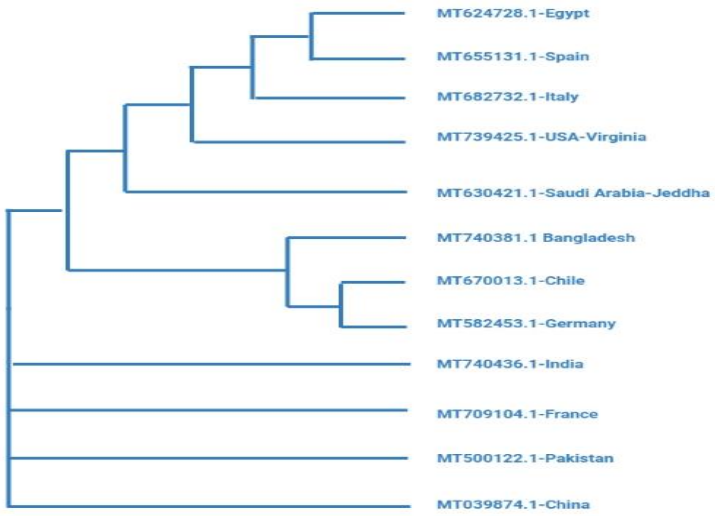

Fig. 3: Evolutionary relationship of 12 Genomes obtained from different countries. MT500122: Pakistan: Karachi, MT740436-29800: India, Gandhinagar, MT447177: Iran, MT740381: Bangladesh, MT630421: Saudi Arabia: Jeddah. Using the Neighbor-Joining process, evolutionary history was inferred. The maximal tree will be seen with the branch length number of = 26.83493485.

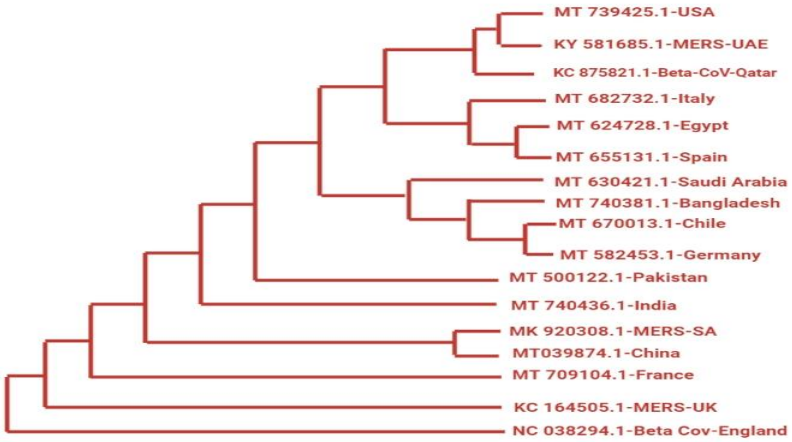

Fig. 4: Evolutionary relationship of COVID-19 with SARS and MERS.

Using the Neighbor-Joining process, evolutionary history was inferred. The maximal tree will be seen with the branch length number of = 26.83493485. The proportion of repeated trees in which in the bootstrap test (500 replicates), the related taxa are grouped is shown next to the divisions. With branch lengths in the same units as those of the developmental distances used to conclude the phylogenetic tree, the tree is drawn to size. The evolutionary distances have been determined using the Maximum Cumulative Probability process and are the number of base substitutions in units per position. This research discovered 16 nucleotide sequences. For each pair of sequences, all ambiguous locations have been deleted for (pairwise deletion option). There were a total of 30123 positions in the final dataset. Evolutionary tests were conducted in MEGA X. NC038294.1 is a MERS genome that has a close relationship with KC164505.1 which is also a MERS genome. MT 447177.1 is a COVID-19 genome, has a close relationship with MERS genome MK 920308.1.

The study revealed that the COVID-19 demonstrates a discordant clustering of the Bat SARS-like coronavirus sequences and showed close relationship to the Bat SARS genome. Nevertheless, the genome from Saudi Arabia still has similarities with the genome of COVID-19 in Iran. A single cluster identified that the SARS-like sequences of coronavirus has half spike regions in the MERS. Consisting of nearly half of the genome with a separate subset of betacoronavirus. Such genomic characteristics and their possible interaction with the phenotype and virulence of the human virus require more study. In Asia, Europe, Africa, North America, South America, and Australasia, beta CoVs, and alpha CoVs were commonly found in cats [13, 24]. Besides, alpha CoVs tends to be more common than beta CoVs. The incidence of alpha CoVs was around twice the incidence of beta CoVs in bats in Hong Kong (**Fig. 6**). From the species level 2019, bat CoV epidemic dynamics may be identified [25].

Three big CoV outbreaks in the past 15 years involved SARS-CoV, MERS-CoV, and SARS-CoV for the MERS-CoV [26], which also has a very recent human source, fleas which were believed to be the cause of SARS-CoV and COVID-19 [28]. In the last 15 years, there were three significant CoV outbreaks. Curiously, it was discovered in bats, especially *Rhinolophus affinis* and *Rhinolophus sinicus* both SARS-CoV and SADS-CoV [29]. The epidemic was found in South-East China, with a broad range of bats (**Fig. 5**) (*Rhinolophus sinicus* and *Rhinolophus affinis*), particularly of horseshoe bats. It means that through the distribution of the various bat communities the next CoV outbreak is predicted globally. Human beings may also be suitable for the four HCoVs in a specific angle. They may be wounded by pandemics [30, 31]. The four HCoVs which trigger mild symptoms are mutually adverse to humans.

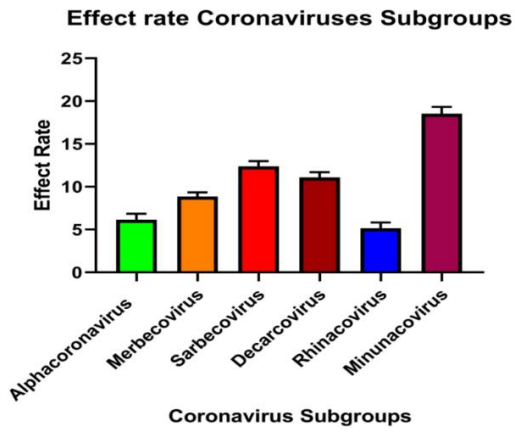

Fig. 5: Chart for each Bat CoV sub-gender, a fairly large detection rate of the common bat CoVs is identified in Hong Kong from 2008 to 2017 from different sub gender alphacoronavirus and betacoronavirus. Some potential zoonotic transmission routes for each Bat CoV sub-gender detected are provided [26, 27].

HCoV-NL63 and HCoV-229E may, according to phylogenetes, be used to classify rodents in conjunction with HCoV-OC43 and HCoV-HCU1 from bat vectors [33, 34]. Bat CoV identified as ARCoV-2, in the North American tricolor specimen, is closely balanced by the HCoV-NL63 [35]. The genetically modified CoV bat reported in Ghana is connected to a host Hipposidero. The chart below demonstrates how well-known HCoVs are perceived from animal sources. To justify it [36] HCoVs that induce harmful diseases have been removed for humans and animals who have acquired serious HCoV anomalies. For humans, the HCoVs will raise significantly to produce adaptive mutations that concur with host restriction factors [37]. The more involved and accessible SARS-CoV-2 outbreaks, the more likely it would be to be completely human-oriented. The four acquired CoVs in the population lives and cause cold inhuman conditions in immunochemical individuals. When completely integrated, isolation or other contamination control strategies may find it impossible to protect their spread to humans. No animal environment is required for these viruses.

SARS-CoV and MERS-CoVs by comparison, are viruses that cannot be tailored easily to people that are discouraged from introducing them to humans. To order to inject one or more of the intermediates onto prone individuals, we must be separated from their zoonotic environments. Both SARS-CoV-2 functions, both of which were acquired into four classes, are SARS-CoV / MARS-CoV and HCoV. For thousands of years, the coronaviruses (viruses) and their offspring, like humans, develop and alter.

The population's HCoV is highly transmissible. Human CoVs (HCoVs) were reported for mild disease until 2003, but not extreme freezing. SARS and Middle East ARS reject the coin as to the likelihood of life-threatening or harmful contact. [38]. The HCoV-229E, HCoV-OC43, HCoVNL63, and HCoV-HKU1 zoonotic injection tests were performed in addition to the comparatively pathogenic HCoV, high ARS significant respiratory syndrome [39].

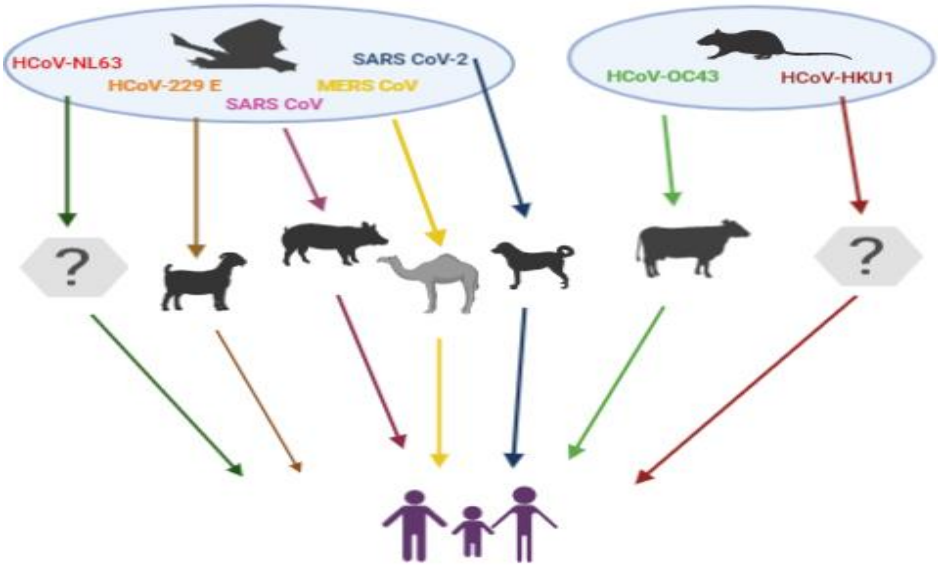

Fig. 6: Types of coronaviruses with their intermediate species. After all, this diagram is pangolin and livestock from humans (SARS-CoV, HCoV transmission in Black, Blue, Purple, Orange, Yellow, brown and dark blue, HCoV-NL63, HCoV-229E, SARS-CoV switch, SARS-CoV sticks, HCoV-OC43, and HCoV-HKU2). Intermediate host(s) are given for HCoV-NL63 and HCoV-HKU [32].

Conclusion

The COVID-19 arises from bats according to genetic studies. The genomes of many countries are closely associated with the above phylogenetic analysis. Besides, this work is applied to a mixture of SARS, MERS, and COVID-19. They are both familiar and of the same roots as COVID-19. Our phylogenetic results indicate that bats were responsible for the epidemic. The effects of the systemic analogical models often propose an alternate intermediate host for coronavirus transmission to human hosts. Further research should also be stressed about the production of spike glycoprotein. The ongoing propagation of COVID-19 can be impacted by this analysis and future outbreaks of zoonotic conditions may be avoided.

Future Perspective

Many groups have been investigating animal CoVs since the discovery of SRAS-CoV, to understand their zoonotic capacity. Checking them is the target. The broad range of bat CoVs and the genetic process to boost genomic separation raise the risk of organism-by-organism transmission. Agreed, the introduction of 2019-nCoV emphasizes that bats are a source for infecting novel humans but also an ideal paradigm for preparing studies and strategies through which potential zoonotic agents are removed. To examine viral advances and pass those to natural hosts, it is also important to step up the effort to classify the virus into many species. The synthesis of the new technologies with traditional virological approaches for viral models for molecular/bioinformatics can include

knowledge about how to prevent dangerous outbursts. In particular, it would help to plan specific surveillance systems to track outbreaks whenever they appear in the context of forecasting distribution between species. Finally, it is necessary to establish vaccination channels since vaccines are the best way to eliminate the spread of the disease. To this point, the identification of new viruses by vaccination can be improved if synthetic biology methods are conveniently sequenced by viral genomes. It must still be remembered that although viral isolation and technological advances can allow the easy and in-vivo use of preventive or treatments. Also essential are evaluation and deployment, which will take time. It is also necessary to engage effectively around the world in control initiatives and to strengthen collaboration on a global preventive and response system for emerging infectious diseases.

Conflict of interest

The authors declare no conflict of interest.

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