

An Updated Literature Based Analysis on the Genetic Aspects of Coronavirus (COVID19) and its Connection with the Viral Genome

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ABSTRACT

World Health Organization has declared in 2020 “coronavirus 2019” (COVID-2019 or 2019-nCoV or SARS-CoV-2 or CoV) as a global endemic. A recent respiratory disease produced by a novel coronavirus was born in Wuhan city of China in late December 2019. CoV is connected with a large family of viruses commonly found in cat, camel, cattle and bats. Severe acute respiratory syndrome (SARS) virus is genetically interrelated with COVID 19 strains which infect bats. MERS-CoV, SARS-CoV and SARS-CoV-2 are affected by humans from the animals. The COVID 19 is known to be the human-to-human transmission. Presently, there is no medication for COVID19, and this disease has been inherited to another global country. Pharma companies will have a major role when genomic medicine goes at the mainstream, and presently, there is no medication for COVID 19. However, genome sequencing analysis can help to design medication (Rx) by pharmacists. The genome sequencing can be identified by the next-generation sequencing (NGS) in the whole viral genome. The advantage of NGS is to identify the disease-causing or novel variants in the human genome. Limited global studies have sequenced the human genome and confirm ~88% of the human genome is similar to the Bats sequence in an effected person of COVID 19. This review will be connected to the pharma companies in designing the Rx for COVID 19. Thus, NGS analysis can be helpful for the pharma companies for scheming medications.

INTRODUCTION

Human Coronaviruses are mostly 4 types (HCoV-OC43, 229E, NL63 and HKU1) as categorized with International committee for the Taxonomy of viruses (Lefkowitz et al. 2018; Zu et al. 2020). One of the types of pneumonia occurred in 2019 novel coronavirus disease (COVID-19) is recognized to be highly infectious disease; declared by World Health Organization (WHO) as a global public

health emergency (Chen et al. 2020). Several recent reviews since then have appeared in literature describing various aspects of the effects of the global pandemic such as biological, economical, social and psychological, (Gralinski and Menachery, (2020) and Miraj and Miraj 2020).

Coronaviruses (CoV) belongs to one of the large family group of viruses that cause starting from illness to common cold which is similarity for Middle-east respiratory syndrome (MERS) and severe acute respiratory syndrome (SARS)-CoV, (Situational Report 2020). Coronavirus-2019 is known to be 2019 novel coronavirus outbreak, illness is termed as COVID-19, and virus is known to be SARS-CoV-2 or 2019-nCoV (Kim 2020). Right now, both WHO and centers for disease controls are monitoring the CoV disease (Lu et al. 2020). Presently, CoV disease is hugely expanding in China and its premises (Sun et al. 2020).

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CoV are documented as zoonotic; which indicates as the disease CoV has been transmitted from animals to people, (Gralinski and Menachery 2020).

CoV are termed as crown-like spikes on their surface; categorized as alpha, beta, gamma and delta sub-types. Between the 1960's, CoV was identified in humans and 229E (α -CoV), NL63 (β -CoV), OC43 (γ -CoV), (δ -CoV), MERS-CoV, SARS-CoV and SARS-CoV2 viruses can infect. Global people are currently affected with α , β , γ and δ Coronaviruses (Xu et al. 2020). Appearance of common signs is cough, fever, shortness of breath, respiratory symptoms and breathing difficulties; amongst the rare cases, SARS, pneumonia, damage of kidney and at last death may also occur (Shanker et al. 2020).

Initially, CoV or COVID-19 is documented in Wuhan city at China in 2019 and is suspected as this disease may be allied with seafood market in Wuhan city. CoV possibly appeared initially from animal source but it seems now, it is dispersion from one affected person to another one (Albarello et al. 2020; Sohrabi et al. 2020a). COVID-19 is presently considered as more attention because it has been documented as novel virus; which was not documented earlier in the humans (Zhu et al. 2020). CoV is a respiratory viruses and others are influence; whereas, COVID-19 is not confirmed till now as droplet or air-borne transmission virus. Subsequently, diagnostic tests have been improved for CoV patients and applied these tests in the suspected cases in the worldwide, (WHO 2020).

Bats are whispered to be familial hosts of α and β CoV and for also SARS and MERS CoV(s) (Anthony et al. 2017). (Lam et al. 2020) studies report the confirmation of COVID 19 associated with CoV in Malayan Pangolins seized in anti-smuggling operations in south region of China. Metagenomic sequencing of pangolins confirms the two-sub lineage sequence in CoV associated with COVID19. Presently, COVID 19 is spreading globally 160 countries and showing no symptoms of slowing down. Worldwide, 2.5 million cases have been registered; USA has 0.8 million; the maximum registered cases in the globe, followed by Spain, Italy, France, Germany, UK, Turkey, Iran and 82,758 COVID cases has been confirmed and in China, till now >77,123 cases were recovered with COVID19 and >4600 deaths occurred whereas the rest of the world has registered 170044 deaths as of 21st April 2020, (WHO, 2020).

In South Korea 10,683 cases have been confirmed. Corona viruses are the largest RNA viruses that infect animals and humans in respiratory and enteric diseases. CoV causes almost one-third of common colds and the newly recognized SARS. Epidemiology of CoV in people harbors anti-corona virus antibodies; however, reinfection is documented as numerous circulating serotypes of viruses are present in the human population, (Sohrabi et al. 2020b). The pathogenesis of CoV is caused due to respiratory and enteric diseases in various animals. In humans, virus replication in the epithelial cells of the respiratory tract and one-third of colds are

affected with CoV. The symptoms of CoV are sore throat, running nose, headache, cough, high grade fever, chills and the incubation period is for 72 hours. The spread of the viral is due to immune response with short life-span. Transmission is done through the transfer of nasal secretions in aerosols caused due to sneezes, (Cascella et al. 2020).

Viruses that infect epithelial cells of the enteric tract causes diarrhea. The infections for CoV are undiagnosed with self-limited diseases. The diagnosis can be confirmed through immuno-electron microscopy and serology. There are no routine anti-viral CoV infections. Severe acute respiratory syndrome (SARS) was documented in 2002 at Southern China, which was also reported in Africa, Asia, Europe and North America. The SARS CoV causes severe respiratory disease and an average incubation period is minimum of 14 days, (Lauer et al. 2020).

The common symptoms involve fever (>380C), malaise, chills, headache, dizziness, sore throat, cough and shortness of breath. The laboratory diagnosis for SARS are based on antigen as well as detection of nucleic acid. The antigen is perceived through Enzyme Linked Immuno Sorbent Assay (Elisa) tests with the high-quality of antiserum. Enteric CoV can be diagnosed using electron microscopy with the stool sample. Polymerase chain reaction (PCR) assays are useful to distinguish CoV nucleic acid in respiratory secretions and in stool samples. The RNA of SARS viruses was seen in plasma through PCR and it is difficult to observe human CoV with cell-culture technique. The SARS viruses are recovered from oropharyngeal specimens through kidney cells in Vero monkeys. Serology, Elisa and hemagglutination tests can also be used for the confirmation of SARS. Currently, there is no treatment for SARS; however, symptoms can be managed and drugs are under progress, (Ahmad et al. 2020; Al-Ahmadi et al. 2020; Albarello et al. 2020; Cleemput et al. 2020; Gallego et al. 2020; Huang et al. 2020; Sohrabi et al. 2020a; Yang et al. 2020). However, numerous vaccine trails have been implemented and none of the vaccines are available till now for COVID19. One of the complications with live virus vaccine is antigenic shift and unpredictable outcomes.

Sequencing analysis: CoV have RNA sequence with huge genomic structures through high error in repetition when equated with host genomics. Numerous coronaviruses can do effective recombination of their genomes after infecting host cells (Luo et al. 2018). Genome sequencing of pathogens is always critical for developing specific diagnostic tests and the identification of potential treatment options (Ma et al. 2019). Sequencing of viral genome, huge sample size with hundreds and thousands of genomes are required to analyze numerous phenomena in which genetics plays a role (Harris et al. 2008). High throughput or next-generation sequencing technique is known as powerful for identifying the disease causing or novel variants for human as well as viral genome sequences (Bogari 2016; Bogari et al. 2020).

Next-generation sequencing (NGS) has driven the research space and is insightful clinical applications with enormous impact. NGS technique can be used for DNA, RNA or methylation sequencing for large-scale genomic and transcriptomic sequencing because of the high-throughput production and outputs of sequencing data. NGS is lowered to cost compared with the traditional first-generation sequencing (FGS) or DNA-Sanger method. One of the differences between first and second-generation sequencing techniques are, FGS can screen the limited variants; whereas, second-generations sequencing (SGS) can be enormously high-throughput from several samples at lower cost (Kulski and Challenges 2016). Based on large sample size, it will be beneficial for detecting the large number of mutations through RNA sequence in the viral genome and will be useful in tracking the spread of COVID19. It is very important to screen towards phenotype for the spreading of viruses (Zhang and Holmes 2020).

The comprehensive diagnostic ability of NGS in documenting pathogens of unknown etiology during specific infections (Schilcher et al. 2019). Genome data is useful in understanding the transmission dynamics for expansion of rapid diagnosis (Cleemput et al. 2020). SGS data is very useful in diagnosis in confirming the rare or novel variants and which may be associate with the human disease. Currently, it is important to identify the basis of its replication, structure, and pathogenicity for discovering a way to the special treatment or the prevention (Mousavizadeh and Ghasemi 2020).

CoV and SGS studies: Lu et al (Lu et al. 2020) have documented 10 genome sequences of COVID19 NGS data which was attained from 9 patients. The COVID19 sequence was found to be similar with 88% in bat resulting from SARS like CoV (bats; SL-CoVZC45 and SL-CoVZXC21). Joyjinda et al (2019) initially studied the human coronavirus (HCoV) in 2004 from Hongkong population and its diagnosis was confirmed through PCR; targeting the CoV RNA dependent RNA polymerase gene. Tao and Tong (2019) have performed the complete genome sequencing SARS of Bats and recognized the CoV strain i.e., BtKY72 or Rhinolophus species in the Kenyan bats. This study also confirmed the sequence of BtKY72 is close to the BtCoV or BM48-31 in the European Bats. The SARS-CoV identified in Rhinolophus bats were from China, Europe and Kenya. Genetic sequence for BtKY72 will facilitate understanding the molecular evolutionary characteristics of bat SARS-related CoV (Tao and Tong 2019).

Recently, Wu et al (2020) have performed the Next-generation metagenomic RNA sequencing in 7 subjects allied with Sea food marker at Wuhan city from China and identified a novel RNA virus Coronaviridae family intended as WH-Human-1 coronavirus. This study also confirms as ~89% of nucleotide sequence was found to be common with Bats sequence in China for a group of SARS-CoV in the β CoV of Sarbecovirus.

Pharmacogenomics and SGS: SGS and RNA-S offers

entire transcriptome and CHIP sequences for complete architecture of the genome. Discovering genetic or novel variants in the affected individuals may be predicted for the disease risk. NGS can also use for predicting the disease risk to predict the response to adverse effects of drugs. Presently, COVID19 is an essential disease has been grown up without any medication (Rx). There is no medication for COVID19 and there is a need for such a personalized medicine which needs to supply the possibility to treat COVID 19 transmitted disease. Pharmacogenomics will always play a major role in discovering the medication for novel diseases based on the SGS technologies and their precise applications in human diseases to foster human health care and personalized medicine (Rabbani et al. 2016).

CONCLUSION

From this current review, limited information is gathered for the pharmacists for developing the medicine using the available genome data from the humans affected with COVID19; as ongoing virus tumbles from animals to cause severe disease in humans. NGS analysis can be helpful for pharma companies for scheming medications. First of all, accurate diagnostic tests with PCR should be implemented to rule out the disease. Furthermore different researches should also be implemented on usage of medicinal plants or herbs for the future treatment perspectives of COVID 19 pandemic.

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