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Short Communication

Animal and Human Coronavirus Disease

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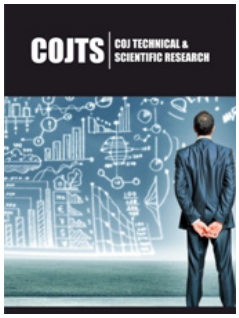
Abstract

In the context of emerging diseases, an important tool to investigate the evolutionary history and viral origin from animals to humans consists in the phylogenetic analysis of molecular sequences of both nucleotides of the viral genome and amino acids, sharing into a common ancestor. In the twenty first century two other zoonotic coronaviruses were introduced, the SARS CoV and the MERS CoV, which differs from the new SARS CoV 2 while containing known viruses predominantly isolated from humans and several species of bats. The current outbreak of a corona virus associated acute respiratory disease called coronavirus disease 19 (COVID 19) has been designated «severe acute respiratory syndrome coronavirus 2» (SARS CoV 2) named based on phylogeny and the viral taxonomy among clusters to the prototype human and bat. As it occurs with other RNA viruses, high genetic variability leads to gene recombination in coronaviruses, because they have similar and non identical genome sequences generating variants of the same virus. The importance of strengthening epidemiological surveillance systems in the early diagnosis and adoption of preventive measures is paramount for controlling viral spread.

Keywords: Emerging diseases; Coronaviruses; Outbreak; RNA; SARS



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Submission: March 18, 2020

Published: April 08, 2020

Volume 2 - Issue 5

How to cite this article: Rachel Siqueira QS. Animal and Human Corona viruses. COJ Technical & Scientific Research. 2(5). COJTS.000547. 2020.

Introduction

The current outbreak of a coronavirus associated acute respiratory disease called coronavirus disease 19 (COVID 19) has been designated "severe acute respiratory syndrome coronavirus 2" (SARS CoV 2) named based on phylogeny and the viral taxonomy among clusters to the prototype human and bat [1]. In the twenty first century two other zoonotic coronaviruses were introduced, the SARS CoV and the MERS CoV, which differs from the new SARS CoV 2 while containing known viruses predominantly isolated from humans and several species of bats. SARS CoV 2 is completely different from the SARS CoV of the outbreak in 2002 2003, although of both viruses share evolutionary histories and are strictly genetically related each other [1]. SARS CoV was first reported in 2002, constituting severe human pneumonia in southern China with cases of death. In 2003, the disease advanced and spread throughout Central and Southern Asia, reaching countries in North America, South America and Europe. In April 2012, another coronavirus was isolated, distinct from the one that caused SARS CoV. The virus was first identified in Saudi Arabia and caused the death of more than 800 people, being transmitted from camelids to humans and named Middle East Respiratory Syndrome (MERS CoV) [2]. The coronaviruses are classified in Riboviria realm, Nidovirales order, Cornidovirineae suborder, Coronaviridae family, two subfamilies, five genera, 24 subgenera that affect 39 species [1]. Unlike SARS COV 2 that occurs only in humans by a clinical respiratory infection, the microorganisms of the Coronaviridade family infect also vertebrates causing diseases in animals as turkeys (enteritis), mouse (viral hepatitis), pigs, dogs, foals (gastroenteritis), cats (peritonitis), calves (neonatal diarrhea), bird and rats (pneumonia). In Brazil, the phylogeny of canine coronavirus (CCoV) based on membrane protein partial a sequence has been investigated by molecular biology techniques. Feline coronavirus (FCoV) is responsible to causing one of the most important infectious diseases that affect domestic and wild felines, called feline infectious peritonitis (PIF) [3]. As it occurs with other RNA viruses, high genetic variability leads to gene recombination in coronaviruses, because they have similar and non identical genome sequences generating variants of the same virus. So, enveloped positive sense RNA viruses with a 27kb genome have the region of the most conserved replicative proteins encoded in the open reading frames 1a and 1b (ORF1a/1b)

of the coronavirus genome. The three dimensional structure of the spike protein of the coronavirus strain SARS Cov 2 has been detected by computational modeling. A 3D map of the protein or blueprint was created using the cryo electron microscopy technique [4]. So, in just 48 hours it was possible to sequence the complete genome of the new coronavirus (COVID 19) from the first confirmed case of the disease in Brazil, showing genomic sequences more similar once to the European viruses in Germany, and another in England, both different from the genome identified in Wuhan, the epicenter of the epidemic in China. In the context of emerging diseases, an important tool to investigate the evolutionary history and viral origin from animals to humans consists in the phylogenetic analysis of molecular sequences of both nucleotides of the viral genome and amino acids, sharing into a common ancestor. Thus it is possible to determine the starting point that originated the infection and to track the viral spread between populations. In a worldwide epidemiological scenario, the COVID 19 was declared to be a public health emergency due to the fast speed of spread of the virus by direct transmission and the contact of infected people. Social isolation is adopted as a preventive measure. Research labs around the world have turned their attention to investigating the new virus responsible for causing major respiratory damages and to be capable of exterminating mainly elderly populations. Three drugs with potential antiviral activity to COVID 19, called Remdesivir, used in Ebola and Marbug virus treatment also, both belonging to the Filoviridae family, have been tested against coronaviruses, including MERS and SARS viruses and others respiratory infections as the respiratory syncytial virus, Junian virus, Lassa fever virus, Nipah virus and Hendra virus. Chinese Company has produced others drugs like Favilavir and Choroquine Phosphate [5] used to prevent and treat malaria and amebiasis also. Moreover, the implementation of stem cell therapy in the treatment of patients infected with COVID 19 capable of repairing the damage caused to the lungs, liver and other organs have been successful [1,2]. The Corona virus pandemic has accelerated molecular studies using genomic tools with Next Generation Sequencing (NGS) for the characterization of viral samples and in genetic engineering for the development of vaccines. Based on the vaccine against infectious bronchitis caused by another type of corona virus that affects chicken, Israeli scientists are developing an oral vaccine against corona virus that will be commercially available in May 2020. Other countries as USA, Brazil, England and China are also developing possible candidates for vaccines against SARS CoV 2 using different strategies such as mRNA synthetic molecules and virus like particles (VLP). In veterinary medicine, the vaccine available against canine corona virus was made by recombinant technology using a live attenuated virus, protecting against other viral infections also. The importance of strengthening epidemiological surveillance systems in the early diagnosis and adoption of preventive measures is paramount for controlling viral spread.

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