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EMERGING ZOONOSIS

AND THE JUMP OF THE SPECIES BARRIER IN THE COVID-19 PANDEMIC

ZOONOSIS EMERGENTE Y EL SALTO DE LA BARRERA DE ESPECIES EN LA PANDEMIA DEL COVID-19

Raúl González Salas[1]
E-mail: rauljoelis68@gmail.com
ORCID: https://orcid.org/0000-0003-1623-3709
Mildre Mercedes Vidal del Río[1]
E-mail: mriovidal69@gmail.com
ORCID: https://orcid.org/0000-0003-3496-5057
Ivan Pimienta Concepción[1]
E-mail: dr.ivan.pimienta@gmail.com
ORCID: https://orcid.org/0000-0002-7623-7499
Aldemar Alejandro Monsalve Guamán[1]
E-mail: aldomonsag@gmail.com
ORCID: https://orcid.org/0000-0001-7106-0746
Darvin Manuel Ramírez Guerra[2]
E-mail: dramirezg@uho.edu.cu
ORCID: https://orcid.org/0000-0001-5934-7779
[1] Universidad Regional Autónoma de Los Andes. Ecuador.
[2] Universidad de Holguín "Oscar Lucero Moya". Cuba.

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ABSTRACT

In recent years, the emergence or re-emergence of many epidemiological events has taken place in the world, which appear in a population for the first time or which existed and in a certain period show an increase in their incidence and geographical distribution. Mammalian coronaviruses, including those that infect humans, evolve from bat coronaviruses. Although SARS-CoV and MERS-CoV are genetically closely related to bat coronaviruses, intermediate hosts are likely involved in the occurrence and inter-species transmission of these new human viruses. More research is needed to elucidate the ecology of coronaviruses. Vigilance must be maintained to rapidly identify newly emerging coronaviruses. The objective of this research is to inform the main aspects of emerging zoonosis and the jump of the species barrier in the COVID-19 pandemic.

Keywords: Emerging zoonosis, Coronavirus, species barrier.

RESUMEN

En los últimos años se ha producido en el mundo el surgimiento o resurgimiento de muchos eventos epidemiológicos, que aparecen en una población por primera vez o que existieron y en un período determinado muestran un aumento en su incidencia y distribución geográfica. Los coronavirus de mamíferos, incluidos los que infectan a los humanos, evolucionan a partir de los coronavirus de murciélago. Aunque el SARS-CoV y el MERS-CoV están estrechamente relacionados genéticamente con los coronavirus de murciélago, es probable que los huéspedes intermediarios estén implicados en la aparición y transmisión entre especies de estos nuevos virus humanos. Se necesita más investigación para dilucidar la ecología de los coronavirus. Se debe mantener la vigilancia para identificar rápidamente los coronavirus emergentes. El objetivo de esta investigación es dar a conocer los principales aspectos de las zoonosis emergentes y el salto de la barrera de especies en la pandemia COVID-19.

Palabras clave: Zoonosis emergentes, coronavirus, barrera de especies.

INTRODUCTION

The term emerging defines diseases that appear in a population for the first time or that existed and in a certain period show an increase in their incidence and geographical distribution PAHO (Lu et al., 2020), is used to identify epidemics such as smallpox or flu, plague, cholera, influenza, Ebola, SARS, MERS (Gralinski & Menachery, 2020),(Llorente-Parrado et al., 2020) that devastated humanity and more recently the Severe Acute Respiratory Syndrome Coronavirus 2 (SARS-Cov-2)(Phan, 2020), (Shang et al., 2020); causing a disease known as COVID-19 (Cao, 2020), (X. Liu et al., 2020).

Coronaviruses (CoVs) are single-stranded, positive-sense RNA viruses that are enveloped, highly diverse, and cause respiratory, neurological, and digestive disorders of varying severity in a wide range of animal species, including humans, who can be seriously ill. CoVs are grouped into four genera: Alphacoronavirus, Betacoronavirus, Gammacoronavirus, and Deltacoronavirus (Heer et al., 2021).

There are two types of Betacoronavirus of great interest to the scientific community and world health: the cause of the severe acute respiratory syndrome, known as SARS-CoV-2, and the cause of the Middle East respiratory syndrome (MERS-CoV). More than enough scientific evidence proves that SARS-CoV-2 is a type of viral zoonosis that originated in wild animals such as bats and then transmitted through other mammals to humans. (Mar Cornelio et al., 2021).

In the last forty years, 70% of emerging infections have been zoonosis, infectious diseases caused by bacteria, viruses, fungi, or parasites transmitted from animals to humans. Routes of transmission can be through direct physical contact, through air or water, or an intermediate host. These zoonotic pathogens do generally not affect the animals in which they reside but could pose a high risk to humans who do not have natural immunity against them. (Garcia-Salido, 2020), (Guerra et al., 2021), (Carralero et al., 2020).

These diseases are of great interest due to their high incidence and convergence of many factors (aging, increase in the global population, trade, travel, urbanization, climate change), in addition to their severity, evolution, and spread, thus constituting a global permanent challenge (Percedo Abreu et al., 2020), (Cordero et al., 2019).

This research aims to support the main aspects of emerging zoonoses and the jump of the species barrier in the COVID-19 pandemic.

DEVELOPMENT

A review was made of articles published in English and Spanish in journals indexed in Elsevier, Springer, Pubmed, and Scimago that contributed to the knowledge obtained regarding emerging zoonoses and the species barrier's jump COVID-19 pandemic. The analyzed period goes from January 2005 to September 2020. The terms used were: Coronavirus, emerging zoonoses, species barrier, pandemic, SARS-CoV-2, intermediate host, mammals, animal pathogen, human exposure, viral evolution (Teruel et al., 2018), (Ricardo et al., 2020).

Stages summarize emergencies in zoonoses: The first refers to contact between a primary source of animal infection with other animals. The second is critical and consists of human infection by exposure to an infected animal reservoir, producing the jump of species for the first time animal-man transmission. In the third, human exposure to the microorganism from the animal is maintained and some human cases appear, these processes can trigger large outbreaks of the disease, ending in an epidemic or pandemic and the disease becomes (or can do it) exclusively of the man (Wong et al., 2020).

Pangolins are the only mammals including bats that have been documented as being infected with a SARS-CoV-2-related coronavirus. Notably, two strains of coronavirus are found in these animals that were independently sampled in different Chinese provinces, and both are also related to SARS-CoV-2. This suggests that they may be important hosts for these viruses, which is striking since they are mostly solitary and, in turn, belong to relatively small populations, so they should be studied further. (P. Liu et al., 2020).

According to studies to identify SARS-CoV-2 coronaviruses in Malaysian pangolins, current data show that there is a high probability that these mammals acquired their SARS-CoV-2-related viruses independently of bats or other animal hosts. (Domínguez & Amador-Bedolla, 2020). Therefore, its role in the emergence of human SARS-CoV-2 has not yet been clarified.

In this context, it has been explained that both strains of coronavirus were obtained from trafficked Malaysian animals, Southeast Asia and that there is an evident lack of knowledge of the viral diversity shown by this species in regions where there is a lack of knowledge of the viral diversity shown by this species it is native. An aspect that allows us to reflect on the degree of transmission of the virus in these populations and the need to carry out a greater number of investigations (Liu et al., 2019).

As for coronaviruses, including those related to SARS-CoV-2, they are present in many wild mammals in Asia (Sharun et al., 2021). It should be noted that although great efforts have been made, studies of pathogenicity, epidemiology, the degree of infection between species, and the transmissibility of coronaviruses in pangolins have not yet been studied. (Domínguez & Amador-Bedolla, 2020), the data presented here suggest that handling these animals requires considerable caution and that their sale in wet markets should be strictly prohibited. Greater vigilance is needed in their natural environment in China and Southeast Asia(Couple-Alcaraz, 2021) to understand its role in coronavirus affectations and the risk of future zoonotic transmissions.

(Zhou et al., 2018) They report that certain coronaviruses that infect animals can be transmitted to humans and subsequently spread between people, although the mechanisms are not yet clarified according to the research. Similar events occur with the virus that caused the current COVID-19 outbreak, it is theoretically held that the virus originated in bats. The first reported infections were linked to a live animal market, but the virus is now spreading from person to person globally, resulting in countless infections and has even claimed the lives of hundreds of people.

Research carried out so far has proven that domestic animals can be infected in the same way as human beings. However, it should also be noted that there is no evidence that pets can transmit the disease to their owners. The World Health Organization states that there is no evidence that cats, dogs, or any pet can transmit COVID-19, which greatly reassures the population that has a great attachment to these companion animals (Segura & Placeres, 2019).

The American Veterinary Medical Association refers to arguments about the contagion to domestic animals, which highlights the story of a dog that currently died and two cats in New York that recovered. It is necessary to consider that these animals were in contact with people with positive diagnoses for COVID-19. It is presumed that their owners infected them, generally many of the pets have the virus in its inactive form. On the other hand, the contagion of a four-year-old tiger was reported at the Bronx Zoo in the United States, which could have been infected with its caretaker in an asymptomatic state.

There is not enough scientific evidence to show that pets could spread SARS-CoV-2. But there is research where cats and ferrets turned out to be the animal species most susceptible to infection. In the case of the latter, SARS-CoV-2 was capable of replicating in the upper respiratory tract without causing signs of serious illness or death, in addition, similar results were obtained in cats, where the transmission of viruses between individuals through microdroplets of respiration. In contrast, dogs showed low susceptibility to SARS-CoV-2 infection, and pigs, ducks, and chickens none.

The possible role of animals as mechanical vectors of this virus has also been reported through hair, skin, or legs after coming into contact or being caressed by a COVID-19 positive person. Although no specific studies have been found in this regard, such a possibility deserves a thorough investigation to continue looking for alternatives for the control and possible prevention of the spread of the virus.

The species jump (of the species barrier) represents the atypical transmission of a pathogen from a host reservoir to a new host. It can occur between animals, domestic or wild, and also, from them to man, in which case we speak of a zoonotic barrier jump, a progressive process in which an animal pathogen establishes itself in man and can cause disease, or even death.

There have been four events of zoonotic jumps of coronavirus from animals to humans that have resulted in epidemics. The first event occurred with a β-coronavirus of the A lineage, which involved nine animal species, including humans. It is hypothesized that the final zoonotic jump of this β-coronavirus was from bovines to humans about 120 years ago, leading to CoV OC43, identified, like HCoV-229E, in the years 1966 and 1967, respectively. HCoV-229E and CoV OC43 were the first coronaviruses to be identified in humans.

For more than 40 years, these coronaviruses were thought to be the only infective. Studies in healthy adult volunteers revealed that infection induced by these two coronaviruses causes symptoms of the common cold. Another symptom observed in HCoV-229E infected individuals is rhinitis, whereas odynophagia occurs in HCoV-OC43 infected patients.

At the beginning of the 21st century, the second zoonotic jump event occurred which involved a β-coronavirus of the B lineage, giving rise to human SARS-CoV in 2003. This event involved bats, palm civets (Pagumalarvata), and humans (33). It is important to note that palm civet meat is a highly valued food in China. In turn, the SARS-CoV was responsible for the epidemic that began in Guandong, which was controlled that same year with the implementation of quarantines.

The third zoonotic event occurred in the C lineage of β-coronaviruses, causing the Middle East respiratory syndrome (MERS-CoV) epidemic, a viral process closely related to CoV HKU4 present in the bat Tylonycteris (Ty-BatCoV HKU4) and the CoV HKU5 present in the bat Pipistrellus (Pi-BatCoV HKU5), both species originating in Hong Kong. On the other hand, outbreaks of the HCoV-NL63 and HCoV-HKU1 viruses appeared in 2004 and 2005, respectively. Thus, these latest human coronaviruses are not new, they simply had not been previously detected. Additionally, there is evidence that genotypes of the HCoV-HKU1 strain recombined naturally, and in the case of β-coronavirus it is well adapted to humans.

The four strains of human coronaviruses mentioned above are classified as common cold viruses that in certain cases severely affect adults with chronic diseases, young children, and the elderly. One theory that is held regarding these pathogens is that at first glance it appears that bats are the natural hosts of the coronaviruses that originated the C-lineage of β-coronavirus. However, a significant number of contagion cases were not related to direct exposure to bats.

A more likely scenario is that a single variant of β coronavirus in bats successfully hopped and established efficiently in an intermediate animal host species, for example, civets and dromedaries, with consequent incidental spread to humans. Such zoonotic events are facilitated through frequent human-intermediate host interactions and possibly through viral adaptations acquired during the initial jump of the species, the range of animal sources, and the transmission routes between species during the period of generation of β-coronavirus lineage C.

The fourth zoonotic event concerns SARS-CoV-2, which is almost impossible to manifest from a laboratory manipulation starting from a related coronavirus. This is because the receptor-binding domain (RBD) on the SARS-CoV-2 spike protein (S) is optimized to bind to the human angiotensin-2 converting enzyme differently from other coronaviruses.

Viruses accumulate genetic changes at great speed, sometimes at the limit of their extinction, an aspect that allows them to develop a property known as learning to jump from one species to another. For this, several factors must be conjugated that allow the virus to accumulate mutations and it is in this way that it recognizes the cells of another species, as an additional requirement there must also be physical contact between individuals of the different species, reaching epidemic proportions if the virus also achieves good human-to-human transmission.

Analysis on a global scale concerning all zoonotic viruses reveals a structured variation among mammalian species that are implicated as a potential source of the spread of the virus to humans.

The new coronavirus (SARS-CoV-2), the causal agent of the COVID-19 pandemic, is the result of natural evolution from coronaviruses present in wild fauna, as shown by the detailed study of its genome. Despite the doubts that still exist, current scientific clues point to the Huanan seafood market, in Wuhan, as the focus where the first infections occurred: the first 41 hospitalized patients had been in the market.

SARS-CoV-2 is related to bat coronavirus, but its jump from the Malayan pangolin is unproven. Several species of pangolin are threatened and are subject to the largest illegal animal trafficking in Asia. Bats, on the other hand, have long been recognized as large reservoirs of zoonotic viruses, and in particular of coronaviruses, in various parts of the planet.

A study conducted in Saudi Arabia with the participation of 16 out of 30 camel workers, to whom a survey was applied showing evidence of previous infection by MERS-CoV through seroconversion and/or virus-specific CD8 + T cell responses without any history of significant respiratory disease. Researchers suggest that camel workers with mild or asymptomatic disease may serve as another route of spread.

Although camels are believed to be the main zoonotic reservoir for human transmission, there is strong evidence that bats are the ancestral reservoir for MERS-CoV. MERS-CoV is a group C betacoronavirus and is phylogenetically related to the BatCoVs identified in various species of bats belonging to the family Vespertilionidae. This includes BatCoV HKU4, BatCoV HKU5, NeoCoV, and PDF-2180. Furthermore, the peak protein of HKU4 and MERS-CoV are very similar, and both use human dipeptidyl peptidase 4 (DPP4) for virus entry.

CONCLUSIONS

SARS-CoV-2 is related to bat coronavirus, but its jump from the Malayan pangolin is not yet proven. It is one of the great emerging infections that humanity has ever faced. In the coming years, more infections between species are expected to occur due to the great variety of factors that influence the presentation of zoonotic infections, the increase in population density, ecology, and the proximity between animals and humans. Therefore, a close watch is needed for emerging pathogens.

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