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Editoriales

Zoonotic emergence of coronavirus: a potential public risk for Latin America

Emergencia zoonótica de coronavirus: un potencial riesgo público para América Latina

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Coronaviruses (CoV) are a group of enveloped RNA viruses, single-stranded (positive sense) belonging to the order Nidovirales, family *Coronaviridae*. They are divided into four main groups: alpha, beta, gamma and delta; it seems, alpha and beta infect humans. The first known human coronaviruses (HCoV), HCoV-229E and HCoV-OC43, cause mild respiratory infections (1).

Coronaviruses are common throughout the world and six of them can make humans sick. Some coronaviruses have existed for a long time and commonly cause mild to moderate illnesses around the world. However, the two most recent coronaviruses, SARS-Coronavirus (SARS-CoV) and Mers-Coronavirus (MERS-CoV) frequently cause severe disease. However, with the exception of the previous coronaviruses, its role in respiratory disease in humans is still a matter of debate. In a multicentre study, where some countries in Latin America and Australia were considered, among others, which included 6.266 pediatric patients with symptoms compatible with influenza; the highest prevalence was Rhinovirus /Enterovirus (42%) and Coronaviruses was only 6%.

In 2002, SARS-CoV appeared in Guangdong province in southern China. It quickly spread to 27 countries, infecting 8.098 people and causing 774 deaths, thus it was declared the first global pandemic of the 21st century. The bats were identified as the reservoir and the probable source of the outbreak. In 2012, the SARS-Cov pandemic was followed by that of MERS-CoV, which emerged in the Middle East with 1.782 confirmed human cases and 640 deaths through September 2016. Camels were identified as the probable source of human infections; however, it was again discovered that bats hosted closely related viruses (similar to MERS), and therefore, it was assumed that bats were the original evolutionary source. Outbreaks of SARS-CoV and MERS-CoV have shown that *Coronaviridae* is a family with potential zoonotic capacity, which has led to an increase in eco-epidemiological studies for the search of coronaviruses in bats.

In addition to camels and bats, coronaviruses can affect different species of animals such as porcine coronavirus, porcine epidemic diarrhea virus, porcine delta-coronavirus (PDCoV), infectious bronchitis virus (IBV) and turkey coronavirus. These coronaviruses have a significant impact on animal health and cause considerable economic costs to farmers (2).

In Brazil, pandemic type II canine coronary coronavirus strains were characterized in tissue samples from five puppies that died as a result of severe gastroenteritis. The reverse transcriptase PCR indicated that they were similar to those found in other countries, suggesting a common ancestor of these Brazilian isolates. This was the first report of pantropic CCoV-II in puppies from Latin America and the results showed that CCoV should be included as a differential diagnosis of canine parvovirus infection. The equine coronavirus manifests as an enteric disease and belongs to the group of beta-coronaviruses; this has recently been isolated from a series of outbreaks in the United States, Europe and Japan. The seroprevalence of equine coronavirus in the United States has been estimated at 9.3%, but there are no studies in Colombia or in Latin America. Finally, the feline enteric coronavirus produces mild or chronic gastroenteritis, many cats are resistant and are only carriers, but the virus has the ability to mutate giving rise to feline infectious peritonitis.

Rarely, these coronaviruses from domestic animals can infect and spread among humans. However, in the future, one or more of these, including other coronaviruses could spread to humans, as happened in the past with dromedaries.

The inter-species spread of coronaviruses in new hosts frequently occurs, SARS-CoV and MERS-CoV are the most notable examples of intra-species infection towards humans. The bovine, canine respiratory, dromedary and human OC43 coronaviruses potentially come from the same common ancestor, demonstrating the viral flexibility to adapt to new hosts. SARS-CoV probably originated in bats, whereas it is likely that PDCoV originated in birds. Therefore, the search for reservoirs in wild animals for CoV is of great interest (2).

The identification of SARS-CoV in *Rhinolophid* bats led to more intensive investigations of coronaviruses in humans and in bats. After the discovery of MERS-CoV as a zoonotic agent, coronavirus NL63 and HKU1 were recently detected as endemic in humans. Recent studies have shown that bat coronaviruses were the source of many human coronaviruses, including SARS-CoV, HCoV-229E and NL63 (1).

In a muticentric study in Africa, Asia and Latin America (Peru, Bolivia, Brazil and Mexico), a total of 19.192 samples were collected between animals and humans, which were analyzed for the presence of CoV by PCR. Two fragments were amplified: one of 434 bp of RNA polymerase (RdRp) corresponding to nucleotides (NT) 15156-15589 and the other of 332 bp of a different peptide downstream of RdRp, corresponding to NTs 18.323-18.654. The majority were bats (n=12.333) and represented 282 species of twelve families. In general, the proportion of positive CoV individuals was 8.6% in bats (n=1.065/12.333) and 0.2% in non-bats (n-17/6.859). In other words, more than 98% of all positive individuals were bats. In the phylogenetic analysis and viral diversity, the intra-genera transmission of bats was higher in Africa and Asia; however, in Latin America the contact and viral exchange is narrower among nearby species of bats, in contrast, in Africa the viruses circulate between more distant bat species. The study also confirmed that viral abundance is related to the abundance of bats. In this sense, Colombia and Venezuela are the countries with the highest biodiversity of bats, so further studies are needed to confirm this argument.

To demonstrate that bats harbor more CoV diversity than other host mammals, phylogenetic analyzes of the alpha and beta-coronavirus genera have been carried out, which were widely found in Chiroptera. The zoonotic origin of four of the six known human CoVs (HCV) has been demonstrated, three of which probably involved bats: SARS-CoV, MERS-CoV and HCoV-229E.

There are no studies on CoV of bats, nor in humans in Colombia and in Latin America are very insufficient. This critical lack of information in a country that holds the greatest diversity of Chiroptera in the region, reveals an ecoepidemiological gap that we have to overcome with the implementation of more studies aimed at better understanding the role of CoV in human health and animal in the region and in the world.

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