



# **Global Trends of Emerging Infectious Diseases and the Impacts on Biodiversity: Spillover, Diversity and the Role of Bats in Evolutionary Relationships as Zoonotic Virus Reservoirs**

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*This work was carried out in collaboration among all authors. Author DPLJ conceived and designed or scope of the review. All other authors contributed to the improvement of the article, carrying out a careful review. All authors read and approved the final manuscript.*

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## ABSTRACT

**Introduction:** It is possible that the evolution of man is associated with manifestations of microscopic beings that have accompanied him since ancient times. Emerging infectious diseases have been warning for decades that habitat fragmentation and degradation, antropization effects, animal trafficking increase the risk of diseases spreading from wildlife to human populations.

**Aims:** The purpose of this study was to review the current events about the pandemics that occurred on the planet and the current situation of bat involvement, their high degree of ecological plasticity that these beings present with the emergence and spread of viruses.

**Methodology:** Review the current knowledge about viral diversity, host condition and possible mammalian reservoirs in the face of pandemics and the close relationship of bats with humans and other possibly incriminated species. Given the epidemics of the last century, it is possible to observe that the increased interaction between humans and wild animals has facilitated the emergence of viral strains of importance for public health.

**Results:** Given the reports argued by the scientific community, bats may be responsible for the air cycle of viral diseases, being considered of great importance in the study of epidemiology.

**Conclusion:** The SARS-CoV-2 epidemic has come to test the ability of humans to face a threat that may be repeated in the future. As part of nature, bats cannot be framed as precursors of viral agents. The knowledge obtained, associated with investment in science, research and education, will put us one step ahead of future pandemic events.

*Keywords: Epidemics; Chiroptera; conservation; virus; COVID-19.*

## 1. INTRODUCTION

Since the beginning, when man stopped living on trees and allowed himself to walk on two legs, this organism went through physical changes that, later, originated the dominant species named *Homo sapiens*. Climate change, habitat destruction, the way across continents, species pressures, and war between peoples, comorbidities, cultural practices, demographic density or mitigation, any of these situations could have caused these hominid ancestors to descend from their trees and cause that the world should be alert, in the face of expectations, desires, benefits and harms that this evolution would bring to the planet.

However, in fact, this possible evolution of man is also associated with manifestations of microscopic beings that have accompanied man since the beginning. Viruses, fungi, bacteria, parasites and other microorganisms, participate in the evolution of humanity and reveal how these microscopic beings have shaped evolution on the planet over millennia and, today, help us to understand our own origin on Earth [1].

Can changes in biodiversity within the bodies of organisms also change the transmission of pathogens? We can know when and how the current epidemics started and how they conditioned human existence, decimating populations, stimulating conflicts, infecting

combatants, promoting exodus, promoting miscegenation, strengthening or weakening peoples.

Mammals of the order Chiroptera, are involved in the emergence and spread of viruses in animals and humans. Endowed with the ability to fly, a diet rich in food, live in colonies and cover long distances during migration, occupying the most varied ecological niches and dispersion on the planet [2].

This remarkable ability has been providing this globally known species, as bats; with idiosyncratic and insuperable characteristics, an evolutionary success and a remarkable propensity for these animals to favor, and become hosts, reservoirs and transmitters, spreading a wide variety of viruses and other potentially pathogenic microorganisms.

Recent advances in science and in improving researchers' ability to detect uncultivable microbial species have made it possible to document the enormous diversity of microorganisms in animals and plants and reporting that when we treat the human species, *Homo sapiens*, 90% of all cells are microbial [3].

Research on emerging infectious diseases has warned for decades that fragmentation and degradation of habitat, biopiracy and trafficking in live animals increase the risk of diseases

spreading from wildlife to human populations. The appearance of several emergencies registered on our planet in this millennium; they can be attributed, at least in part, to the increase in human impacts on natural systems [4,5].

The objective of this work was to address the main factors involved in the emergence and reemergence of pandemic diseases. Here, we present as a methodology a review based on the current literature, to serve as a source for consultations and information on the historical reports of the pandemics that have plagued the planet and the recent concepts and classifications in virology and biodiversity actions. In this article, we list the characteristics of the current pandemic COVID-19, with an emphasis on aspects and characterization of the Coronaviridae family, viral morphology and its structures and taxonomy. We present the relationship and interaction with the chiropteran hosts and the occurrences presented by habitat fragmentation, the intimate relationship between viruses and mammals of this order, evaluating the role that bats play as potential reservoirs and transmitters of viral genera, performing an eco-epidemiological and the epidemics that occurred in the world.

The world we live in is changing and the current concept of biodiversity has pointed out situations in which the planetary population must be prepared to answer the questions, especially if we must maintain the view that the health of the planet has meaning, relevance and importance in prevention the spread of viruses and other pathogenic microorganisms and the interaction with pandemics.

## 2. METHODS

In this review, we carried out a bibliographic survey emphasizing updated topics using the available databases, addressing a focus on understanding the epidemics and pandemics that occurred in the world and also those related to the current pandemic situation of COVID 19 (SARS-CoV-2) providing a critical assessment and rational discussion about the available knowledge, in order to have a clear view of the action of these pathogens and the close relationship with the bat species distributed throughout the planet.

## 3. RESULTS

After consultation and evaluation, 100 scientific articles available in the databases were used as

a basis for the results and relevant discussion of this review. The results show an analysis of the historical reports of the pandemics that devastated the planet and the recent facts about the current viral pandemic that devastated the planet. The results were grouped and compared into themes and are presented below.

## 4. WHAT IS THE ORIGIN OF THE NEW OUTBREAK?

In the 14th century, an unknown disease killed about 50 million people, panic made people isolated, afraid and terrified of coming into contact with people and objects, nobody going out on the streets; a terrifying fear of coming into contact with particles, supposedly infectious in the air, would be involving the deadly disease [1].

The black plague was decreed and generated panic in the population much like what we are experiencing in the times of Coronavirus. But today, we know that in the air, there was nothing, and that the disease in question: the bubonic plague (formerly known as the black plague) was transmitted and caused until today, by the zoonotic bacteria *Yersinia pestis*, which lives in wild rodents and their fleas and which end up being transmitted to humans through the bites that infest mice and other rodents.

A few decades ago, it was believed that in intact natural environments and in tropical forests full of wildlife and exotic fauna, distributed around the world, they were a threat to humans, as they harbored viruses and various pathogens that cause new diseases, such as Dengue, Ebola, Nipah, SARS, MERS, HIV [6]. The U.S. Center for Disease Control and Prevention (CDC) estimates that 3/4 of the emerging infectious diseases that infect humans originate in exotic and wild animals [7-9].

Nowadays, a genetic analysis of the virus and comparing it with the genetic information about these microorganisms and their different relatives from various geographical locations and their respective host species, the researchers concluded that the pandemic virus, which causes major impacts on public health in global scale, initially called WHCV, in allusion to the city of Wuhan, China, where the pandemic began, later 2019-nCoV, and more recently SARS-CoV-2, [10] the last name received for the viral etiologic agent and named by WHO (World Health Organization) as COVID-19, appears to be a

virus formed from a combination of a Coronavirus found in bats and another Coronavirus of unknown origin [11].

The Coronaviridae Study Group (CSG) of the International Committee on Taxonomy of Viruses (ICTV), in a recent Consensus [10], emphasizes the situation with SARS-CoV-2 is fundamentally different because this virus is assigned to an existing species that contains hundreds of known viruses predominantly isolated from humans and diverse bats. All these viruses have names derived from SARS-CoV, although only the human isolates collected during the 2002–2003 outbreak have been confirmed to cause SARS in infected individuals.

The virus resulting from this possible interaction has developed a mutation or "recombination" of its viral proteins that recognizes and binds to receptors on host cells. This recognition is essential to allow viruses to enter host cells, which can lead to infections and diseases [12].

## 5. VIRUS, A MUTANT MICROORGANISM

There is no single coronavirus. There are several, say virologists. The name does not refer to a specific virus, but to a group of viruses that have common characteristics and have been responsible for several public health crises in recent decades around the world.

Three diseases observed in animals were the subject of initial study on the Coronaviridae family and these diseases were caused by viruses, without establishing a degree of kinship between them. Veterinarians were unaware of the effect of these diseases on animals, but coronavirus were already manifesting causing bronchitis in chickens and intestinal disease in pigs.

These infectious manifestations were responsible for avian infectious bronchitis (IBV), a disease first observed in 1937, for poultry farming in Brazil and worldwide. Another in 1946; disease known as swine gastroenteritis (TGEV), and finally, in 1951, murine hepatitis (MHV) transmitted by mice [13] were diseases that produced great economic losses and had something in common.

Later, it was discovered that the IBV, TGEV, MHV viruses had the same characteristic morphology observed in electron microscopy "in the shape of a crown", then the name

Coronavirus (1968) appeared, establishing that these groups of parasites that cause disease in animals they belonged to the same group of viruses that caused colds in humans.

All viruses evolve over time, accumulating mutations as they replicate imperfectly within a host's cells in an extraordinary amount and then spread through the population, with some of these mutations persisting through natural selection [13].

The new coronavirus looks practically the same phenotypically everywhere it appeared, and there is no evidence that some strains are more deadly than others. These acellular microorganisms go beyond the barriers of species by hosting animals in animals, and remain trapped and inert in their primary hosts and remain for a long time in these hosts, without even causing disease.

## 6. EPIDEMICS AND PANDEMICS

The stories of the origins of epidemic outbreaks remain at a very controversial level, however, considering that mammals, including bats, were the sources of different zoonosis and reported as the protagonists of scientific reports.

For a classification, since we are talking about epidemic and pandemics, we will first conclude that an epidemic occurs when there is an increase in the number of cases, much higher than expected for a given region, already a pandemic is more comprehensive; where cases affect several countries and continents.

In general, terms, there are six classes of zoonotic pathogens: viruses, bacteria, protozoa, fungi, chlamydia and helminths. It is known that there are 219 virus species, from 27 families, capable of infecting humans, still 538 bacteria and rickettsia, 307 fungi, 66 protozoa and 287 helminths [14].

Epidemic diseases are usually zoonotic, that is, the transmitting agents are caused by parasites of other non-human animals. According to Taylor et al. [14] of the 1,415 known pathogens, 61% are zoonotic and have been lent to humans of other species. Woolhouse & Gaunt [5] in a systematic literature search report 1,399 species of human pathogens.

Throughout history, numerous pandemic outbreaks have been identified and reported, with viral spikes, in 1761, 1781, 1789, 1833, 1836, 1847, 1889, 1900, 1918, 1957, 1968, 2003, 2006, 2009, 2013, 2019-20 with very

irregular time intervals in different parts of the globe, with more or less deaths.

Historical reports, recorded of a great epidemic in Russia in 1781 and one in Asia, in 1830, the best known was the devastating "Spanish flu", between 1918-20, caused by the Influenza H1N1 virus, responsible for millions of deaths. Influenza pandemics, such as the "Asian flu" of 1957-60 (H2N2 virus) and the "Hong Kong Flu" of 1968-69 (H3N2 virus), also claimed millions of lives [15-17] (Table 1).

In 1901, the first "infiltrating agent" discovered to infect humans was the yellow fever virus [18]. According to Quammen [19] examples of these microorganisms and other diseases that have reached man, we can mention the measles that may have jumped into us from domesticated sheep and goats. Alternatively, other examples, the Hantavirus (HTV), from the Hantaviridae family, transmitted by rodents and the Lassa virus (LASV), from the Arenaviridae family, first identified in 1969 in Nigeria; these diseases started to leave their rodent hosts, causing hemorrhagic fevers in humans.

Some diseases, such as rabies and plague, crossed and even crossed the barrier between the species that existed between animals and men, we have observed for centuries how tenuous this barrier is, and it is increasingly clear that it is impossible to separate animal and human health.

Some viruses, such as Zika (ZKV) and West Nile Fever (WNV) virus, which originated in Africa, have mutated and settled on other continents. West Nile disease, for example, which affects humans and horses, is caused by a flavivirus that is also found in different species of birds, wild and domestic mammals, as well as species of mosquitoes and ticks [20-22].

As an example, we mention those belonging to the Filovirus family, the Marburg virus (MARV) in 1967, where the disease originated from green monkeys of the genus *Chlorocebus* spp. and in 1976, Ebola (DVE) in Africa, also caused hemorrhagic fevers. Suspicions fell, under the transmission of different species of fruit bats (Pteropodidae), but investigations were rare and of unknown origin and the evidence could be just coincidences [23,24]

More recently, in light of new discoveries of viral fragments, Ebolaviruses are associated with bats:

a new Ebolavirus, discovered by American researchers [25] called Bombali virus (BOMV) was detected in free-tailed bats of the Molossidae family (*Chaerephon pumilus*) and (*Mops condylurus*) registered in Sierra Leone. Recently, Kupferschmidt [26] reported the existence of an Ebolavirus supposedly sequenced from a species of insectivorous bat in the family Miniopteridae (*Miniopterus inflatus*), captured in 2016 in Liberia.

The Hendra virus (HeV) 1994, in Australia, transmitted by horses and the Nipah virus (NPV) 1998, in Malaysia, belonging to the Paramyxovirus family, has the bats *Pteropus* spp. like their primary hosts [27], in the most likely epidemiological scenario, pigs became contaminated with the Nipah virus by eating leftover fruit eaten by bats establishing pig-to-pig transmission, and the pathogen spread from pigs and ended up infecting humans when they come into contact with mucous membranes and excreta from infected pigs [28]. This is due to the fact that these animals are considered intermediate hosts of these viruses, due to their upper respiratory tract having receptors for different virus species, as well as for the swine/human virus (SA- $\alpha$ -2,6) and for avian influenza (SA- $\alpha$ -2,3) that reaches wild, aquatic and domestic birds [29].

Drexler [30] in research carried out, identified 66 new species of Paramyxovirus in bats and rodents, and drew attention to the fact that the Hendra and Nipah viruses probably had their rise in Africa, where they circulate in these mammals. The HIV-1 virus itself got in our way from chimpanzees. Thus, there is a certain diversity of origins and mysteries. But a large fraction of all the new scary viruses have been jumping on bat humans [19].

Still, in relation to historical facts, the influenza viruses (Orthomyxoviridae), which cause influenza, they transfer from wild and migratory birds to domestic birds, and after a period of visiting pigs, they complete their adaptive processes and then decide to affect humans [19,31]

Influenza is recognized worldwide for its ability to generate epidemic and pandemic waves with notes of the main virological, clinical and epidemiological characteristics, including its mortality and lethality and the context of its occurrence in a pandemic character. Antigens of viral surfaces H1, H2 or H3 and N1 or N2 are probably responsible for influenza infections to the present day [32].

The role of bats in the emergence and transmission of new influenza viruses is not yet fully understood, although influenza A viruses H17 and H3N2 have been discovered in species of the family Phyllostomidae (*Sturnira liliium*) and Vespertilionidae (*Nyctalus noctula*) [33].

## 7. THE CORONAVIRUS TAXONOMY

Coronavirus have become the focus of research since the first global epidemic caused by Severe Acute Respiratory Syndrome (SARS). The recent discovery of a wide variety of new Coronavirus in different host species encouraged the reclassification of the order Nidovirales, subdivided into 8 suborders, which have 14 families: Abyssoviridae, Arteriviridae, Cremagaviridae, Gresnaviridae, Olifoviridae, Coronaviridae, Mesioniviridae, Medioniviridae, Nanghoshaviridae, Nahypoviridae, Euroniviridae, Roniviridae and Tobaniviridae [34].

The current classification of coronavirus includes this group of viruses in the Riboviria kingdom, Order Nidovirales, suborder Cornidovirineae, family Coronaviridae, recognizing two subfamilies Letovirinae and Orthocoronavirinae (four genera ( $\alpha$ ,  $\beta$ ,  $\gamma$ ,  $\delta$ -CoV), 25 subgenera and 45 species) [10,34]. The Coronaviridae family (RNA virus), which comprises important human and veterinary pathogens, are responsible for causing respiratory, gastrointestinal, cardiovascular and neurological diseases [35]. In the Baltimore classification, taking into account the nature of the nucleic acid and the replication strategies. Coronavirus belong to class IV (ssRNA) positive sense [36].

With the wealth of phylogenies of Coronavirus generated after the SARS epidemics; the Orthocoronavirinae sub-family, according to the International Virus Taxonomy Committee; consists of four genera based on their genetic properties, including the genera Alphacoronavirus ( $\alpha$ -CoV), Betacoronavirus ( $\beta$ -CoV), Gammacoronavirus ( $\gamma$ -CoV) and Deltacoronavirus ( $\delta$ -CoV) [34]. The first two genera mainly affect mammals in general, while Gammacoronavirus are found in birds and mammals, including isolation records in Swan goose (*Anser cygnoides*), Asian leopards (*Prionailurus bengalensis*), beluga whales (*Delphinapterus leucas*) and nose dolphins (*Tursiops aduncus*) [13,35,37-41] (Fig. 1)

In their records, Woo et al. [39] suggest that the Gammacoronavirus of dolphins and beluga

whales are characterized as distinct species of cetacean Coronavirus (Fig. 1). And finally, the recent findings of Deltacoronavirus identified in pigs and birds [42,43] as the isolates described in Brazil by Barbosa et al. [37] from avian species *Anser cygnoides* and *Rhynchops niger* (Black-skimmer) and Gammacoronavirus in water birds of the genus *Calidris* (Scolopacidae) (Fig. 1).

There are seven human Coronavirus (HCovs) recognized for causing diseases: HCoV 229E (1965), SARS-CoV-1 (2002), MERS-CoV (2003), HCoV-NL63 (2004) and SARS-CoV-2 (2019) have bat virus viruses as ancestors, while the main animal host of SARS-CoV are horseshoe bats (*Rhinolophus sinicus*) [44]. MERS-CoV is phylogenetically related to the coronavirus of several bat species belonging to the Vespertilionidae family, with exceptions being HCoV-OC43 (1967) and HCoV-HKU1 (2005) that appear to originate from rodent coronavirus. SARS-CoV-1, MERS-CoV and SARS-CoV-2, cause serious infections and epidemics, while the other four Coronavirus (HKU1, NL63, OC43 and 229E) are common causes of colds, associated with mild symptoms [11,12,42,45,46]. These two informal subgroups were recently recognized as subgenera Sarbecovirus and Merbecovirus integrating with other 3 subgenera Embecovirus, Nobecovirus and Hibecovirus, all belonging to the genus Betacoronavirus [10].

While the coronavirus CoV-229E and HCoV-NL63 belong to the genus Alphacoronavirus, the viruses HCoV-OC43, HCoV-HKU1, SARS-CoV, MERS-CoV and SARS-CoV-2 are part of the genus Betacoronavirus [38,42,43,47,48].

The Betacoronavirus (Beta-CoVs) of greatest clinical importance for humans are OC43 and HKU1 of strain A; SARS-CoV and SARS-CoV-2 (COVID-19) of strain B, and MERS-CoV of strain C. MERS-CoV, which caused cases in the Middle East, Europe and Africa, are also phylogenetically close related to coronavirus of bats of the Vespertilionidae family of the genera Pipistrellus, Tylonycteris, Nyctalus, Epseticus, Myotis and Hypsugo, and the first betacoronavirus belonging to the C strain that infects humans is known. Coronavirus strains D include coronavirus from bats of the family Pteropodidae: *Rousettus* spp. [2,12,38,42-44,47,48].

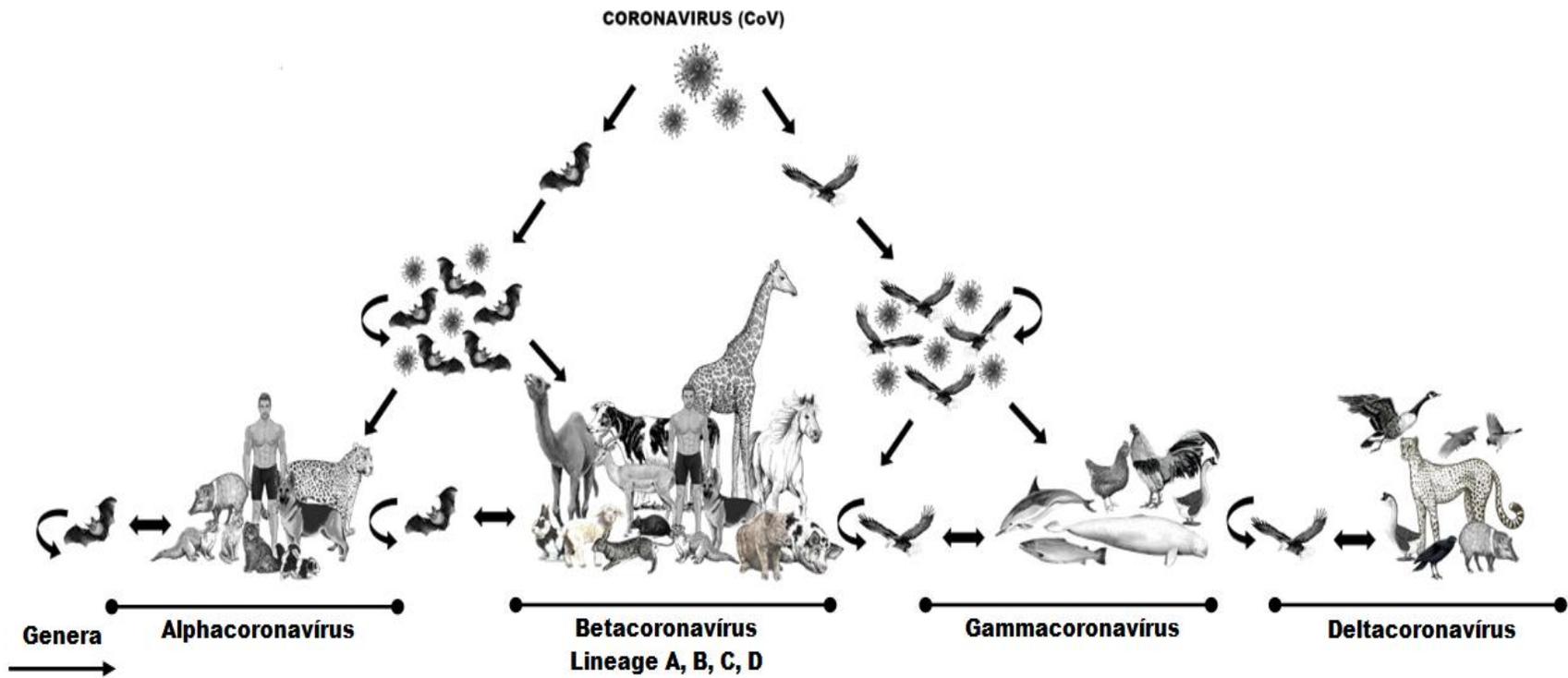
**Table 1. Characterization and descriptions of the main epidemics and pandemics of viral and bacterial origins registered on the planet in the XIX, XX, XXI centuries**

Year/Registration	County of Occurrence	Event	Disease	Etiologic agent/ Genus/Specie	Taxonomic family	Reservoirs/Transmission	Symptoms
1343-1351	China	Black plague	Bubonic plague	<i>Yersinia pestis</i> (bacteria)	Enterobacteriaceae	Fleas ( <i>Xenopsyla cheopis</i> and <i>Pulex irritans</i> ) and rodents ( <i>Rattus rattus</i> and <i>Rattus norvegicus</i> )	Fever, headaches, vomiting and rash in the ganglia
1685	Africa	Arbovirosis	Yellow fever	Flavivirus	Flaviviridae	Non-human primates. Mosquitoes <i>Haemagogus</i> spp. e <i>Sabethes</i> spp. (wild) <i>Aedes aegyti</i> (urban)	Sudden fever, chills, severe head and back pain, body aches, nausea and vomiting, fatigue and weakness. Icteric.
1770-1780	Asia	Arbovirosis	Dengue	Flavivirus (DENV 1,2,3,4)	Flaviviridae	Mosquito <i>Aedes aegypti</i> and <i>Aedes albopictus</i>	Fever, chills, severe head and back pain, body aches, nausea and vomiting, fatigue and weakness. Hemorrhage.
1817, 1832, 1852, 1863-1875, 1866, 1892, 1899, 1951-1966	Asia Europa Africa	<i>Cholera morbus</i> (8 global pandemics)	Cholera	<i>Vibrio choelerae</i> (bacteria)	Vibrionaceae	Contaminated water and food	Severe diarrhea, vomiting and nausea
1824-1840	Índia	Great fire or Spotted death	Smallpox	<i>Orthopoxvirus variolae</i>	Poxviridae	Infected secretions	fever, body and throat rasches. Eradicates in 1980.
1850-1950	Europa	White plague	Tuberculosis	<i>Mycobacterium tuberculosis</i> (bacteria)	Mycobacteriaceae	Humans. Aerosols. cough and sneeze droplets	It affects the respiratory system. Chronic cough with expulsion of blood, sputum, fever, night sweats and weight loss.

Year/ Registration	County of Occurrence	Event	Disease	Etiologic agent/ Genus/Specie	Taxonomic family	Reservoirs/Transmission	Symptoms
1889-1990	Russia	The flu	Influenza A	<i>Mixovirus influenzae</i> Subtypes (H2N3 or H3N2)	Orthomyxoviridae	Aerosols. Cough and sneeze droplets	acute high fever, headache, joint pain, nasal constipation and sore throat and cough.
1918-1920	USA	Spanish flu	Influenza A	<i>Mixovirus influenzae</i> Subtype (H1N1)	Orthomyxoviridae	Swine and poultry	acute high fever, headache, joint pain, nasal constipation and sore throat and cough.
1918-1922	Europa	Exanthematic typhus (rickettsiosis)	Typhus	<i>Rickettsia prowazekii</i> (bacteria)	Rickettsiaceae	Fleas ( <i>Xenopsyla cheopis</i> ) and rodents	headache and joint pain, high fever, delusions and hemorrhagic rashes.
1947	África	Arbovirosis	Zika	Flavivirus (ZKV)	Flaviviridae	Rhesus monkey ( <i>Macaca mulata</i> ) Mosquito <i>Aedes aegypti</i> and <i>Aedes albopictus</i>	Fevers, body and joint pain, neurological complications such as encephalitis, Guillain Barré syndrome, microcephaly
1953	Tailândia	Arbovirus	Chikungunya	Alphavirus (CHIKV)	Togaviridae	Mosquito <i>Aedes aegypti</i> and <i>Aedes albopictus</i>	Fever, headache, malaise, body aches and a lot of joint pain, red spots or blisters on the body
1957-1958	China	Asian flu	Influenza A	<i>Mixovirus influenzae</i> Subtype (H2N2)	Orthomyxoviridae	Humans, pigs, horses, other mammals and birds. Contaminated fluids and objects	Acute high fever, headache, joint pain, nasal constipation and sore throat and cough.
1968-1969	China	Hong Kong flu	Influenza A	<i>Mixovirus influenzae</i> Subtype (H3N2)	Orthomyxoviridae	Humans, pigs, horses, other mammals and birds. Contaminated fluids and objects	Acute high fever, headache, joint pain, nasal constipation and sore throat and cough.
1977-1978	Asia Europa Africa America	Russian flu	Influenza A	<i>Mixovirus influenzae</i> Subtype (H1N1)	Orthomyxoviridae	Humans, pigs, horses, other mammals and birds. Contaminated fluids and objects	Acute high fever, headache, joint pain, nasal constipation and sore throat and cough.

Year/ Registration	County of Occurrence	Event	Disease	Etiologic agent/ Genus/Specie	Taxonomic family	Reservoirs/Transmission	Symptoms
1980 – 1982	Africa	HIV/AIDS	Acquired immunodeficiency syndrome	Lentivirus HIV1	Retroviridae	Primates (Monkeys, gorillas, chimpanzees and humans) Blood and body fluids	Fever, headache and myalgia, evolving, vomiting and diarrhea. Deterioration of the immune system. It lasts until the present day.
2002-2003	China	Asian pneumonia	Acute respiratory syndrome	Betacoronavirus SARS-CoV-1	Coronaviridae	Bats Aerosols. Cough and sneeze droplets	Fever, cough, breathing difficulties. Pneumonia
2003-2004	Ásia	Avian flu	Influenza A	<i>Mixovirus influenzae</i> Subtype (H5N1)	Orthomyxoviridae	Humans, pigs, horses, other mammals and birds. Contaminated fluids and objects	Acute high fever, headache, joint pain, nasal constipation and sore throat and cough.
2009-2010	México	Gripe Suína	Influenza A	<i>Mixovirus influenzae</i> (H1N1) pdm09	Orthomyxoviridae	Humans, pigs, horses, other mammals and birds. Contaminated fluids and objects	Fever, cough, sore throat, chills and body pain.
2012-2013	Saudi Arabia	Pneumonia	Acute respiratory syndrome	Betacoronavirus MERS-CoV	Coronaviridae	Bats and Dromedaries Aerosols. Cough and sneeze droplets	Fever, cough, breathing difficulties. Pneumonia
2013-2016	Africa	Hemorrhagic fever	Ebola	Ebolavirus (6 subsp.) Bombali, Zaire, Sudan, Tái, Bundibugyo and Reston	Filoviridae	Bats are the most likely Contaminated fluids and objects	High fever, body aches, vomiting and bleeding
2019-2020	China	Asian pneumonia	Acute respiratory syndrome	Betacoronavirus SARS-CoV-2	Coronaviridae	Bats? Reservoir? Aerosols. Cough and sneeze droplets	Fever, cough, breathing difficulties. Pneumonia

Sources: ICTV [34]; WHO [98]; Hay [99]; Tibayrenc [100]



**Fig. 1. The four genera of Coronavirus: Alphacoronavirus, Betacoronavirus, Gammacoronavirus and Deltacoronavirus and their respective reservoirs and hosts. Bats and wild birds are seen as genetic sources for the spread of viruses, based on epidemiological, virological and phylogenetic evidence. Only coronavirus A and B have the ability to infect humans**

*Sources: Shereen et al., [11]; Woo et al. [42]. Adapted: Leite-Jr, D.P.*

In view of the reports, it has been proposed that bat CoVs are the genetic source of all Alphacoronavirus and Betacoronavirus in the wild, while avian CoVs are considered the genetic source of all Gammacoronavirus and Deltacoronavirus [12,42,44]. Coronavirus can infect humans and many different animal species, including birds, cetaceans, bats, giraffes, ferrets, minks, rabbits, camels, cats, pigs, cattle, horses, dogs, rodents, snakes and other wildlife [11,39,49] causing a variety of respiratory, enteric, liver and central nervous system diseases.

According to Botto Nuñez et al., [50] the spread of wildlife pathogens to humans or pets requires a number of conditions to align with space and time. Bats are known to be reservoirs for a variety of mammalian pathogens, including viruses, fungi and bacteria. Genomic analysis revealed that SARS-CoV-2 is phylogenetically related to bat viruses like severe acute respiratory syndrome (SARS type), so bats can be the possible primary reservoir, [10,11,48,51] which was recently concluded in the coding of a new RmYN02 found in a bat sharing 96% similarity of its RNA with that of SARS-CoV-2 [52].

Of the viruses that affect humans, coronavirus is a relatively large viral group, have 125 nanometers in diameter and for viruses that use RNA to replicate, they have the largest genomes with 30,000 genetic bases, and the group are responsible for most diseases emerging. In relation to other viruses, their genomes are three times larger than those of HIV and hepatitis C and more than twice that of the Influenza virus [52,53].

The coronavirus genome is subdivided into a variable number of open reading sequences (ORF, 6 to 9), which encode a set of non-structural proteins with RNA polymerase function (Pol -1a, b), and four main proteins structural: Spicula glycoprotein (S), Membrane (M), Envelope (E) and Nucleocapsid (N). In addition to these, there are non-structural proteins with unknown functions and group-specific position in the genome [54] (Fig. 2).

The spike (S) protein, a type I membrane glycoprotein, is primarily responsible for the entry of the virus into susceptible cells through initial interaction with specific cell receptors and subsequent mediation of the fusion between the virus-cell membranes and consequently the entry of the virus in the cytoplasm [55] (Fig. 2)

The particles have projections emanating from the envelope in the form of spikes, formed by trimers of protein S (spike protein). These projections generate a crown aspect, hence the name Coronavirus. In the case of SARS-CoV-2, which causes the current pandemic of COVID-19, protein S recognizes the receptor through its receptor binding domain (RBD), a gateway that is a protein called ACE2 (angiotensin-converting enzyme) 2) present on the outside of lung cells and throat, cells of humans, ferrets, cats, monkeys, bats and other species with high homology of receptors [56].

Once installed inside the human body, SARCoV-2 uses a diverse arsenal of strange and dangerous molecules. Evidence of their physiology and genetics suggests that the viral form was close to humans, hidden in nature for many decades, using animals as a "smoke screen", and then manifesting themselves in humans in the form of a pandemic.

Brazilian researchers, [57] in a more recent study analyzing the evolutionary characteristics of the virus, emphasize that the SARS-CoV viruses have been evolving and becoming more apt to attack humans and have found answers to these variations in human genes of our hominid ancestors, the Neanderthal man (*Homo neanderthalensis*).

In fact, the taxonomic demarcation of this acellular group; between genus, species complex, variations, species and serotypes or other specific names; it can be somewhat arbitrary. Nevertheless, a study of currently recognized 'species' is a natural starting point for attempts to characterize and interpret patterns of virus diversity [5].

The SARS virus, which stands for Severe Acute Respiratory Syndrome, which plagued China, killed more than 700 people and spread to 30 countries in 2002-2003, infecting humans on different continents including countries in Asia, Europe, America and Oceania. A Coronavirus, the SARS-CoV-1, which is a "relative" of our pandemic enemy that causes COVID-19 disease, called SARS-CoV-2, [19,31,49] caused this syndrome.

The most recent outbreak of viral pneumonia in China, which started in December 2019 and has spread to other continents, has some possible origins of the outbreak. Studies by Chinese researchers [47,58] observed that some patients infected by the virus were exposed to wild

animals in a wholesale market, where seafood, birds, reptiles, bats and rural animals were sold.

The emergence of SARS marked the beginning of the intensive study on Coronavirus [44,59] and has registered its mark in the 2020s. Among the 23 coronavirus classified as Alphacoronavirus and Betacoronavirus, with the complete genomic sequence available, nine of them come from bats. In addition, bats are also hosts for another 103 coronavirus identified worldwide, recorded in the researcher's work, [2,12,42,60,61,62] including in South America [63,64].

Many hypotheses were created, for the beginning of the outbreak, where the transmission of the virus jumped from its natural reservoir, a probable bat (*Rhinolophus sinicus*), to the man probably occurred through contact, in the wildlife markets with carnivorous mammals like the masked palm civet Himalayan (*Paguna larvata*), Chinese ferret-badger (*Melogale moschata*), raccoon dogs (*Nyctereutes procyonoides*) and Malayan pangolins (*Manis javanica*) [31,44,65,66]. The studies carried out, in this sense, never proved the existence of the live virus in a bat, however in 2005, Chinese researchers [59] isolated natural strains of coronavirus similar to SARS-CoV.

Regarding the origin of the virus, it was initially suggested that snakes would be the most likely animal reservoir for 2019-nCoV. [12,47,58] More current research has concluded that genomic sequences are more closely related to SARS-CoV-2 originating from bats (BatSL-CoVZC45), with 96% similarity in sequential confirmation with a group of coronavirus type SARS-CoV (Betacoronavirus) [12,49,67].

However, despite this link with these mammals, several factors suggest that another animal, still unknown, may be acting as an intermediate host between bats and humans [11,12] Discover the missing link present in the leap of coronaviruses, which highlight and incriminate bats as probable transmitters for humans.

Wang et al, [68] indicated in their studies; carried out on viruses and their hosts suggested that viruses tend to evolve in the codon use bias when comparable to those of their hosts. Féllez-Sánchez et al., [69] using assays with HPV viruses, they call that synonymous codons are used by the parasite and are not the same ones used by the host, this is called bias in the use of codons, since each virus uses the cellular machinery for replication using its codons to be

translated and in addition to the recombination between taxa of the same virus family, there may also be recombination between close families, due to cross infections.

In view of these perspectives, Lu et al., [12] emphasize that genetic analyzes suggest that COVID-19 and the most similar genomes with the bat Coronavirus and the codon use bias more similar to that of snakes; emphasizing that this homologous recombination of unknown origin can occur within the virus glycoprotein; which perhaps could explain its interspecific transmissibility and that this spread would be limited from person to person [70].

Chinese researchers, [11,12] revealed that the analyzes carried out confirmed a homologous recombination between the bat Coronavirus and a Coronavirus of unknown origin in the viral peak glycoprotein gene, even if no evidence has been found so far isolating the presence of the virus in animals, only in humans. According American researchers [53] this recombination in bats happens frequently, as these mammals get to host 61 viruses that infect humans; some species harbor up to 12 different types.

However, Chinese researchers indicate that a close relative of SARS-CoV-2 found in bats offers more evidence of natural evolution. Although not a direct evolutionary precursor to SARS-CoV-2, Chinese researchers have described a bat coronavirus in Yunnan province, recently identified RmYN02, which contains amino acid insertions at the junction of the S1 and S2 subunits at the peak of the virus similar to SAR-CoV-2, the results found suggest that this type of apparently unusual insertion event can occur naturally in wildlife, indicating an evolution with strong evidence that these insertion events can occur naturally in animal beta-coronavirus [52,37].

Another infection by viruses of the Coronaviridae family is the MERS-CoV Respiratory Syndrome; they are new viruses for humans and are spreading globally. The primary animal reservoir of the MERS-CoV is the dromedary (*Camelus dromedarius*), which occurred in the Middle East, which has been confirmed by experimental infections in these animals and which also transmits this virus to man, although most of the cases so far known inter-human transmission. Chinese researchers report that SARS-CoV and MERS-CoV originated from bats, both species left their natural reservoir and jumped to infect humans through different intermediate hosts [48,51].

Evidence showed that the genetic analyzes found in feces samples of the bat species of the family Emballonuridae, known as the Egyptian tomb bat (*Taphozous perforatus*) were reported by Memish et al., [71] defining that bats are the main reservoir of MERS-CoV and the intermediate reservoir dromedaries. We can observe with these results that the risk of pathogens being transmitted to humans has always existed and will be present whenever natural barriers are overcome.

## 8. WHAT IS THE FAULT OF BATS, ABOUT ALL THIS?

Let us start our conversation by clarifying first that bats are not to blame for what happened in pandemics. According to reports in various surveys, 75% of all emerging and reemerging infectious diseases that threaten public health are zoonotic, most of which spread from wild reservoirs directly to humans or through domestic animals [5,8,9]. The program developed by the USA on Emerging Pandemic Threats, published a report that also complies and recorded this information, alerting this situation [7].

After the Rodentia order, bats constitute the second largest order of mammals, making up 20% of species of the Mammalia class. Taxonomically, bats are classified in the order Chiroptera, subdivided into two sub-orders, Microchiroptera and Megachiroptera, commonly referred to as microbats and megabats [2]. Currently these sub-orders are known as Yangochiroptera and Yinpterochiroptera, respectively [72] Among all mammalian species of this order they present a high degree of ecological and behavioral plasticity, diversity of species existing throughout the world and a range of physiological and immunological resources (Table 2).

Bats are one of the main sources of zoonotic viruses worldwide [53]. Tropical forests are full of bats, currently there are 9 families, 68 genera, 181 bat species officially registered in Brazil and more than 1,400 described worldwide [73], bats come in all shapes and sizes. Each species has its own range, in which ecologists call "functional characteristics", which are biochemical, physiological or behavioral characteristics, exclusive to the animal [74] (Table 2).

In the face of the epidemics of the last century, it is possible to observe that the increased interaction between humans and wild animals

has facilitated the emergence of viral strains of importance for public health. Bats, responsible for the aerial cycle of viral diseases, have shown great epidemiological importance, specimens of chiropterans are being found in urban centers, harboring the virus in the salivary glands, blood, feces, urine and other secretions, allowing its spread [33,75].

Exposures to infected aerosols generated during urine and defecation have been suggested as possible routes of intra-species and inter-species transmission of bat viruses. Bats can also transmit viruses to humans and other animals through bites and scratches, as in the case of rabies [33,76].

In fact, bats are crucial to the health of the terrestrial ecosystems in which they live. They play an important ecosystem role, both in the pollination and dispersion of various plant species, and in the control of insect pests in all places where these mammals are found, including in Brazilian biomes [77]. Monitoring bat species and their population dynamics can act as an important indicator of ecosystem health, as they are particularly sensitive to habitat conversion (bioacoustics), climate change and anthropic impact actions on biodiversity [38, 78].

This order of mammals appears to be one of the main reservoirs for viruses potentially terrible to humans. The implication of Coronavirus in humans, suggests that bats are natural reservoirs of a variety of viruses, as these winged mammals are not usually very sick.

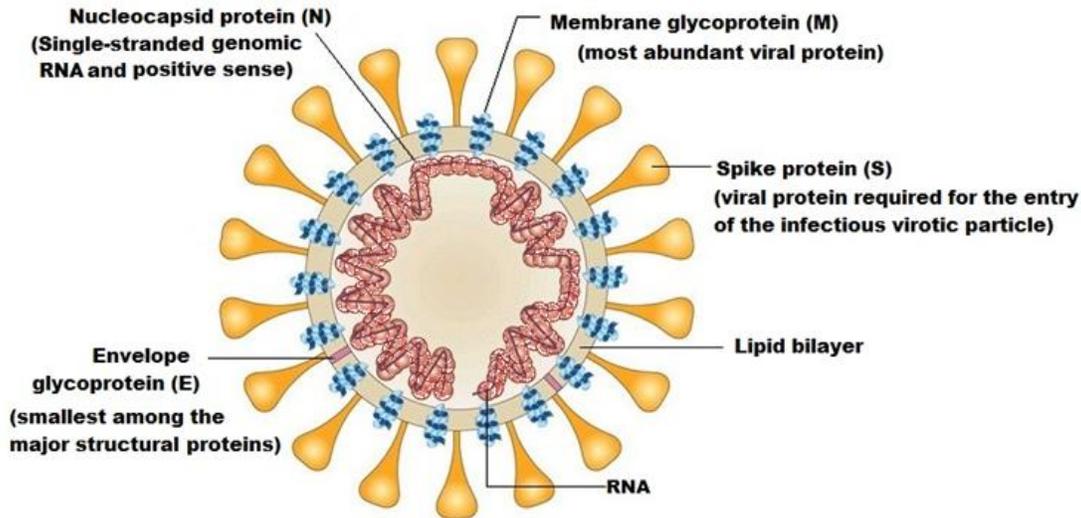
In view of this premise, it would be interesting to consider the potential role that these animals can have as sentinels, especially with regard to the introduction of pathogens in commercial creations or even in the human population [22]. Comparisons of bat genomes with other mammal species provide new insights into bat biology and evolution [79].

Portuguese researchers [74] emphasizes that this is due to the capacity and functional characteristics, exclusive of these winged mammals that have an impressive capacity to spread pathogens over a great distance and in a very wide way, implying in transmitting these agents to humans; when the natural balance undergoes intervention. And it is a fact, that this intervention is always associated with the action of human beings.

**Table 2. Taxonomic classification of bat families recorded by around the world. Families highlighted with "asterisk" are found in Brazil**

Kingdom: Animalia – Phylum: Chordata – Subphylum: Vertebrata – Class: Mammalia – Infraclass: Placentalia				
Order	Suborder	Family	Record the number of species	common name of bats
<b>Chiroptera</b>	<b>Yangochiroptera (Microchiroptera)</b>	Craseonycteridae (Hill, 1974)	1	Kitti's hog-nosed bat, Hog-nosed or bumblebee bat
		Cistugidae (Lack et al, 2010)	2	Wing-gland bats
		Emballonuridae * (Gervais & Castelnou, 1855)	54	Sheath-tailed bats or sac-winged bats
		Furipteridae* (Gray, 1866)	2	Smoky bats
		Hipposideridae (Lydekker, 1891)	88	Old World leaf-nosed bats
		Megadermatidae (Allen, 1864)	6	False vampire bats or greater false vampire bat
		Molossidae* (Gervais & Castelnou, 1855)	126	(Mexican or Brazilian) Free-tailed bats
		Mormoopidae* (Saussure, 1860)	18	Leaf-chinned bats or Ghost-faced bats
		Miniopteridae (Dobson, 1875)	38	Bent-winged, Long winged bat or Free-tailed bats
		Mystacinidae (Dobson, 1875)	2	New Zealand short-tailed bats
		Myzopodidae (Thomas, 1904)	2	(Madagascar) Old World sucker-footed bat
		Natalidae* (Gray, 1825)	12	(Cuban or Bahaman) Funnel-eared bats
		Noctilionidae* (Gray, 1821)	2	(Greater) Bulldog bats or fisherman bats
		Nycteridae (Van de Hoeven, 1855)	15	Hollow-faced bats or Slit-faced bats
		Phyllostomidae* (Gray, 1825)	217	American leaf-nosed bats (vampire bats)
		Rhinolophidae (Gray, 1825)	109	(Greater or Chinese) Horseshoe bats
		Rhinopomatidae (Bonaparte, 1838)	6	(Greater) Mouse-tailed bats
		Rhinonycteridae (Gray, 1866)	9	Trident bats
	Thyropteridae* (Miller, 1907)	5	(Spix's) Disk-winged bats	
	Vespertilionidae* (Gray, 1821)	496	Vesper bats or simple nose bats (common bats)	
	<b>Yinpterochiroptera (Megachiroptera)</b>	Pteropodidae (Gray, 1821)	191	Flying foxes, fruits bats or Old World fruit bats

\*List of chiropterans from Brazil. Garbino et al, [73]



**Fig. 2. Schematic representation of the SARS-CoV and SARS-CoV-2 (Coronavirus) virus structure. Viral surface proteins (spicule, envelope and membrane) are incorporated into a lipid bilayer envelope derived from the host cell. The single-stranded positive viral RNA is associated with the nucleocapsid protein. Proteins S, M and E are considered major structural proteins**

Source: Stadler et al. [97], Adapted: Leite-Jr, D.P.

These warm-blooded vertebrates exhibit high species biodiversity, migratory behavior, diverse shelters, associated with a unique adaptive immune system, and have characteristics favorable to dissemination, becoming immune or even a reservoir for a cocktail of different viruses to mix generation of new recombinant RNA viruses. Trait-related responses to habitat fragmentation in Amazonian bats. Trait-related responses to habitat fragmentation in Amazonian bats [76].

This conclusion brings us to facts in the history of some bat-related disease outbreaks and these facts require analysis of the immune systems of these animals, which seem to explain why they are potential hosts for a great diversity of viruses without apparently developing diseases caused by these viruses.

Reports described by Towner et al. [65] these researchers found that bats can carry an infectious form of Marburg virus (MARV) for months without showing any visible symptoms of loss of balance in their colonies, but that these mammals could transmit the viral source, eliminating in its saliva, feces and urine, making it an important fact in the host-parasite puzzle, and that other viruses could also be housed in a similar way.

Bats are the only mammals capable of sustained flight and are notorious reservoir hosts for some of the most highly pathogenic viruses in the world, including Nipah, Hendra, Ebola and SARS-CoV [6,79].

Investigative analyzes indicate factors that may also be related to the ease of adaptation of viruses in this order of animals. The first hypothesis refers that among the more than 5,400 mammal species identified in the world (including humans), more than 20% are bats. This diversity can provide a large number of different cell types for different Coronavirus. The second hypothesis emphasizes that the different environmental pressures to which these winged mammals are exposed, which would have provided the different species of bats with different selective pressures for parasitism of different Coronavirus. The third hypothesis characteristic of these mammals would be the habit of bats perching, resulting in a large number of animals gathered, which consequently could also have facilitated the exchange of glass particles. The last characteristic, perhaps the one that most emphasizes the adaptability of these mammals, would be the ability to fly. This facilitates the movement of these animals,

leaving them free from obstacles faced by land mammals. Bats can be found at altitudes up to 5,000 m. The ability to fly would have facilitated the possible exchange of glass particles and / or their genetic materials between different types of living organisms [28,33,42,43,80-82].

The emergence of the ability to fly is believed to be the key to explaining these animals' resistance to viruses and other pathogens. Studies developed by researchers [53,79,83] indicate that the apparent virulence to viral infections in these animals may be related to the increase in higher body temperatures during flight, and consequently the increase in metabolism and immunological activities. During the flight, there is an increase in metabolism, resulting in higher levels of oxygen free radicals, which, in turn, generate genetic changes. In order to avoid unwanted inflammatory responses to damaged DNA, bats have developed mechanisms to suppress inflammation, thus this immune trick provides these mammals with an evolutionary adjunct to their immune systems, providing a powerful selective force against virulence and promoting the diversity of viruses that infect bat populations, an evolutionary factor due to the body temperature spikes that occur in these mammals.

Whether viral activities in bats are related to the metabolism of these animals; on the other hand, if the reduction of the metabolic activity and of the immune system during periods of rest or low activity can contribute for pathogens adapted to adverse physical conditions to invade and decompress the body machinery of these mammals, as in the case of the fungal pathogen that causes white nose syndrome (WNS). Currently, the white nose syndrome in bats epidemic, which initially occurred with North American species, since its detection in the United States in 2006, has as a catastrophic example and causal agent a fungus psychrophilic *Pseudogymnoascus destructans* (Pseudeurotiaceae) [84].

This disease, caused by the cold-loving fungus responsible for zoonosis that has earned the name of white ring that forms around the snouts of these animals. Animals infected by this eukaryotic agent are no longer able to control their body temperature: during hibernation periods, they deplete their reserves and starve to death [85] decimating bat populations and harming their survival.

This disease has affected several species of chiropterans. In North America, the fungal agent has infected at least eleven bat species of the genera *Myotis*, *Eptesicus*, *Perimyotis*, *Corynorhinus*, *Tadarida*, *Lasiurus*, *Lasionycteris*, and in Europe and Asia, bat species that have been shown to harbor *P. destructans* include bats of the genera, *Myotis*, *Eptesicus*, *Miniopterus*, *Rhinolophus*, *Barbastellus* and *Plecotus* [86].

The bat's immune system may be a key mechanism to explain bats' long life and virus reservoir status. But when it comes to flight, since bats are the only species of mammal capable of flying and this interaction with viruses is so evident; reaching the conclusion that the flight can also be an adjunct and assist other animal species, as is the case of the insects that transmit pathogens of the genus *Aedes*, transmitters of the Dengue, Chikungunya, Zika and Yellow fever virus in the Americas, the transmitting agents of malaria protozoa (*Plasmodium* spp.), mosquitoes of the genus *Anopheles*, with wide worldwide distribution and also the genus *Lutzomyia* (*Leishmania* spp.), a species of sandflies found in the New World, distributed in areas of southern North America and throughout the neotropical zone, since all these species of arthropods use flight to reach their hematophagous sources.

Does this lead us to believe that bats are found guilty? In view of the reports, we need to respect their habitat more and try to understand the dynamics of it all. Bats are in the spotlight, but they are not the big "villains" of disease outbreak. In Brazil; mainly this order of mammals, carry the stigma due to its famous history for being hosts of the Rabies virus, a zoonosis of great relevance in the country. In the case of Coronavirus, it is not an exception, and we can consider a solution, before anyone thinks about exterminating them from planet hearth.

Because they are associated with the night and their dark nature, on the contrary, these animals have much more positive and heroic characteristics like the character in the Batman comics, than being stigmatized as Count Dracula, in literature and cinema. Voigt & Kingston [6] report that human beings are moved by their visual system and are more concerned with the animals that we see and interact during the day, therefore, they tend to neglect the dark side of conservation, that is, the protection of animals nocturnal.

According to reports by primatologist Jane Goodall [87] shortly after the explosion of COVID-19, a strict ban on wildlife trafficking has been implemented in China, including a ban on the import, sale and consumption of wild animals. Other countries, such as Vietnam, have also fostered the initiative and are following suit. These palliative measures seek to minimize global threats to wildlife, especially trafficking. Therefore, we must be much more vigilant about not being too close to the wildlife to protect them and ourselves.

According to Moratelli et al. [66] in most cases, the only evidence that associates bats with zoonotic infections would be the isolation or detection of pathogens in bats and humans in areas where diseases have arisen. In some cases, the same virus can be found in other terrestrial vertebrates, such as primates, antelopes and birds, or even in arthropods. This does not prove that bats are reservoirs; it is just evidence that, like mammals, humans and bats are similar enough to serve as temporary reservoirs for the same virus.

The reports found in the literature show that so far there is no evidence that SARS is a disease whose potential vector is bats, there are speculations that indicate that this species of mammal, is a potential vector, but incriminating it indistinctly is a mistake. What the reports actually show us is that, while scientists struggle to learn more about coronaviruses and their controversial conclusions, they qualify their conclusions and emphasize with the famous phrase: "More work is needed so that there is a better understanding of the proposed results".

## 9. BIODIVERSITY AND PATHOGEN TRANSMISSION

In Brazil, bats are protected by environmental legislation, and infractions are subject to civil, criminal and administrative penalties (Law on Fauna Protection - Federal Law No. 5,197, of January 3, 1967; Environmental Crimes Law - Federal Law No. 9,605, of February 12, 1998; Federal Decree No. 6,514, of July 22, 2008 - Provides for administrative infractions and sanctions on the environment, establishes the federal administrative process for investigating these infractions, and gives other measures) [88,89].

The legislation is very clear about the misfortune on wildlife, establishing severe penalties for offenders. Legal protection for bats has already

been implemented in Australia, Bulgaria, Czech and Slovakia, Denmark, East and West Germany, Finland, Hungary, Italy, Mexico, Poland, Russia, Yugoslavia and the United States [88].

Voigt & Kingston. [6] report in their book that 15% of bat species are listed as endangered by IUCN, that is, they are considered Critically Endangered, Endangered or Vulnerable. About 18% of the species are data deficient, highlighting the scarcity of ecological studies that can support conservation status assessments.

According to the latest edition of the Red Book of Threatened Brazilian Fauna of Extinction ICMBio [90], several species of chiropterans in Brazil are in endangered (EN) and vulnerable (VU) situations. Bat species of the sub-order Microchiroptera (currently Yangochiroptera), [72] belonging to the families Emballonuridae (16 spp.); Molossidae (27 spp.); Thyropteridae (4 spp.) Noctilionidae (2 spp.); Furipteridae (1 sp.) being *Furipterus horrens* (VU); Natalidae (1 sp.) being *Natatus macrourus* (VU); Vespertilionidae (28 spp.) being *Eptesicus taddeii* (VU) and ending the Phyllostomidae family (92 spp.) being *Xeronycteris vieira*, *Lonchorhina aurita*, *Glyphonycteris behnii* in a situation of vulnerability and *Lonchophylla dekeyseri* considered in danger.

In view of the above, we observed that the protection of the habitat of these mammals, through the actions and awareness of the conservation units can still be considered the main tool of action to reduce the risk of extinction of the species, but these actions of conservation and maintenance of biodiversity the fauna of Brazil and the world, cannot depend on a single type of standardization instrument for defense and awareness.

Pandemics originating from zoonosis are nothing more than a reflection of human intervention in the environment. In the desire to conquer, expand and acquire humanity, it invades the territories of others, causing these microscopic beings, hitherto asleep and even forgotten in their reservoirs, to emerge, thus becoming a problem originating from natural sources.

We use as a classic and practical example, among the risk factors are related to the presence of human beings in rural and wild areas, the infections generated by infected mosquitoes and that, perhaps, will bite human beings, who will present distinct symptoms, of according to each person and the level of

severity of the disease. These diseases, called arboviruses, cause infections, and the causes are viruses of the family Flaviviridae, such as West Nile Fever (WNV), Dengue (DENV), Zika (ZKA), Chikungunya (CHIKV), Yellow fever (YFV) and Mayaro Fever (MAYV) of the *Togaviridae* family [91]

The loss and decrease of biodiversity can affect the transmission of the disease by several mechanisms, as each species has a different effect on the transmission of pathogens and the decline in diversity can equally likely to cause a decrease or an increase in the transmission of diseases in the remaining species. As an example, the West Nile virus is a virus transmitted by mosquitoes, for which several species of passerine bird's act as hosts, the low diversity of birds increases human risk and the incidence of diseases, amplifying the virus, inducing a high prevalence of infection in mosquitoes. [28]

Kilpatrick [20] reports that many invasive species that have been disseminated by the globalization of commerce and travel are infectious pathogens, using the paradigmatic case of the introduction of the West Nile virus (WNV) that occurred in urbanized and agricultural habitats, with adaptation of the virus to infect local mosquito vectors and also associated with the feeding patterns of WNV mosquito vectors that are important for transmission.

Let it be said, in passing, that diseases transmitted by mosquitoes, the connection between the emergence of arboviral epidemics, deforestation and disorderly invasion of explored green areas is already established, although here in this article, we deal less with the loss of habitats than with their transformation.

According to Woolhouse & Gaunt [5] the "viral species" itself is an imprecise designation, citing as an example the influenza A virus, where different serotypes can have different epidemiologies and impacts on health; constantly causing ministries and health organizations to carry out vaccination campaigns in an attempt to contain outbreaks.

Like other animals, which live in forests among other biomes, bats are under great pressure because the landscape changes around them and their homes become more and more fragmented and inhospitable to their survival. Understanding how species' functional characteristics interact with environmental

characteristics can help scientists predict how biodiversity could be affected in the future [74].

Keesing et al., [28] reports that reduced biodiversity can affect the transmission of infectious diseases from humans, other animals and plants. In principle, the loss of biodiversity can increase or decrease the transmission of diseases and new pathogens. These researchers draw attention to the remaining issues, indicating that current evidence regarding the preservation and maintenance of intact ecosystems and their endemic biodiversity should generally reduce the prevalence of infectious diseases.

Bats are particularly susceptible to anthropogenic changes due to their low reproductive rate, longevity and high metabolic rates [6]. Natural habitat disturbances play a role in these changes, but the greatest pressure is often derived from the impact of the changes creating a set of biological, ecological, socioeconomic and anthropogenic factors and their related activities such as livestock, agriculture, mining, construction of dams under different scenarios, disordered land use, forest loss, deforestation and habitat fragmentation [5,74]. According to the report by the U.S. Agency for International Development [7] they point to the Amazon region, in South America, among one of the future "hot spots" for these invasion processes of intact and isolated environments.

Today, several researchers and environmentalists suggest that it is really the destruction of biodiversity by humanity that create conditions for the emergence of new viruses and diseases like COVID-19, the viral disease that appeared in China in December 2019, generating profound economic and social impacts in health; both in rich and developing countries [31]. Among these destructions, urbanization is seen as the most ecologically damaging change to land use worldwide, presenting significant threats to global biodiversity [6].

It is a fact that, since the 1990s, climatic and environmental factors have been anticipated as a dramatic global scenario for the coming decades, with global warming leading to the proliferation and displacement of mosquito vectors for arboviral diseases, as well as other vectors [4]. A recently published study, involving 178 research centers distributed across the planet, shows that trees, causing changes, have felt the thermal sensitivity of tropical forests, where climate

change has been showing greater thermal resilience. Researchers warn of the long-term climate adaptation potential of tropical forests requires protecting them and stabilizing the Earth's climate [92].

A recently published study, involving 178 research centers spread across the planet, reports information on the thermal sensitivity of tropical forests. Climate change has shown greater thermal resilience and is being felt by trees, causing changes. Researchers warn of the long-term climate adaptation potential of tropical forests requires protecting them to stabilize the Earth's climate [92].

The result of these global climate changes was observed in 2019, when a strong heat wave, reaching more than 42°C, in northern Australia (Queensland) killed almost one third of the bats of the sub-order Megachiroptera (=Yinpterochiroptera) [72] known as spectacled flying fox (*Pteropus conspicillatus*), black flying fox (*Pteropus alecto*) and gray-headed flying fox (*Pteropus poliocephalus*) considered an endangered species in the country [93-95]. According to the red list, has been showing a catastrophic picture of this scenario, where reports from that country show that more than 1,800 species of plants and animals and ecological communities are at risk of extinction [93,34].

These statements continue to open up new perspectives in the wild, bringing us closer to animals and the range of exotic disease-causing viruses that are housed in them, producing ideal conditions for this storm of emerging and reemerging infections.

In view of these records, we observed that new information should be obtained and analyzed in order to have an evolutionary understanding of viral groups, which are highly significant and necessary for this understanding. Many gaps in knowledge and behavior about bats and viruses of zoonotic origins still need clarification. Simply, associating these animals with contamination and the proliferation of these pandemics, spread fear and accurate information is highly regarded as ignorance, which is not acceptable.

According to Reis et al., [88] an enlightened society should execute fauna conservation programs without prejudice, which does not include only animals of public interest. Bats are threatened by insecticides, deforestation and

even motivated by legends and superstitions about them.

And finally, even though they are considered transmitters of viral agents, bats interact socially during illnesses that affect some of their individuals; American researchers [96] observed the social distance that vampire bats present when individuals in the group are sick, and promote this distance to avoid contamination of the group. What we can quote before these facts is that humanity still needs to learn a lot from the concepts of nature.

In fact, what we must adopt is the insertion of a new discipline, planetary health, which focuses on the increasingly visible connections between the well-being of human beings and the way of life and behavior of other living beings, and even entire ecosystems [31]. These actions together transform and aim at the conscious use of nature, while harmoniously respecting the renewal of natural resources with use based on sustainability.

## 10. CONCLUSION

Evidence suggests that there is still a considerable group of undiscovered human virus species. Many specialized human viruses have their origin in registered in different animal groups, and when there is a natural breakdown of their reservoirs, they pass to humans and can also infect other non-human hosts.

Exterminating populations of certain animal species can cause an imbalance in the ecosystem services provided by these animals. Ignoring the potential role of winged mammals, and their close relationship in the maintenance, circulation and transmission of pathogens to humans, which these animals coexist with, can be considered a mistake.

The SARS-CoV-2 epidemic came to test the ability to face a threat that could be repeated in the future. Increasingly, we must learn from our mistakes and be better prepared than before, for what seems inevitable that new human viruses will continue to emerge.

Often the spread of epidemics and their impact on human populations are and have often been influenced by environmental, social and political factors. In addition, these epidemic events can affect different groups in a society in different ways and varying degrees, taking on proportions

that often provoke different explanations and meanings, often inaccurate and sometimes divergent.

Given this premise, perhaps we should move forward against these pandemic events using the knowledge already acquired by investing even more in science, research, education and extension, in studies of disease spread and epidemiological control. Educational efforts are needed to prevent future repercussions of virus transmitted by bats and to further protect bats from unnecessary slaughter. That way we can use this knowledge to try to stay one step ahead and better prepare for future pandemic events.

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### COMPETING INTERESTS

Authors have declared that no competing interests exist.

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