Aquatic biota is not exempt from Coronavirus infections: An overview.

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Abstract

Coronaviruses are pathogens recognized for having an animal origin, commonly associated with terrestrial environments. However, although in a few cases, there are reports of their presence in aquatic organisms like fish, frogs, waterfowls and marine mammals. None of these cases has led to human health effects when contact with these infected organisms has taken place, whether they are alive or dead. Aquatic birds seem to be the main group carrying and circulating these types of viruses among healthy bird populations. Although the route of infection for CoVID-19 by water or aquatic organisms has not yet been observed in the wild, the relevance of its study is highlighted because there are cases of other viral infections known to have been transferred to humans by aquatic biota. It is encouraging to know that aquatic species, such as fish, marine mammals, and amphibians, shows very few cases of coronaviruses and that some other aquatic animals may also be a possible source of cure or treatment against then, as some evidence with algae and marine sponges suggest.

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1. Introduction

The current Severe Acute Respiratory Syndrome coronavirus 2 (SARS-CoV-2) or CoVID-19 pandemic, as it is commonly known, brought society's interest in one of the families of high-risk pathological-infectious viruses, known as Coronavirus (CoVs)[1]. The impact that the CoVID-19 has had on human dynamics is undoubtedly enormous. The mortality and public health impacts caused by CoVID-19, caught the attention of scientists to try to slow down its effects and look for a vaccine. This virus is already present in every continent, and as previous events with other viruses such as SARS or HIV (Human Immunodeficiency Virus), humans will have to learn how to live with it. However, this situation also makes us wonder about what other organisms may be subject to coronavirus infection? Which organisms can be vectors or reservoirs? That is that they may have the virus in their body, transport it and spread it in other areas or to other organisms, without suffering the symptoms of the infection. Moreover, can the coronavirus infect and affect aquatic organisms? These questions, indeed some present in the scientific and non-scientific communities may eventually be answered in a particular way over time for SARS-CoV-2. However, at the moment, scientific efforts are focused on the public health aspects at the global level [2,3]. Thanks to previous studies on the subject, we can have access to information that allows us to understand more about the possible scenarios associated with these questions. Moreover, to be able to make more specific approaches to the impact of SARS-CoV-2 on aquatic organisms, based on the general knowledge that is available on coronaviruses. Due to the above, this review aims to synthesize the information available in the scientific literature on the detection and presence of coronavirus in organisms and promote its study, not only for the ecological and public health impacts but also its potential as treatment sources. This work has been focused on the coronavirus basic features, presence in aquatic environments, detection in aquatic organisms (fish, marine mammals, waterfowls, amphibians, crustacean and molluscs), some viral infections on humans from aquatic organisms, and further considerations involving biological aspects or potential use of biomolecules produced by aquatic biota, in search of a treatment or control against coronavirus exposures. This review highlights the proven CoVs cases, discuss if their features could be an indication of future CoVs infections, taking into account previous infections from similar viruses, as well as the possible implications in its dispersion. It also mentions the potential that aquatic organisms can represent in the search for control or treatment against these highly pathogenic viruses. The importance of carrying out broad and specific studies on coronavirus presence, abundance, pathologies, dispersion and affectations in aquatic biota is discussed.

1.2 Coronavirus features

CoVs are pathogens associated with epithelial cells infections such as gastrointestinal (gastroenteritis) and respiratory (respiratory infections) [4–6]. Its structure consists of three components: 1) genetic material with which it replicates or reproduces within infected cells, known as RNA (ribonucleic acid of a chain between 26 and 32 kb in length), 2) an external protein that surrounds it known as caps (viral wrap) and 3) a membrane that surrounds and envelops the protein cover, which is covered in turn, with spicules that give the shape of a "crown", from which they are called coronavirus, and that allows them to recognize and come into contact with the membrane of the cell that will infect [7,8]. These spicules are called the "S" protein [7].

It is recognized that CoVs have its origin in bats, with several varieties or viral species depending on poly-protein or full genome analyses [8,9], which include some of the most toxic and lethal strains of recent decades. CoVs mainly affect terrestrial organisms, such as humans, bats, felines, camels and birds [8,10]; however, their potential to infect the aquatic life has been demonstrated.

Coronaviruses are part of the Family Coronaviridae of the Order Nidovirals, which in addition to infecting terrestrial mammals and birds, have also been found in a frog, fish and marine mammals [6,8,11]. Four genera are recognized based on their phylogeny and genomic structure, from the subfamily Orthocoronavirinae, of which *Alphacoronavirus, Betacoronavirus*, *Gammacoronavirus* and *Deltacoronavirus* stand out, for their ability to infect humans and non-human respiratory tracts, and other organisms at the digestive level (enteritis) [8]. Within this group of Nidovirals, we find viruses such as the widely known SARS-CoV and MERS-CoV (Middle East Respiratory Syndrome), both belonging to the genus *Betacoronavirus* and subgenus *Sarbecovirus* and *Merbecovirus,* respectively [6,8]. These two types of viruses are recognized as infectious of zoonotic origin, that implies a transmission from an animal, as a result of direct interactions with an animal carrying the infection. The other subfamilies within the Coronaviridae are the Torovirinae, formed in turn by two genera, *Torovirus* and *Bafinivirus*, and Letovirinae with *Alphaletovirus* (LeV*),* respectively. *Bafinivirus* has been identified in a teleost fish [12,13] and LeV in a frog [11], a clear example that it is possible to find coronaviruses in aquatic environments.

2. Coronavirus and aquatic environments

The presence of CoVs in natural waters has been determined with low percentages, compares to another type of viruses; however, they have been detected recently, as is the case of the Ilé river basin in Kazakhstan [14].

Interest in virus transmissions in aquatic media focuses on those with public health relevance, which often enter natural water from treated and untreated wastewater discharges [4,15]. In the 1980s, it was recognized that as far as pathogenic viruses are concerned, more than 100 different types are excreted by man or by animals through their faeces [16]. The stool is one of the main materials for viruses transfer to water bodies. The transfer to the mouth as a result of poor hygiene, or the intake of contaminated water, allows viruses to enter the digestive system, infecting and replicating itself in the gastrointestinal tract, and then being expelled in large numbers again in the faeces produced by infected people or animals [17]. It is estimated that about 10 billion viral particles are present for every gram of excrement [18]. Sewages, especially in countries with limited capacities for treatment and adequate sanitization, poses a risk of contamination when discharged or overflowing into the bodies of natural water occurs [18]. Unfortunately, this scenario becomes more complicated considering that also hospital waste, biological-infectious and sanitary waste (intimate towels, mouth covers, gauze, body protectors among others), can eventually reach lakes, lagoons, rivers and seas, due to their mishandling as solid waste, becoming vectors of viruses towards the aquatic environment. Recently, a study has shown the presence of SARS-CoV-2 from the waste discharge activities of infected communities [19].

Some CoVs transmitted through contaminated food or water include *Alphacoronaviruses* such as 229E and NL63 or *Betacoronaviruses* such as OC43 and HKU1 (not well-known frequencies) and SARS (with occasional frequencies) [5]. Infections related to contaminated water can have various routes of contagion that may include aspiration, inhalation of aerosol droplets, penetration by the skin or mucous membranes, as well as by intake [20]. For CoVs in general, it is reported that they can continue active or infectious for up to several weeks in water, including wastewaters [21]. Thus, viruses can come into contact with free-living aquatic organisms or in aquaculture farms and then be transmitted to humans when they become pets or food, and that, in the near future, it could be the way for new coronavirus outbreaks, which will need to be evaluated particularly for CoVID-19.

2.1 CoVs and aquatic organisms

The aquatic biota is constituted by those organisms that inhabit aquatic environments temporarily or permanently. Within them, we find amphibians, molluscs, fish and waterfowls. Studies focusing on viral infections in aquatic organisms have targeted mainly those species of commercial importance and especially those of aquaculture exploitation [22], or those associated with captivity and tourism industry, such as marine mammals in aquariums and water parks [23]. However, aquatic biota includes various types of organisms, which, although they do not have direct commercial or exploitative importance for man, there are part of aquatic ecosystems and, therefore, are exposed to viral infections in this type of environments. Such is the case of amphibians such as frogs and salamanders, or different aquatic birds such as gulls or pelicans.

Within the CoVs that have been identified in aquatic organisms and also associated to important pathological infections, we find those that affect fish, marine mammals, frogs (Table 1) and waterfowls (Table 2 and 3). No mollusc and crustacean infections by CoVs have been reported so far.

2.1.1 Fishes

In the case of fish, viruses of the *Bafinivirus* group have been reported [6,13,24,25]. It is recognized that the first report of CoVs was in a European cyprinid known as white brema (*Blicca bjoerkna*), which showed a bacilliform structure, related to the viruses of the subfamily Torovirinae, giving rise to a new genus defined as *Bafinivirus* [13]. There are cases since the late 1980s, where CoVs have been identified, particularly in Japan by 1988, in the common carp *(Cyprinus carpio),* widely cultivated and consumed in the world [26,27]. Production involvements reached 70% mortality within 20 days, with pathological damage including renal and hepatic tubular necrosis, as well as damage to renal hematopoietic tissue [24], skin and abdomen bleeding [13]. However, *Bafiniviruses,* together with *Gammacoronaviruses* detected in marine mammals, are usually found mainly in the digestive tract of the host or infected organisms [5]. Most recently, this genus has been reported in *Pimephales promelas* or bighead face fish [28,29] and on the salmon, *Oncorhynchus tshawytscha* [30], identified as two different types of *Bafinivirus* (Table 1).

Some Chinese electronic media have stated that CoVID-19 cannot be transmitted through fish, under the argument of the virus's thermo-tolerance and the low body temperature of fish, compared to those of mammals [31]. However, this

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must be confirmed and might be not necessarily true. Recent and specific tests of SARS-CoV-2 tolerance to thermal gradients have demonstrated tolerance between 4ºC and 20ºC in the air [32]. This temperature range is below the human body temperature (36.6ºC), which are resisted and tolerated by SARS-CoV-2 during human infections. In drinking water, SARS-CoV-2 dispersion seems to decrease at 23ºC [33]. In addition, we must recognize that this would have relevant implications for viral tolerance, if we consider that fish are ectothermic, that is, their body temperature is equal to that of the environment around them (except tuna, which is heterothermic)[34], and fish that have already shown the presence of CoVs are tolerant to a wide range of temperatures, from temperate to warm conditions (like cyprinid fish that lives or reproduces between 17 ºC and 30ºC [35]). This aspect is important in the case of the CoVID-19 because it might imply that under that temperature range, its incorporation by fish could be possible, just considering the body temperature as a limit factor for its infection. On the other hand, marine mammals regulate body temperatures in a lower range than humans (29-32ºC [36]). Despite this, marine mammals have developed CoVs infections, as can be seen in Table 1. Under this evidence, the body temperature would not be a limiting factor on the possible future infection of SARS-CoV-2 to fish and marine mammals, or at least once they have already entered the body of the organism.

2.1.2 Waterfowl.

Waterfowl is the group of animals most representative that can harbor CoVs [37] associated with aquatic environments, birds appear to be the group with the higher diversity of CoVs, with at least 88 genetically identified varieties found during a recent review [38] and here updated (Table 2 and 3), within two of the four genera (75 *Gammacoronavirus* and 13 *Deltacoronavirus,* respectively) of the subfamily Orthocoronavirinae [39]. Different types of birds, such as gulls (*Laurus hyperboreus*; *L. galucesceus*), geese (*Branta bernicla*, *Anser caerulescens*), spatulas (*Platalea minor*), herons (*Ardea cinerea*, *Ardeola bacchus*), cormorants (*Phalacrocorax carbo*) and ducks (*Anus Americana*, *A. crecca*, *A. clypeata, A. penelope*, *A. acuta*, *Dendrocygha javanica*) are confirmed carriers of CoVs. The ducks of the genus *Anas sp*. and *Anser sp*. are the most represented and capable of carrying even strains of SARS-CoV. Particularly noteworthy are *Anas domestica, Anas platyhynchos* and *Anser anser* (Table 2).

A review carried out by Wartecki and Rzymski [37] highlighted that the prevalences of coronavirus in waterfowl vary according to the geographical region, from a low incidence in South America (Brazil) up to 19% in Scandinavia and that their infections can range from asymptomatic to mild or severe. Waterfowl faeces deposited directly in the water are considered a critical CoVs source to aquatic environments, contributing to viral spread, an idea that it is considered still to be confirmed [37]. The contribution of waste and carcasses from bird clutches to water bodies where they live, allow CoVs to enter the aquatic food chain and can then be distributed with the potential of infection to other organisms or even compromise the chain [37,40].

Recently, in an evaluation of infectious agents in the penguin *Spheniscus magellanicus*, the presence of four variants of CoVs (Avian coronavirus M41, C46, A99 and JMK) were detected, with ACoVC46 being the one with the highest representation, causing bronchitis [41]. The seroprevalence analysis in penguins, which evaluates the percentage of the population that has developed antibodies against CoVs, shows a low prevalence in two more known species as *Eudyptes chrysocome* (Southern Rockhopper) [42] and *Spheniscus humboldti* (Humbolt penguin) [43], respectively.

Some birds, such as cormorant and ducks are migratory, and that would allow wide geographical distribution of these types of viruses. Although no reports of human infection originated from waterfowl, have been detected [37], the ecological study of these correlation becomes indispensable, to understand better the relationship of birds and CoVs, and their epidemiology among birds and other species within their ecosystems [39]. It has been suggested that Deltacoronaviruses through recombination processes of their genome, could lead to their propagation through new hosts [37].

2.1.3 Amphibians

Recent research on the nido-like virus by Bukhari et al. [11], have revealed the presence of sequences encoding proteins similar to proteinases of the coronavirus. Through these analyses, the authors discovered an RNA transcript of 22.3 Kb from nine tadpoles belonging to *Microphyla fissipes* (ornamented pygmy frog) the only amphibian host reported so far (Table 1), on the best of our knowledge. This virus has been named *Microphyla letovirus* (MLeV), which was included in the nidovirus taxonomy list published by the International Committee on the Taxonomy of Viruses in 2018 [11].

2.1.4 Marine mammals.

Regarding marine mammals, the first report of CoVs dates back to the 1970s associated with the death of several seals *(Phoca vitulina)* in a Florida aquarium [44] and other free-living pinnipeds off the coast of California [45]. This infection was known as HSCoV (Harbor Seal coronavirus), identified as deadly haemorrhagic pneumonia caused by *Alphacoronavirus* group [45]. Years later, in 2008, the presence of other CoVs was detected in a beluga whale *(Delphinapterus leucas)* under captivity (BWCoV SW1) [9,46]. In 2014, the presence of CoVs was detected in faeces from bottlenose dolphins [9], from the Indo-Pacific (*Tursiops aduncus*), which was called BdCoV HKU22 (Bottlenose dolphin CoV). These latter two were recognized within the *Gammacoronavirus* group, which caused viral bronchitis to those infected animals [9]. The gregarious behavior of several marine mammal species may promote the contagion and dispersal of these types of pathogens in wild populations, so their monitoring becomes essential and necessary for their health and avoid further transmission to others aquatic organisms.

Gammacoronavirus detected in marine mammals, unlike *Bafinivirus* in fish, can also be found in the respiratory tracts of terrestrial and marine mammals and not only in the digestive tracks [5]. Viruses such as influenza A and B have been reported in mammals such as seals and cetaceans [5,23], which have come to be considered as reservoirs and vectors towards humans [5]. This scenario opens up the possibility that other viruses, including CoVs, could be transmitted to humans when interacting and coming into contact with seals, sea lions and dolphins in water parks and aquariums. Working with infected wildlife, or using them as food sources, especially in communities such as Asian ones, might also be another route of transmission.

2.1.5 Crustaceans and molluscs

Crustaceans are recognized as a group capable of accumulating in their exoskeleton or body cover human pathogens [47]. However, no coronavirus infections have been reported until the best of our knowledge. In shrimps, however, the "Yellow head virus" or YHV [48], was reported in 1990 in East and Southeast Asia, affecting *Penaeus monodon* shrimp farmed. There are unconfirmed reports in Mexico for *P. Stylirostris* and *P. vannamei* [48–50]. This virus belongs to another family of Nidovirales, known as Roniviridae, specifically the *Okavirus* genus [10]. Although it does not belong to the Coronaviridae family, is a closely related virus, which illustrates very well the possibility that in the future, it could also be possible to find CoV infections in crustaceans. Genetic studies have shown that YHV had undergone significant recombination processes, apparently attributable to international trade with wild and farmed shrimp in the Asia-Pacific region, promoting a faster genetic diversity of the virus, as a result of several recombination events [51]. So it cannot be ruled out the possibility that this type of events is taking place in the wild, for coronavirus species.

In the case of molluscs, there are also no reports of the presence of CoVs in scientific literature. However, there are reports of other RNA virus infections, both encapsulated and unencapsulated. Arenaviridae or Retroviridae (encapsulated) families, as well as the Biriaviridae, Reoviridae and Picornaviridae (unencapsulated), have been found in bivalves [22].

As it was mention in section 2.1, CoVs are RNA genome virus with a protein cap, feature share with the Arenaviridae and Retroviridae families (all three are RNA encapsulate viruses). As in the case of crustaceans, represents the possibility that in the future, similar RNA encapsulated viruses such as CoVs could develop infection patterns in molluscs, similar to those observed, for example, in the cases of *Hyriopsis cumingii* plague virus (HcPV, Arenaviridae) or B-type retrovirus (Retroviridae), the first one reported in the freshwater mussel *H. cumingii*, and the second in the marine clam *Mya arenaria* [22].

It is also not possible to rule out that future environmental and genetic changes may cause new routes of spread and transmission of coronavirus species through vector organisms such as crustaceans and molluscs. The Arenaviridae viruses are considered enteric viruses of interest for the WHO (World Health Organization); they are rarely detected (low frequency) in water or food during human transmission studies [5]. Nevertheless, some arenavirus infections such as Lassa fever, caused by the *Lassa mammarenavirus* and transmitted by mice to humans, are considered to have the potential to increase its transmission under climate change scenarios [52]. The same case might apply to all virus, including Retrovirals, which usually are associated with swimming pool [13], and fish infections [12,13].

Analyzing the different aspects related to the presence of coronavirus in the above-mentioned aquatic organisms, especially the detection of its presence in marine mammals such as dolphins and seals, as well as its biological similarity with other viruses detected in other groups of animals such as crustaceans or molluscs (which presence has been associated with transfers to humans due to their use as food), leads us to one of the main questions in case of the SARS-CoV-2 infects an aquatic ecosystem, would SARS-CoV-2 from aquatic organisms infect humans?.

3.- Some viral infections to humans from aquatic organisms

During this review, no published studies on the actual risk of SARS-CoV-2 contagion from aquatic organisms were found. There is a history of other viral respiratory infections transmitted to humans from either wild or captive animals [17,23]. That is the case with influenza-A, caused by the H7N7 virus, in people infected during a necropsy performed to a seal [44], or by coming into contact with the sneeze of a seal in captivity [23], causing conjunctivitis, rather than typical influenza or respiratory disease. A similar case has also been identified for Influenza B [5,23]. Moreover, a historical review carried out by Petrovic et al. [17], has shown numerous viral outbreaks (not CoVs related) associated with shellfish. These outbreaks, included human enteric viruses, mainly those of type NoV (norovirus). HAV (hepatitis virus A), EV (Enterovirus), HAdV (human adenovirus) and HRV (human rotavirus) are reported in shellfish in different countries, but not CoVs. Oysters and clams have been associated with NoV and HAV between 1976 and 1999, in the United States alone. The presence of these viruses has also been identified in molluscs in Europe, both in fish and sea markets and in oyster farms associated with human enteric viruses between 1990 and 2006 [53,54] and all are good examples of food as a source of viral infections. For the World Health Organization and the Food and Agriculture Organization Joint Committee, coronaviruses related to Severe Acute Respiratory Syndrome (SARS-CoV) are viruses of concern by contaminated food [55]. There are other types of water-viruses associated with birds, such as H5N1 avian influenza and avian influenza A1, also highly infectious, and recognized for their transmission to humans from duck meat and blood [56,57]. Due to these examples, there are required extensive monitoring studies since ducks are one of the main groups of birds capable of carrying CoVs (Table 2).

At the moment, as long as there are no more significant scientific elements to be certain of the non-spread of the SARS-CoV-2 pandemic through natural waters and aquatic organisms, it is best to follow the indications that the health authorities have been issuing in this regard. These indications highlight those made by the World Health Organization [58], which recommends avoiding unprotected contact with wild and farm animals, and has even been recommended not to approach public markets where wild animals are under sale, both live and slaughtered [8].

4.- Further considerations about CoVs and aquatic biota

The efforts of the scientific community will continue over the coming years to learn more about CoVID-19. Genetic adaptation, including mutation and recombination, identify routes of zoonotic (animal) origin, new vector organisms (birds, mammals, fish, amphibians, molluscs or crustaceans), animal-human transmission events, wild natural storage and contagion risks, which will allow effective and realistic programmes to control the transmission of coronaviruses, particularly SARS-CoV-2. It is recognized that viral genotypes with epidemiological potential can become very variable, as a result of their genetic characteristics, which allow them to endure and survive, as well as spread and even mutate along trophic chains [47]. It is encouraging to know that even other aquatic organisms, such as seaweed or sponges, could play a key role in the treatment of CoVs infections. It has been observed through laboratory tests with *Halimeda tuna* algae, a natural product known as diterpene aldehyde or halitunal [59], with an antiCoV effect. Other examples are the sponge *Mycale sp*, which produces a substance called micalamide A, both with antiviral capacity against the A59-CoV of murine origin [60,61].

Another good example is the *Axinella corrugata* sponge that produces an ethyl ester of esculetin-4-carboxylic acid against SARS-CoV [62]. Natural marine compounds are being found to be inhibitors against the main proteases of SARS-CoV-2 [63]. Eight antiviral compounds have been recently reported against SARs-CoV-2 protease, particularly a compound identified as Esculetin ethyl ester from *A. corrugata*, which has shown to be the most effective antiprotease [64]. These molecules are considered bioactive compounds that act as replication inhibitors to SARS-CoV in Vero cells (kidney cells from an African green monkey; [62]), among others that can act as effective antiviral drugs [64]. These substances, together with other products of natural origin [61,65], could be the sources of some control against coronavirus like SARS-CoV-2 in the future.

5.- Conclusions

Although some scientists speculate that CoVs will not last long in the environment, especially in tropical and subtropical environments [52], due to their intolerance to high temperatures, the diversity and presence of CoVs in aquatic organisms should be monitored. Their varieties identified adequately in infected wild populations, to better understand their infectious potential and avoid future outbreaks in the wild, which eventually could also reach humans.

The presence of CoVs in aquatic environments is a reality, which has demonstrated its ability to be transmitted to organisms in wildlife, aquaculture farms and animals under captivity. The presence observed in farmed fish such as carp, or a frog, although they have not reported significant effects or consequences on human health, could be of potential risk in the near future. Knowledge of other cases such as marine mammals, where seals have shown to be carriers of respiratory infections, which have eventually been transmitted to humans, with effects on eye membranes, even in infections as dangerous as influenza diseases, most be taken in consideration. Waterfowl show to be a natural reservoir, mainly ducks, which, due to their migratory behaviors, deserve to be studied in more detail. The high adaptive capacity of viruses, the wide distribution and recombination potential of their genetic material, could be factors that favor their eventual pathogenicity through aquatic environments. Although crustaceans and molluscs are not infected with CoVs, their antecedents as vectors or carriers of other viruses, including close related viruses taxonomically and biologically, to CoVs, make them suitable for monitoring for possible future infections.

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Table 1. Coronavirus found in aquatic organisms. Taxonomical groups, according to de Groot et al. [6] and Kasmi et al. [10].

Group		**Genus**	**CoV type**	**Host**	**Health Effects**	**Year**	**Reference**
Order	Nidoviales						
Suborder	Cornidovirinea						
Family	Coronaviridae						
		*Coronavirus(?)**	Carp CoV	Common carp (Japan)	Erythema, necrosis (abdomen and liver)	1988	[22,25]
		*Coronavirus(?)**	Carp Viremia-Associated Ana-Aki-Byo	Common carp (Japan)	Dermal ulcerations, necrotic lesion. Found in spleen and hematopoietic tissue	1997-1998	[25,66]
Subfamily	Orthocoronavirinae						
		Alphacoronavirus	HsCoV	Harbor seals (Aquatic Park, Florida, USA)	Acute enteritis, pulmonary edema	1987	[44]
			HsCoV	Pacific Harbor seals (California, USA)	Pulmonary congestion, consolidation and hemorrhage, pneumonia	2000	[67]
		Betacoronavirus	Not reported				
		Gammacoronavirus	BWCoVSW1	Beluga whale (Aquatic Park, California, USA)	Hepatic necrosis and pulmonary disease	2008	[6,46]
			BdCoV HKU22	Bottlenose Dolphin (Aquatic Park, Hong Kong)	Found in faeces		[9]
		Deltacoronavirus	Not reported				
	Torovirinae						
		*Torovirus(?)**	CIVH 33/86	Grass carp (Hungary)	Not known	1986	[25]
		Bafinivirus	WBV DF24/00	White bream fish (Saxonia-Anhalt, Germany)	Not known	2000	[12,25]
			FHMNV	Fathead minnow fish (Arkansas, USA)	Eyes and skin haemorrhage, tissue lesions (spleen, liver and kidney)	1997	[28,29]
			Chinook Salmon Bafinivirus	Chinook salmon (Ontario, Canada)	Not known	2014	[25,30]
	Letovirinae	*Alphaletovirus*	Microhyla letovirus MLeV	Ornamental pygmy frog	Not reported	2018	[11]

*still unclassified.

Table 2. Coronavirus found in waterfowl of the Order Anseriformes.

Order	*Genus*	*Specie*	Type of bird	Type of CoV	References
Anseriformes	*Anas*	*domestica*	Duck	Gamma (SARS-CoV)	[68]
		platyhynchos	Spotbill duck	Gamma (SARS-CoV)	[68]
		americana	American wigeon	Delta (JQ065048.1)	[69]
		crecca	Common teal	Gamma (J0109, J0121, J0126, J0559, J0579, J1393); Delta (J1420)	[39,70,71]
		clypeata	Northern shoveler	Gamma (K547, K554, K561, K589, J0554, J0807, J1300, J0901, J1491); Delta (J0590)	[39,71]
		penelope	Euroasian wigeon	Gamma (K596, J0588, J1561)	[39]
		acuta	Northern pintail	Gamma (J1375, J1393, J1404, J1407, J1435, J1616, J1451, PBA-10, PBA-15, PBA-16, PBA-25, PBA-37, PBA-124)	[39,70,71]
		erythrorhyncha	Red-billed duck	Gamma (KM093874, KM093875, KM093876, KM093877)	[71]
		hottentota	Hottentot teal	Gamma (KM093880)	[69]
	Clangula	*hyemalis*	Long-tail duck	Gamma (Fin14395)	[70]
	Cygnus	*cygnus*	Whooper swan	Gamma (Fin4983)	[70]
	Dendrocygna	*javanica*	Lesser whistling duck	Gamma (KH08-0852)	[39,69]
		viduata	White-faced whistling duck	Gamma (KM093872, KM093873, KM093878)	[71]
	Aythya	*fuligula*	Tufted duck	Gamma (J1482)	[39]
	Anser	*caerulescens*	Snow goose	Gamma (WIR-159)	[39,69]
		anser	Greylag goose	Gamma (SARS)	[68]
		cygnoides	Swan goose	Gamma (DPV_16). Delta (DPV_5, DPV_10)	[69]
	Branta	*bernicla*	Brent goose	Gamma (KR-69, KR-70, KR88)	[39,69,71]

Table 3. Gammacoronavirus and Deltacoronavirus reported in aquatic birds.

Order	***Genus***	***Specie***	**Type of bird**	**Type of CoV**	**References**
Pelecaniformes	*Ardeola*	*bacchus*	Pond heron	Delta (KH08-1475, KH08-1474)	[39]
	Ardea	*cinerea*	Gray heron	Delta (K581, K513)	[39]
	Bubulcus	*ibis*	Heron	Gamma (KM093897)	[69,71]
	Platalea	*minor*	Black-faced spoonbill	Delta (J0569)	[39]
	Phalacrocorax	*carbo*	Great cormorant	Delta (J0982, J1517)	[39]
Gruiformes	*Rallus*	*madagascariensis*	Madagascar rail	Gamma (KM093896)	[71]
	Porphyrula	*alleni*	Allen´s gallinule	Gamma (KM093890, KM093891, KM093892 KM093893, KM093894)	[69,71]
	Gallinula	*chloropus*	Common moorhen	Gamma (KM093881, KM093885, KM093887). Delta (JQ065049.1)	[69,71]
Charadriiformes	*Charadrius*	*pecuarius*	Kittlitz`s plover	Gamma (KM093879, KM093883, KM093884)	[69,71]
	Gallinago	*macrodactyla*	Madagascan snipe	Gamma (KM093888, KM093889, KM093895)	[71]
	Calidris	*mauri*	Wester sandpiper	Gamma (KR-28)	[69]
		ptilocnemis	Rock sandpiper	Gamma (CIR-66187, CIR-665821, CIR-665828)	[39,69,71]
		alba	Sanderling	Gamma (PNLP100)	[69]
		fuscicollis	White-rumped sandpiper	Gamma (PNLP159)	[69]
	Larus	*sp*	Gull	Delta (JX548304)	[69]
		argentatus	Hearing gull	Gamma (Fin9211, Fin10877, Fin10879, Fin12822, Fin13125)	[70]
		hyperboreus	Glaucous gull	Gamma (PBA-173)	[39]
		fuscus	Lesser Black-back gull	Gamma (Fin10059)	[70]
		glaucescens	Glaucous-winged gull	Gamma (CIR-66002, GU396682)	[39]
	Chroicocephalus	*ridibundus*	Black-headed gull	Gamma (CIR-66187, GU396679, GU396680, GU396683, KX588674, Fin10083)	[39,70]
	Rostratula	*benghalensis*	Greated Painted-snipe	Gamma (KM093883)	[69]
	Rynchops	*niger*	Black skimmer	Delta (PNLP115)	[69]
Sphenisciformes	*Spheniscus*	*magellanicus*	Magellanic penguin	Avian CoV M41, C46, A99, JMK	[41]
		humboldti	Humbolt penguin	Avian CoV M41, C46, A99	[43]
	Eudyptes	*chrysocome*	Southern rockhopper	Avian CoV C46, A99, JMK	[42]