

Aquatic biota is not exempt from Coronavirus infections: An overview

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Abstract

Coronaviruses are pathogens recognized for having an animal origin and commonly associated with terrestrial environments. However, although in few cases, there are reports of their presence in aquatic organisms like fish, crustaceans, waterfowls and marine mammals. None of these cases have even led to human health effects, when contact with these infected organisms, whether they are alive or dead. Aquatic birds seem to be the main group in carrying and circulating these types of viruses in healthy bird populations and play an important role in these environments. Although the route of infection for CoVID-19 (Coronavirus disease 2019) 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 (no coronavirus), which are known to have been transferred to the human by aquatic biota. What is even better, it becomes encouraging to know that aquatic species shows very few cases in fishes, marine mammals, and crustaceans, and some other aquatic animals may also be a possible source of cure or treatment against coronaviruses, as some evidence with algae and marine sponges suggests.

Keywords: Coronavirus, aquatic organisms, fish, marine mammals, crustaceans, birds.

Declarations

Funding: Not applicable.

Conflicts of interest/Competing interests: The author declares no conflict of interest.

Availability of data and material: Not applicable.

Ethics approval: Not applicable

Consent to participate: Not applicable.

Consent for publication: Not applicable.

Code availability: Not applicable.

Authors' contributions: G.N-N. contributed to the study conception and design, and A.A.G-B and G.N-N material preparation, data collection, analyses, and approved the final manuscript.

Acknowledgement

The author G.N-N recognizes the support provided by the PII SNI-UJAT program and the assistance of Enrique Núñez-Jiménez to improve this manuscript.

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.

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 Nidovirales, which in addition to infecting mammals and birds, have also been found in crustaceans, fish and marine mammals [6,8]. 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 subfamily within the Coronaviridae is the Torovirinae, formed in turn by two genera, *Torovirus* and *Bafinivirus*, respectively. *Bafinivirus*, in fact, has been identified in a teleost fish [11,12].

2. Coronavirus and aquatic environments

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 [4,13]. 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 [14]. 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 [15]. It is estimated that about 10 billion viral particles are present for every gram of excrement [16]. 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 [16]. 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 [17]. For CoVs in general, it is reported that they can continue active or infectious for up to several weeks in water, including wastewaters [18]. 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.

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 [19].

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 [20].

2.1 CoVs and aquatic organisms

Studies focusing on viral infections in aquatic organisms have targeted mainly those species of commercial importance and especially those of aquaculture exploitation [21], or those associated with captivity and tourism industry, such as marine mammals in aquariums and water parks [22].

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

2.1.1 Crustaceans

Crustaceans are recognized as a group capable of accumulating in their exoskeleton or body cover human pathogens. However, their role in the transmission of diseases to humans has not been proven [23], perhaps by the culinary habits and customs of removing body covers before ingesting them. In shrimps, the "Yellow head virus" or YHV [24], was reported in 1990 (Table 1) in East and Southeast Asia, affecting *Penaeus monodon* shrimp farmed. There are unconfirmed reports in Mexico for *P. stylirostris* and *P. vannamei* [24–26]. Genetic studies showed 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 [27].

2.1.2 Fishes

In the case of fish, viruses of the *Bafinivirus* group have been reported [6,12,28,29]. 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 [30,31]. 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 [28], skin and abdomen bleeding [12]. However, *Bafiniviruses*, together with *Gammacoronaviruses* detected in marine mammals, are usually found mainly in the digestive tract of the host or infected organisms [5]. It is also recognized that the first report of CoVs was in another 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* [12]. Most recently this genus has been reported in *Pimephales promelas* or bighead face fish [32,33] and on the salmon *Oncorhynchus tshawytscha* [34], 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 [35]. However, this must be confirmed. Recent and specific tests of SARS-CoV-2 tolerance to thermal gradients have demonstrated tolerance between 4°C and 20°C in the air [36]. This temperature range is below the human body temperature (36.6°C), which are resisted and tolerated by SARS-CoV-2 during human infections. In drinking water, its dispersion seems to decrease at 23°C [37]. In addition, we must recognize that this would have relevant implications for tolerance, if we

consider that fish and crustaceans are ectothermic (some fishes can be heterothermic, like tuna), that is, their body temperature is equal to that of the environment around them [38], and fish that have shown the presence of CoVs have a tolerance to a wide range of temperatures, from temperate to warm conditions (like cyprinid fish that lives or reproduces between 17 °C and 30 °C [39]), which in the case of the CoVID-19, could allow its incorporation by fish, just considering their body temperature as a limit factor for its infection. On the other hand, Peneid shrimps are tropical (between 24 °C and 32 °C [40]), and marine mammals regulate body temperatures in a lower range than humans (29-32 °C [41]). 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 crustaceans, fish and marine mammals, or at least once they have already entered the body of the organism.

2.1.3 Waterfowl.

Of the groups of animals associated with aquatic environments, birds appear to be the group with the higher diversity of CoVs, with at least 96 genetically identified varieties found during this review (Table 2 and 3), within two of the four genera (71 *Gammacoronavirus* and 13 *Deltacoronavirus*, respectively) of the subfamily Orthocoronavirinae [42]. 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 (*Anas Americana*, *A. crecca*, *A. clypeata*, *A. penelope*, *A. acuta*, *Dendrocygna 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).

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, 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 [42].

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 [43] and other free-living pinnipeds off the coast of California [44]. This infection was known as HSCoV (Harbor Seal coronavirus), identified as deadly haemorrhagic pneumonia caused by *Alphacoronavirus* group [44]. Years later, in 2008, the presence of other CoVs was detected in a beluga whale (*Delphinapterus leucas*) under captivity (BWCoV SW1) [9,45]. 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 [5,22], 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. These 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.- Virus 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 [15,22]. That is the case with influenza-A, caused by the H7N7 virus, in people infected during a necropsy performed to a seal [43], or by coming into contact with the sneeze of a seal in captivity [22], causing conjunctivitis, rather than typical influenza or respiratory disease. A similar case has also been identified for Influenza B [5,22]. Moreover, a historical review carried out by Petrovic et al. [15], 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 [46,47] 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 [48]. 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 [49,50]. 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 [51], 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.- Conclusions

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, in farmed and wild populations of penaeid shrimp, 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, must 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 molluscs are not infected with CoVs, their antecedents as vectors of other viruses, make them suitable for monitoring for possible future infections.

5.- Further considerations for 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, 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 [23]. 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 [52], 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 or rodent origin [53,54]. Another good example is the *Axinella corrugata* sponge that produces an ethyl ester of esculetin-4-carboxylic acid against SARS-CoV [55]. These substances together with other products of natural origin [54,56], could be the sources of some control against to coronavirus like SARS-CoV-2 in the future.

Although some scientists speculate that CoVs will not last long in the environment, especially in tropical and subtropical environments [57], 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.

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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 Suborder Family	Nidovirales Coronavirineae Coronaviridae	<i>Coronavirus(?)</i> *	Carp CoV	Common carp (Japan)	Erythema, necrosis (abdomen and liver)	1988 [21,29]
		<i>Coronavirus(?)</i> *	Carp Viremia-Associated Ana-Aki-Byo	Common carp (Japan)	Dermal ulcerations, necrotic lesion. Found in spleen and hematopoietic tissue	1997-1998 [29,58]
Subfamily	Orthocoronavirinae	<i>Alphacoronavirus</i>	HsCoV	Harbor seals (Aquatic Park, Florida, USA)	Acute enteritis, pulmonary edema	1987 [43]
			HsCoV	Pacific Harbor seals (California, USA)	Pulmonary congestion, consolidation and hemorrhage, pneumonia	2000 [59]
		<i>Betacoronavirus</i>	Not reported			
		<i>Gammacoronavirus</i>	BWCoV SW1	Beluga whale (Aquatic Park, California, USA)	Hepatic necrosis and pulmonary disease	2008 [6,45]
			BdCoV HKU22	Bottlenose Dolphin (Aquatic Park, Hong Kong)	Found in faeces	[9]
		<i>Deltacoronavirus</i>	Not reported			
	Torovirinae	<i>Torovirus(?)</i> *	CIVH 33/86	Grass carp (Hungary)	Not known	1986 [29]
		<i>Bafinivirus</i>	WBV DF24/00	White bream fish (Saxonia-Anhalt, Germany)	Not known	2000 [11,29]
			FHMNV	Fathead minnow fish (Arkansas, USA)	Eyes and skin haemorrhage, tissue lesions (spleen, liver and kidney)	1997 [32,33]
			Chinook Salmon Bafinivirus	Chinook salmon (Ontario, Canada)	Not known	2014 [29,34]
Family	Roniviridae	<i>Okavirus</i>	YHV (Yellow Head Virus)	Peneid shrimps in East / Southeast Asia, and Mexico (?)	Lymphoid organs and hepatic abnormalities	1990 [25,27]

*still unclassified.

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

Order	Genus	Specie	Type of bird	Type of CoV	References
Anseriformes	Anas	<i>domestica</i>	Duck	Gamma (SARS-CoV)	[60]
		<i>platyhynchos</i>	Spotbill duck	Gamma (SARS-CoV)	[60]
		<i>americana</i>	American wigeon	Delta (JQ065048.1)	[61]
		<i>crecca</i>	Common teal	Gamma (J0109, J0121, J0126, J0559, J0579, J1393); Delta (J1420)	[42,62,63]
		<i>clypeata</i>	Northern shoveler	Gamma (K547, K554, K561, K589, J0554, J0807, J1300, J0901, J1491); Delta (J0590)	[42,63]
		<i>penelope</i>	Euroasian wigeon	Gamma (K596, J0588, J1561)	[42]
		<i>acuta</i>	Northern pintail	Gamma (J1375, J1393, J1404, J1407, J1435, J1616, J1451, PBA-10, PBA-15, PBA-16, PBA-25, PBA-37, PBA-124)	[42,62,63]
		<i>erythrorhyncha</i>	Red-billed duck	Gamma (KM093874, KM093875, KM093876, KM093877)	[63]
		<i>hottentota</i>	Hottentot teal	Gamma (KM093880)	[61]
		<i>hyemalis</i>	Long-tail duck	Gamma (Fin14395)	[62]
	Clangula	<i>cygnus</i>	Whooper swan	Gamma (Fin4983)	[62]
	Cygnus	<i>cygnus</i>	Whooper swan	Gamma (Fin4983)	[62]
		<i>javanica</i>	Lesser whistling duck	Gamma (KH08-0852)	[42,61]
	Dendrocygna	<i>viduata</i>	White-faced whistling duck	Gamma (KM093872, KM093873, KM093878)	[63]
		<i>fuligula</i>	Tufted duck	Gamma (J1482)	[42]
	Anser	<i>caerulescens</i>	Snow goose	Gamma (WIR-159)	[42,61]
		<i>anser</i>	Greylag goose	Gamma (SARS)	[60]
		<i>cygnoides</i>	Swan goose	Gamma (DPV_16). Delta (DPV_5, DPV_10)	[61]
	Branta	<i>bernicla</i>	Brent goose	Gamma (KR-69, KR-70, KR88)	[42,61,63]

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Table 3. Gammacoronavirus and Deltacoronavirus reported in aquatic birds.

Order	Genus	Specie	Type of bird	Type of CoV	References
Pelecaniformes	<i>Ardeola</i>	<i>bacchus</i>	Pond heron	Delta (KH08-1475, KH08-1474)	[42]
	<i>Ardea</i>	<i>cinerea</i>	Gray heron	Delta (K581, K513)	[42]
	<i>Bubulcus</i>	<i>ibis</i>	Heron	Gamma (KM093897)	[61,63]
	<i>Platalea</i>	<i>minor</i>	Black-faced spoonbill	Delta (J0569)	[42]
Gruiformes	<i>Phalacrocorax</i>	<i>carbo</i>	Great cormorant	Delta (J0982, J1517)	[42]
	<i>Rallus</i>	<i>madagascariensis</i>	Madagascar rail	Gamma (KM093896)	[63]
	<i>Porphyryla</i>	<i>alleni</i>	Allen's gallinule	Gamma (KM093890, KM093891, KM093892, KM093893, KM093894)	[61,63]
	<i>Gallinula</i>	<i>chloropus</i>	Common moorhen	Gamma (KM093881, KM093885, KM093887). Delta (JQ065049.1)	[61,63]
Charadriiformes	<i>Charadrius</i>	<i>pecuarius</i>	Kittlitz's plover	Gamma (KM093879, KM093883, KM093884)	[61,63]
	<i>Gallinago</i>	<i>macroductyla</i>	Madagascan snipe	Gamma (KM093888, KM093889, KM093895)	[63]
	<i>Calidris</i>	<i>mauri</i>	Wester sandpiper	Gamma (KR-28)	[61]
		<i>ptilocnemis</i>	Rock sandpiper	Gamma (CIR-66187, CIR-665821, CIR-665828)	[42,61,63]
		<i>alba</i>	Sanderling	Gamma (PNLP100)	[61]
		<i>fuscolis</i>	White-rumped sandpiper	Gamma (PNLP159)	[61]
	<i>Larus</i>	<i>sp</i>	Gull	Delta (JX548304)	[61]
		<i>argentatus</i>	Herring gull	Gamma (Fin9211, Fin10877, Fin10879, Fin12822, Fin13125)	[62]
		<i>hyperboreus</i>	Glaucous gull	Gamma (PBA-173)	[42]
		<i>fuscus</i>	Lesser Black-back gull	Gamma (Fin10059)	[62]
		<i>glaucescens</i>	Glaucous-winged gull	Gamma (CIR-66002, GU396682)	[42]
	<i>Chroicocephalus</i>	<i>ridibundus</i>	Black-headed gull	Gamma (CIR-66187, GU396679, GU396680, GU396683, KX588674, Fin10083)	[42,62]
	<i>Rostratula</i>	<i>benghalensis</i>	Greater Painted-snipe	Gamma (KM093883)	[61]
	<i>Rynchops</i>	<i>niger</i>	Black skimmer	Delta (PNLP115)	[61]

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