Short Communications

Resurgence of Morbillivirus infection in Mediterranean dolphins off the French coast

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IN the past 20 years, epizootics of *Morbillivirus* infection have occurred among several marine mammal populations worldwide (Van Bressem and others 2001). From 1990 to 1992, dolphin *Morbillivirus* spread to the striped dolphin (*Stenella coeruleoalba*) population of the Mediterranean sea, causing the deaths of thousands of animals. Following this, other striped dolphin populations were seen to be at risk for new epizootics (Van Bressem and others 1993, 2001) and two new outbreaks of *Morbillivirus* infection were recently confirmed from the Mediterranean coast of Spain (Fernández and others 2008, Raga and others 2008). This short communication reports the resurgence of *Morbillivirus* off the coast of France during the same period and discusses the possibility of coinfection with *Photobacterium damselae*.

Between August 2007 and March 2008, unexpected strandings of 143 dolphins occurred on the French Mediterranean coast (Table 1, Fig 1). The epizootic started with a low rate of strandings at the beginning of August 2007, a progressive increase during autumn and winter, and a peak in February 2008. In contrast to the 1990/91 episode, which mainly affected adults of more than 180 cm long (Bompar and others 1992), in 2007/08, a larger proportion of stranded animals were juveniles, ranging from 80 to 180 cm in length (Wilcoxon unilateral

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TABLE 1: Numbers of different species of cetacean found stranded, sampled and that tested positive for *Morbillivirus* infection (MI) or *Photobacterium damselae* infection

Species of cetacean	Stranded	Sampled	MI+/ tested*	MI PCR+/ tested	P damselae infected/tested
Striped dolphin (Stenella coeruleoalba)	119	32	1/4	9/32	8/14
Bottlenosed dolphin (Tursiops truncatus)	5	3	1/2	1/3	0/1
Pilot whale (Globicephala melas)	1	1	0	1/1	0
Undetermined dolphin species	18	0	0	0	0
Total	143	36	2/6	11/36	8/15

^{*} Animals with microscopic evocative lesions suggesting MI on histological examination

test, W 7358, P=0.002, α =0.05). Both sexes were similarly affected by the disease (chi-squared test for sex ratio 1, c 1.5, df 1, P=0.22, α =0.05).

Postmortem examination of 36 animals revealed severe bilateral pneumonia, oedematous and enlarged lymph nodes (especially lung-associated and mesenteric lymph nodes) and enteritis; these are all usual findings in cases of *Morbillivirus* infection in cetaceans. The animals were generally in a poor nutritional state and massively infested by parasites. Most of their stomachs were empty. Histology was performed on six animals, two of which showed highly characteristic lesions: pyogranulomatous splenitis and lymphadenitis in a striped dolphin, and interstitial suppurative pneumonia with severe lymphoid depletion of the spleen and lymph nodes in a bottlenosed dolphin. Multinucleated cells were present in all of the lesions.

RT-PCR on frozen tissues from 36 dolphins was performed using a set of universal *Morbillivirus* primers based on the P genes (Barrett and others 1993). Morbilliviral RNA present in nine striped dolphins, one pilot whale (*Globicephala melas*) and one bottlenosed dolphin (*Tursiops truncatus*) (Table 1) was detected from the brain, lung, spleen, thymus and lymph nodes. The kidneys, intestines and livers were negative. The P gene fragment from the virus identified in the three species and from the Spanish strain (GenBank accession number EU039963) showed complete homology. *P damselae* was isolated in pure culture from several organs in eight animals, including the lung, liver, kidney, spleen, mesenteric lymph nodes and brain, suggesting septicaemia as a possible cause of death.

The present study confirms the presence of Morbillivirus infection in cetacean populations along the French Mediterranean coast. Both episodes, from 2007 to 2008 and from 1990 to 1991 (Bompar and others 1992), showed similar patterns of infection; however, results from the present study illustrate three new epidemiological aspects. First, during the 1990 epizootic, Morbillivirus infection could only be demonstrated in the striped dolphin population, while the present study found two other species to be infected. Infection of the bottlenosed dolphin has rarely been described in the Mediterranean Sea, where *Morbillivirus* could be a major threat to the preservation of the species given the very low density of bottlenosed dolphins in the area; the Mediterranean population is estimated to be less than 10,000 animals. Secondly, during 2007/08 the chronological pattern appeared to be different from the 1990/91 episode, possibly due to variations in dominant winds, which could alter carcase recovery on the coast. Finally, juvenile striped dolphins were more frequently affected, which could be due to a lack of immunity against the virus, as the results of Van Bressem and others (2001) showed the absence of seropositive immature dolphins.

The source of infection was unknown in each case. The virus may have an Atlantic origin as both epizootics began in the Gulf of Valencia (Raga and others 2008). However, the genetic relation-

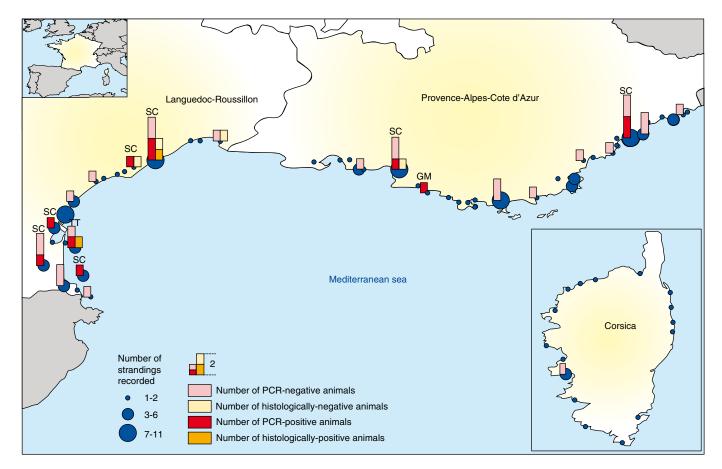


FIG 1: Geographical distribution of strandings and localisation of animals infected with *Morbillivirus*. The number of individual strandings are represented by a coloured bar (scale bar=two animals). GM Pilot whale (*Globicephala melas*), SC Striped dolphin (*Stenella coeruleoalba*), TT Bottlenosed dolphin (*Tursiops truncatus*)

ship between viruses of distinct geographical origin suggests that isolates form distinct geographical clusters (G. Libeau, personal communication).

In some cases, other causes of mortality were diagnosed, particularly infection by *P damselae*. This bacteria has already been considered as a primary pathogen in dolphins (Fujioka and others 1988), but it is also possible that the strong immunosuppressive effect of *Morbillivirus* infection predisposed the animals to infection with *P damselae*.

In conclusion, the causes of mortality in the cetacean population need monitoring, especially in the Mediterranean Sea where cetaceans are already under great pressure from human activities. Particularly, the phylogeny of morbilliviruses and the consequences of selective pressure induced by repeated outbreaks on dolphin populations should be evaluated.

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