

Marine Science Review - 166

Pathogens and disease



In this review:

- A. Recent articles – no abstract available
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A. Recent articles – no abstract available

Ohishi, K., Maruyama, T., Ninomiya, A., Kida, H., Zenitani, R., Bando, T., Fujise, Y., Nakamatsu, K., Miyazaki, N., and Boltunov, A.N. **Serologic investigation of influenza A virus infection in cetaceans from the western North Pacific and the Southern oceans.** *Marine Mammal Science* 22(1): 214-221, 2006.

Goldstein, T., Gulland, F.M.D., Braun, R.C., Antonelis, G.A., Kashinsky, L., Rowles, T.K., Mazet, J.A.K., Dalton, L.M., Aldridge, B.M., and Stott, J.L. **Molecular identification of a novel gamma herpesvirus in the endangered Hawaiian monk seal (*Monachus schauinslandi*).** *Marine Mammal Science* 22(2): 465-471, 2006.

Sakayaroj, J., Benzies, C., Chuaypat, J., and Plathong, S. **Aspergillosis of the gorgonian sea fan *Annella* sp after the 2004 tsunami at Mu Ko Similan National Park, Andaman Sea, Thailand.** *Coral Reefs* 25(2): 296, 2006.

Behringer, D.C., Butler, M.J., and Shields, J.D. **Avoidance of disease by social lobsters.** *Nature* 441(7092): 421, 2006.

Baskin, Y. **Sea sickness: The upsurge in marine diseases.** *BioScience* 56(6): 464-469, 2006.

Dierauf, L.A., Karesh, W.B., Ip, H.S., Gilardi, K.V., and Fischer, J. R. **Avian influenza virus and free-ranging wild birds.** *Journal of the American Veterinary Medical Association* 228(12): 1877-1882, 2006.

B. Recent articles with abstracts

Del Piero, F., Stremme, D.W., Habecker, P.L., and Cantile, C. **West Nile flavivirus polioencephalomyelitis in a harbor seal (*Phoca vitulina*).** *Veterinary Pathology* 43(1): 58-61, 2006.

Notes: A 12-year-old male harbor seal presented with progressive signs of neurologic dysfunction including head tremors, muzzle twitching, clonic spasms, and weakness. Lesions included polioencephalomyelitis with glial nodules, spheroids, neuronophagia, ring hemorrhages, and a few neutrophils. Neurons, fibers, and glial nodules were multifocally colonized with intracytoplasmic West Nile flavivirus antigens that were demonstrated using indirect immunohistochemical analysis. Flavivirus on cultured cells also was isolated and was identified by use of monoclonal antibodies and reverse transcriptase-polymerase chain reaction analysis. Clinical signs of disease and lesion morphology and distribution were similar to those of equine West Nile virus infection. Similar to horses, alpacas, humans, dogs, and reptiles, seals can be dead-end hosts of West Nile virus.

Croquer, A., Weil, E., Zubillaga, A.L., and Pauls, S.M. **Impact of a white plague-II outbreak on a coral reef in the archipelago Los Roques National Park, Venezuela.** *Caribbean Journal of Science* 41(4): 815-823, 2005.

Notes: During the last quarter of 2000, an outbreak of white plague disease (WPD-II) caused significant coral tissue mortality in several reef building species (*Montastraea* species complex, *Colpophyllia natans* and *Stephanocoenia intersepta*) in a fringing reef

along Madrizqui Key, Los Roques National Park, Venezuela. Coral cover and abundance by species, and cover of other substrates (i.e., algae, sand, etc.) were measured using eleven 1 m² quadrats (divided in 100 areas of 100 cm² each) separated by two meter intervals along each of the eight, 20 m long transects haphazardly placed between 5-12 m depth. Measurements were taken at the onset of the epizootic event and a year later. The average coral cover and cover of other substrates were compared using a Friedman ANOVA, while changes in relative cover by species were tested using a t-test. *C. natans* and the *Montastraea* species complex showed the highest significant (t-student, $p < 0.05$) loss in live cover, from 12.28% to 8.11% and 38.34% to 34.84%, respectively. Overall, the average live coral cover decreased significantly (Friedman = 581.5, $p < 0.05$) from 35% in 2000 to 29% in 2001, with a corresponding significant increase in algal and bare substrate cover from 33% to 44%. Similar to other Caribbean areas, the results of this study indicated that outbreaks of WPD-II may cause fast and extended coral tissue mortality, with significant reductions in live coral cover with a corresponding increase in algal cover in a relatively short period of time.

Cipriano, R.C. and Coll, J. **Historical record of *Yersinia ruckeri* and *Aeromonas salmonicida* among sea-run Atlantic salmon (*Salmo salar*) in the Penobscot River.** *Bulletin of the European Association of Fish Pathologists* 25(6): 280-283, 2005.

Notes: Despite restoration efforts, only about 2,000 Atlantic salmon (*Salmo salar*) salmon have annually returned to New England Rivers and more than 71% of these fish migrate to the Penobscot River alone. This report provides a historical compilation on the prevalence's of both *Yersinia ruckeri*, cause of enteric redmouth disease, and *Aeromonas salmonicida*, cause of furunculosis, among mature sea-run Atlantic salmon that returned to the Penobscot River from 1976 to 2003. *Aeromonas salmonicida* was detected in 28.6% and *Yersinia ruckeri* was detected among 50% of the yearly returns. Consequently, Atlantic salmon that return to the river are potential reservoirs of infection.

Thieltges, D.W. **Parasite induced summer mortality in the cockle *Cerastoderma edule* by the trematode *Gymnophallus choledochus*.** *Hydrobiologia* 559: 455-461, 2006.

Notes: In late summer 2004, a conspicuous cockle (*Cerastoderma edule*) mortality event was observed on a tidal flat in the northern Wadden Sea (North Sea, Germany) with many fresh valves and still living cockles lying on the sediment surface. To investigate whether trematode parasites utilizing the cockle as first or second intermediate host were involved in this mortality, buried and surfaced cockles were sampled and analyzed, and a laboratory experiment conducted. The field survey showed no statistical difference in intensity of parasites encysted in the foot of cockles. Three species of *Himasthla* utilizing the cockle as second intermediate host and known to impair the cockle's burrowing ability were found in buried cockles with 148.4 +/- 111.1 metacercariae/foot and in surfaced cockles with 164.2 +/- 84.4. There was also no difference in infection levels of parasites utilizing the cockles as second intermediate host in other cockle tissues between buried and surfaced cockles. In contrast, surfaced cockles showed a ten times higher prevalence (71.0%) than buried cockles (7.4%) of the trematode *Gymnophallus choledochus* - a parasite utilizing the cockle as first (and second) intermediate host - filling almost the entire body cavity and eliminating gonad structures. In an aquarium experiment of 14 days, all cockles found buried on the tidal flat survived compared to only 23.3% found on the surface. This suggests *G. choledochus* to be a castrating agent and a serious mortality factor in adult cockle populations.

Morton, A. and Routledge, R. **Mortality rates for juvenile pink *Oncorhynchus gorbuscha* and chum *O. keta* salmon infested with sea lice *Lepeophtheirus salmonis* in the Broughton Archipelago.** *Alaska Fishery Research Bulletin* 11(2): 146-152, 2005.

Notes: Wild juvenile pink *Oncorhynchus gorbuscha* and chum salmon *O. keta* were captured and sorted by the number of sea lice *Lepeophtheirus salmonis* infecting each fish. These fish were placed in groups of 60 in flowthrough containers immersed in seawater near the site of capture. There were 3-4 replicates for each infection category and 3 consecutive trials or Series run to assess the impact of sea lice on short-term fish mortality. Control groups of lice-free fish were included to measure handling and containment effects. In each trial or Series, significantly more fish died in the categories with sea lice than in the lice-free category. The majority of fish infected with motile-stage sea lice died. These observations indicate that short-term mortality of wild juvenile pink and chum salmon is increased by infestations of 1-3 sea lice.

Kelly, T.R., Greig, D., Colegrove, K.M., Lowenstine, L.J., Dailey, M., Gulland, F.M., and Haulena, M. **Metastrongyloid nematode (*Otostrongylus circumlitus*) infection in a stranded California sea lion (*Zalophus californianus*)—a new host-parasite association.** *Journal of Wildlife Diseases* 41(3): 593-598, 2005.

Notes: A stranded yearling male California sea lion was admitted to a rehabilitation center June 2003. On presentation, the sea lion was emaciated and had diarrhea and neutrophilia. Two weeks later, the animal became anorexic, blood and mucus were observed around the oral cavity, and corneal opacity was noted in the right eye. Hematology results at that time included leukocytosis consisting of neutrophilia with a left shift, anemia, and thrombocytopenia. Despite supportive care, the sea lion died. On post mortem examination, there were multiple areas of hemorrhage scattered throughout all lung lobes, and pulmonary blood vessels were occluded by fibrin thrombi. Nematodes identified as immature forms of *Otostrongylus circumlitus* were found in the right ventricle and pulmonary arteries. Histologic findings in the lungs included severe suppurative and necrotizing arteritis with vascular thrombosis, interstitial pneumonia, and large areas of pulmonary hemorrhage. This report of *O. circumlitus* infection in a California sea lion (*Zalophus californianus*) might indicate a potentially new host-parasite association.

Bracht, A.J., Brudek, R.L., Ewing, R.Y., Manire, C.A., Burek, K.A., Rosa, C., Beckmen, K.B., Maruniak, J.E., and Romero, C.H. **Genetic identification of novel poxviruses of cetaceans and pinnipeds.** *Archives of Virology* 151: 423-438, 2006.

Notes: Novel poxviruses were identified in skin lesions of several species of cetaceans and pinnipeds using polymerase chain reaction targeting DNA polymerase and DNA topoisomerase I genes of members of the subfamily *Chordopoxvirinae*. With the exception of parapoxviruses, no molecular data of marine mammal poxviruses were available to infer genetic and evolutionary relatedness to terrestrial vertebrate poxviruses. Viruses were assigned to a cetacean poxvirus 1 (CPV-1) group based on nucleotide and amino acid identities of gene fragments amplified from skin lesions of Asian bottlenose (*Tursiops aduncus*), Atlantic bottlenose (*Tursiops truncatus*), rough-toothed (*Steno bredanensis*), and striped (*Stenella coeruleoalba*) dolphins. A different poxvirus was detected in skin lesions of a bowhead whale (*Balaena mysticetus*) and provisionally assigned to a CPV-2 group. These viruses showed highest identity to terrestrial poxviruses of the genera *Orthopoxvirus* and *Suipoxvirus*. A novel species-specific poxvirus was also identified in skin lesions of Steller sea lions (*Eumetopias jubatus*). None of these poxviruses were found to have amplifiable hemagglutinin gene sequences. Novel parapoxviruses were also identified in skin lesions of Steller sea lions and spotted seals (*Phoca largha*). A significant degree of divergence was observed in sequences of Steller sea lion parapoxviruses, while those of spotted seals and harbor seals (*Phoca vitulina*) were highly conserved.

Castinel, A., Duignan, P.J., Pomroy, W.E., Lyons, E.T., Nadler, S.A., Dailey, M.D., Wilkinson, I.S., and Chilvers, B.L. **First report and characterization of adult *Uncinaria* spp. in New Zealand Sea Lion (*Phocarctos hookeri*) pups from the Auckland Islands, New Zealand.** *Parasitology Research* 98: 304-309, 2006.

Notes: Two species of hookworms (*Uncinaria lucasi* and *Uncinaria hamiltoni*) have been formally described from pinnipeds, but dissimilar types are noted from these hosts. This report is the first description of hookworms (*Uncinaria* spp.) from the New Zealand sea lion, *Phocarctos hookeri*. The nematodes were collected from dead pups on Enderby Island (Auckland Islands, 50°30', 166°17') during January and February, 2004. Standard measurements of male and female hookworms were obtained, providing a general morphometric characterization of the hookworm species in *P. hookeri*. Considerable variations in the body length of adult hookworms were noted within the same host. The arrangement of some of the bursal rays differs from that described for *U. lucasi* and *U. hamiltoni*.

Bull, J.C., Jepson, P.D., Ssuna, R.K., Deaville, R., Allchin, C.R., Law, R.J., and Fenton, A. **The relationship between polychlorinated biphenyls in blubber and levels of nematode infestations in harbour porpoises, *Phocoena phocoena*.** *Parasitology* 132(4): 565-573, 2006.

Notes: Post-mortem examinations of harbour porpoises, *Phocoena phocoena*, regularly reveal heavy parasitic worm burdens. These same post-mortem records show varying levels of polychlorinated biphenyls (PCBs) accumulating in the blubber of porpoises. Although a number of papers have documented geospatial and temporal changes of PCBs and their detrimental

effects on marine mammal health, as yet none have examined their role in determining nematode burdens in wild marine mammal populations. Using a data set consisting of harbour porpoises stranded in the UK between 1989 and 2002, we found a significant, positive association between PCB levels and nematode burdens, although the nature of the relationship was confounded with porpoise sex, age and cause of death. It was also apparent that individuals with the heaviest infestations of nematodes did not have the highest PCB level: while PCBs are important, they are clearly not the sole determinants of nematode burdens in wild populations of the harbour porpoise around the UK.

Maniscalco, A.M. and Shields, J.D. **Histopathology of idiopathic lesions in the eyes of *Homarus americanus* from Long Island Sound.** *Journal of Invertebrate Pathology* 91(2): 88-97, 2006.

Notes: In 1999, American lobsters, *Homarus americanus*, from western Long Island Sound (WLIS) experienced a significant mortality. In 2001 and 2004, the eyes and eyestalks of lobsters from WLIS and central LIS were examined for histopathological changes. Idiopathic lesions were identified in the ommatidia and optic nerve fibers proximal to the ommatidia in 29 (56%) of the lobsters from LIS. Lesions were categorized as either moderate or severe. Moderate lesions had altered rhabdoms, clumped pigment, and altered optic nerve fibers. Severe lesions were marked by absent rhabdoms, clumped pigment in both the ommatidial region and in the optic nerve region; and optic nerve fibers that had been completely destroyed and were replaced by vascular tissue. Idiopathic lesions occurred primarily in the central and ventral regions of the eye, and with much less frequency in the dorsal region. In addition, damage to the dorsal area tended to occur only when the severity of lesions was high, indicating a spatially progressive pattern to the lesion development. The lesions occurred in both western and central Long Island Sound, with no significant differences in severity between locations. The prevalence of lesions did not vary between years, but in 2004, several eyes had less severe pathology than those from 2001. These data indicate that the etiological agent is present throughout a large portion of the Sound, and that lobsters are probably continually exposed to it.

Mallory, M.L., Forbes, M.R., and Galloway, T.D. **Ectoparasites of northern fulmars *Fulmarus glacialis* (Procellariiformes: Procellariidae) from the Canadian Arctic.** *Polar Biology* 29(5): 353-357, 2006.

Notes: We studied the prevalence and intensity of infestation of ectoparasites on northern fulmars (*Fulmarus glacialis* L.) from a breeding colony in Arctic Canada in June-August 2003. No fleas or ticks were found on any fulmars, but three species of chewing lice (Phthiraptera) were recorded: Ischnocera: *Perineus nigrolimbatus* (Giebel 1874), Ischnocera: *Saemundssonina occidentalis* (Kellogg 1896), and Amblycera: *Ancistrona vagelli* (Fabricius 1787). Non-breeding birds had a higher prevalence of lice than breeding birds, and prevalence varied markedly among louse species. Our study is an important baseline for the occurrence of ectoparasites on northern fulmars in the high Arctic, a region undergoing extensive environmental change due to global warming, and an area where parasites are expected to extend ranges or increase in prevalence under changing annual temperature regimes.

Morton, A. and Routledge, R.D. **Fulton's condition factor: Is it a valid measure of sea lice impact on juvenile salmon?** *North American Journal of Fisheries Management* 26(1): 56-62, 2006.

Notes: Condition factor formulas have been developed and are used to assist in assessing the state of fish health. Fulton's condition factor has been used to measure anthropogenic impacts on fish, such as oil spills, and has provided results that, at times, are contentious. Recently, it has been used to suggest that infestation rates of sea lice *Lepeophtheirus salmonis* currently reported for juvenile pink salmon *Oncorhynchus gorbuscha* and chum salmon *O. keta* in the Broughton archipelago, British Columbia, may have no impact on fish health. Here, we show that Fulton's condition factor values will remain high in salmon fry lethally infected with sea lice until shortly before death. Furthermore, we report that as condition factor values declined, the affected fish exhibited high predator risk behavior. We conclude that Fulton's condition factor does not provide a reliable indicator of the impact of sea lice infestations on juvenile pink and chum salmon.

Fuenzalida, L., Hernandez, C., Toro, J., Rioseco, M.L., Romero, J., and Espejo, R.T. ***Vibrio parahaemolyticus* in shellfish and clinical samples during two large epidemics of diarrhoea in southern Chile.** *Environmental Microbiology* 8(4): 675-683, 2006.

Notes: Large epidemics of diarrhoea associated with seafood consumption and *Vibrio parahaemolyticus* occurred during the austral summers of 2004 and 2005 in the environs of Puerto Montt, Chile (41°29'S 72°24'W). There are no reports of *V. parahaemolyticus* infections before 2004 in this region, their absence being explained by the low ocean temperatures which seldom reach 16°C. We analysed *V. parahaemolyticus* obtained from shellfish and clinical samples during epidemics. Isolates were examined using conventional protocols and an improved method for restriction enzyme analysis using total bacterial DNA which permits direct genome restriction enzyme analysis by conventional gel electrophoresis (DGREA) with a similar discrimination index as restriction fragment length polymorphism-pulsed field gel electrophoresis (RFLP-PFGE). Analysis of clinical samples showed that the epidemics were caused by the *V. parahaemolyticus* O3:K6 pandemic clonal group. On the other hand, analysis of shellfish samples during both epidemics showed that 53% contained *V. parahaemolyticus* (3-93 g(-1)). Detailed analysis of 50 positive shellfish samples showed that only three contained detectable levels of the pandemic clone. Most *V. parahaemolyticus* isolates obtained from shellfish corresponded to non-pandemic clones differentiated into 14 groups by DGREA. In summary, the causative agent during epidemics was only a minor component of a small but diverse population of *V. parahaemolyticus* in shellfish.

Costantini, V., Loisy, F., Joens, L., LeGuyader, F.S., and Saif, L.J. **Human and animal enteric caliciviruses in oysters from different coastal regions of the United States.** *Applied and Environmental Microbiology* 72(3): 1800-1809, 2006.

Notes: Food-borne diseases are a major cause of morbidity and hospitalization worldwide. Enteric caliciviruses are capable of persisting in the environment and in the tissues of shellfish. Human noroviruses (HuNoVs) have been implicated in outbreaks linked to shellfish consumption. The genetic and antigenic relatedness between human and animal enteric caliciviruses suggests that interspecies transmission may occur. To determine the occurrence of human and animal enteric caliciviruses in United States market oysters, we surveyed regional markets. Oysters were collected from 45 bays along the United States coast during the summer and winter of 2002 and 2003. Samples were analyzed by reverse transcription-PCR, and results were confirmed by hybridization and sequence analysis. Nine samples (20%) were positive for HuNoV genogroup II after hybridization. Animal enteric caliciviruses were detected in 10 samples (22%). Seven of these samples were positive for porcine norovirus genogroup II, and one sample was positive for porcine sapovirus after hybridization and confirmation by sequencing. Bovine noroviruses were detected in two samples, and these results were confirmed by sequencing. Five HuNoV samples sequenced in the polymerase region were similar to the norovirus genogroup II US 95/96 subset (genogroup II-4) previously implicated in diarrhea outbreaks. Different seasonal and state distributions were detected. The presence of animal enteric caliciviruses was associated with states with high livestock production. Although the presence of human caliciviruses in raw oysters represents a potential risk for gastroenteritis, disease confirmation by investigation of outbreaks is required. The simultaneous detection of human and animal enteric caliciviruses raises concerns about human infection or coinfection with human and animal strains that could result in genomic recombination and the emergence of new strains.

Ravindran, J. and Raghukumar, C. **Pink-line syndrome, a physiological crisis in the scleractinian coral *Porites lutea*.** *Marine Biology* 149(2): 347-356, 2006.

Notes: Coral diseases are one of the major factors that alter coral cover and their diversity. We have earlier reported the "Pink-line syndrome" (PLS) in the scleractinian coral *Porites lutea* wherein a colored band appears between the dead and healthy tissue of a colony. About 20% of the *P. lutea* colonies were affected in Kavaratti of the Lakshadweep Islands in the Arabian Sea during April 1996 and the incidence increased fourfold within the next 4 years. Fungi were associated in both PLS-affected and healthy specimens, whereas the cyanobacterium *Phormidium valderianum* occurred exclusively in the PLS-affected specimens. There was an increased expression of a 29 kDa protein without any significant increase in total protein content in the PLS-affected colonies. A reduced number of zooxanthellae and an increase in zooxanthellae size, mitotic index, and chl *a* concentrations were some of the characteristics of the PLS-affected colonies. PLS induction experiments conducted using selected fungi and the cyanobacterium *P. valderianum* isolated from the affected colonies and abiotic factors, such as CO₂ enrichment and the effect of cyanobacterial photosynthesis inhibition, indicated that the CO₂ build-up around the host tissue caused the pink coloration. We hypothesize that these physiological changes disturb the mutualism between the zooxanthellae and the host. When the symbiosis is disturbed by the external CO₂, the host loses control over the zooxanthellae, causing their

uncontrolled division. This process may lead to a break in photosynthate transfer to the host, thereby resulting in starvation and finally leading to partial mortality. We further hypothesize that these degenerative processes are triggered by the CO₂ produced by *P. valderianum* through its carbon concentration mechanism. In this context, any opportunistic cyanobacteria or other agents having potential to interfere with the physiology of the host or the symbiont can cause such a physiological disorder. The mechanism of PLS formation is an early warning to protect corals as the increasing atmospheric CO₂ could induce PLS-like physiological disorder in corals.

Thompson, F.L., Barash, Y., Sawabe, T., Sharon, G., Swings, J., and Rosenberg, E. ***Thalassomonas loyana* sp. nov., a causative agent of the white plague-like disease of corals on the Eilat coral reef.** *International Journal of Systematic and Evolutionary Microbiology* 56(2): 365-368, 2006.

Notes: The taxonomic position of the coral pathogen strain CBMAI 722(I) was determined on the basis of molecular and phenotypic data. We clearly show that the novel isolate CBMAI 722(I) is a member of the family *Cobwelliaceae*, with *Thalassomonas ganghwensis* as the nearest neighbour (95 % 16S rRNA gene sequence similarity). CBMAI 722(I) can be differentiated from its nearest neighbour on the basis of phenotypic and chemotaxonomic features, including the utilization of cellobiose and L-arginine, the production of alginase and amylase, but not oxidase, and the presence of the fatty acids 12 : 0 3-OH and 14 : 0, but not 10 : 0 or 15 : 0. The DNA G+C content of CBMAI 722(I) is 39.3mol%. We conclude that this strain represents a novel species for which we propose the name *Thalassomonas loyana* sp. nov., with the type strain CBMAI 722(I) (=LMG 22536(I)). This is the first report of the involvement of a member of the family *Cobwelliaceae* in coral white plague-like disease.

Soniati, T.M., Klinck, J.M., Powell, E.N., and Hofmann, E.E. **Understanding the success and failure of oyster populations: Climatic cycles and *Perkinsus marinus*.** *Journal of Shellfish Research* 25(1): 83-93, 2006.

Notes: *Perkinsus* (=Dermocystidium) *marinus* is a major cause of mortality in eastern oysters, *Crassostrea virginica*. Because initiation of infection and progression of disease are favored by high temperature and high salinity, we hypothesized that climatic cycles influence cycles of disease. Analyses of a 10-y time series of disease prevalence and intensity, chlorophyll *a*, suspended sediments, water temperature and salinity from a Louisiana site, using a wavelet technique, show a teleconnection between the El Niño-Southern Oscillation (ENSO) and oyster disease in the northern Gulf of Mexico. Salinity increases precede increased disease prevalence by several months. The changes in salinity that trigger changes in disease prevalence and intensity are strongly driven by ENSO events. Interannual variation is important in the initiation and intensification of disease and salinity is the primary driving factor. The patterns in the environmental and disease time series suggest that epizootics can be initiated within 6 mo of a La Niña event, which produces increased water temperature and salinity. This relationship suggests an approach for predicting epizootics of *P. marinus* from climate models, which in turn can inform the management of oyster populations.

Hall, A.J., Hugunin, K., Deaville, R., Law, R.J., Allchin, C.R., and Jepson, P.D. **The risk of infection from polychlorinated biphenyl exposure in the harbor porpoise (*Phocoena phocoena*): A case-control approach.** *Environmental Health Perspectives* 114(5): 704-711, 2006.

Notes: The objective of this study was to determine whether the risk of mortality from infectious disease in harbor porpoise in U.K. waters increased with high exposure to polychlorinated biphenyls (PCBs), using a case-control study design. This is the first time that data from a long-term marine mammal strandings scheme have been used to estimate any increase in risk. The exposure odds ratio (OR) from a logistic regression model with infectious disease deaths as cases and physical trauma deaths as controls, after controlling for the effect of confounding factors, was 1.048 [95% confidence interval (0), 1.02-1.07]. To further adjust for the difference in energetic status between cases and controls and account for the negative relationship between PCBs (sum of 25 chlorobiphenyl congeners) and blubber mass, we also "standardized" the blubber PCBs to an optimal blubber mass. This lowered the OR to 1.02 (95% CI, 1.00-1.03). Thus, for each 1 mg/kg increase in blubber PCBs, the average increase in risk of infectious disease mortality was 2%. A doubling of risk occurred at approximately 45 mg/kg lipid. In this study, we have endeavored to avoid selection bias by using controls that died of physical trauma as representative of the exposure prevalence in the population that gave rise to the cases. In addition, we controlled for the effect of variation in

energetic status among the cases and controls. However, as with case-control studies in human and veterinary epidemiology, unforeseen misclassification errors may result in biased risk estimates in either direction.

Siebert, U., Tolley, K., Vikingsson, G.A., Olafsdottir, D., Lehnert, K., Weiss, R., and Baumgartner, W. **Pathological findings in harbour porpoises (*Phocoena phocoena*) from Norwegian and Icelandic waters.** *Journal of Comparative Pathology* 134(2-3): 134-142, 2006.

Notes: A study of 37 by-caught harbour porpoises from Icelandic and Norwegian waters showed that most were in good or moderate nutritional condition and none were severely emaciated. Mild infection with lungworms (*Halocercus invaginatus*, *Pseudalius inflexus*, *Torynurnus convolutus*) was found in 84% of the Icelandic and 91% of the Norwegian animals, usually associated with bronchopneumonia which was rarely severe. Most (91%) of the animals had parasites in the stomach and intestine (*Anisakis simplex*, *Contracaecum osculatum*, *Pholeter gastrophilus*), and *Campula oblonga* was present in the liver and pancreas of 88 and 21%, respectively. Oesophagitis, gastritis, cholangitis, pericholangitis, pancreatitis and lymphadenitis were almost exclusively associated with parasitic infection and usually mild. Bacterial isolates were obtained from 50 to 55% of the animals but were not considered to be clinically significant. There was no indication of morbillivirus infection. Icelandic and Norwegian animals showed a thicker blubber layer and a lower incidence of severe lesions, especially in the respiratory tract, as compared with reports of by-caught animals from the Baltic Sea.

Olsen, B., Munster, V.J., Wallensten, A., Waldenstrom, J., Osterhaus, A.D.M.E., and Fouchier, R.A.M. **Global patterns of influenza A virus in wild birds.** *Science* 312(5772): 384-388, 2006.

Notes: The outbreak of highly pathogenic avian influenza of the H5N1 subtype in Asia, which has subsequently spread to Russia, the Middle East, Europe, and Africa, has put increased focus on the role of wild birds in the persistence of influenza viruses. The ecology, epidemiology, genetics, and evolution of pathogens cannot be fully understood without taking into account the ecology of their hosts. Here, we review our current knowledge on global patterns of influenza virus infections in wild birds, discuss these patterns in the context of host ecology and in particular birds' behavior, and identify some important gaps in our current knowledge.

Le Guyader, F.S., Loisy, F., Atmar, R.L., Hutson, A.M., Estes, M.K., Ruvoën-Clouet, N., Pommepuy, M., and Le Pendu, J. **Norwalk virus-specific binding to oyster digestive tissues.** *Emerging Infectious Diseases* 12(6): 931-936, 2006.

Notes: The primary pathogens related to shellfishborne gastroenteritis outbreaks are noroviruses. These viruses show persistence in oysters, which suggests an active mechanism of virus concentration. We investigated whether Norwalk virus or viruslike particles bind specifically to oyster tissues after bioaccumulation or addition to tissue sections. Since noroviruses attach to carbohydrates of the histo-blood group family, tests using immunohistochemical analysis were performed to evaluate specific binding of virus or viruslike particles to oyster tissues through these ligands. Viral particles bind specifically to digestive ducts (midgut, main and secondary ducts, and tubules) by carbohydrate structures with a terminal N-acetylgalactosamine residue in an α linkage (same binding site used for recognition of human histo-blood group antigens). These data show that the oyster can selectively concentrate a human pathogen and that conventional depuration will not eliminate noroviruses from oyster tissue.

Thieltges, D.W., Hussel, B., and Baekgaard, H. **Endoparasites in common eiders *Somateria mollissima* from birds killed by an oil spill in the northern Wadden Sea.** *Journal of Sea Research* 55(4): 301-308, 2006.

Notes: Mass mortalities of common eiders *Somateria mollissima* have been ascribed to high parasite loads. However, the actual role of parasites in mortalities is disputed as in the case of a mass mortality of eiders in the Wadden Sea in the winter of 1999/2000. A critical evaluation of the role of parasites in eider mass mortalities is hampered by (1) a lack of data on actual parasite loads of the birds involved, (2) missing regional data for comparison, and (3) a lack of unbiased samples: investigations are often based on dead beached individuals, which are presumably the more heavily infected birds of a population and thus

more likely to die and be washed ashore. Although published data on parasite loads in birds of the winter 1999/2000 mortality are available, no data on background parasitism in eiders from the Wadden Sea exist, making an evaluation of the potential role of parasites in this mortality event difficult. By investigating endoparasites of 102 eiders affected by an oil spill in the northern Wadden Sea in winter 1998/1999, we provide a data set of background parasitism in wintering eiders from the Wadden Sea. We found 13 different parasite taxa with high prevalence values (% infected birds) in the acanthocephalan *Proflicollis botulus*, the nematode *Amidostomum acutum*, cestodes and trematodes. In some taxa we observed pronounced differences in prevalence values between juvenile eiders and adults, as well as between adult sexes. The parasite composition shows that bivalves, crabs (*Carcinus maenas*) and other crustaceans are important sources of infections by being intermediate hosts. This is partly mirrored in the food content of eider stomachs where bivalves and crabs were predominantly found. Intensities of the acanthocephalan *P. botulus*, suspected of causing eider mortalities, were especially high in juveniles (1112 +/- 416 ind per infected host), but lower in adult males (40 +/- 7) and adult females (81 +/- 18). However, no extraordinary mortality event was observed in the winter of 1998/1999, indicating no or a very weak effect of the parasites on host condition. A comparison with the parasite loads of eiders from the mass mortality in the winter of 1999/2000 shows that parasite numbers were by no means exceptional for birds from the area. Hence, parasites alone are unlikely to have caused this mortality. Regional background parasite loads are important to differentiate between primary and secondary roles of parasites in anomalous mortality events.

Manire, C.A., Smolarek, K.A., Romero, C.H., Kinsel, M.J., Clauss, T.M., and Byrd, L. **Proliferative dermatitis associated with a novel alphaherpesvirus in an Atlantic bottlenose dolphin (*Tursiops truncatus*)**. *Journal of Zoo and Wildlife Medicine* 37(2): 174-181, 2006.

Notes: Herpesviruses and herpes-like viruses have been reported in only a small number of species of cetaceans, and, to date, clinical manifestations have been either as a life-threatening, disseminated infection or as a non-life-threatening dermatitis. A stranded juvenile Atlantic bottlenose dolphin, *Tursiops truncatus*, was admitted to the Dolphin and Whale Hospital for rehabilitation. On initial physical examination, the rostral skin had multifocal regions of hyperplasia, and the skin of the dorsum contained a large number of small papules. Histologically, epithelial hyperplasia was evident, and clusters of epithelial cells contained 5-15mm intranuclear inclusion bodies. Transmission electron microscopic investigation revealed numerous 170-190nm enveloped virions in both the intracellular spaces and the cytoplasm of epithelial cells, with numerous nucleocapsids noted in epithelial cell nuclei. Consensus primer polymerase chain reaction identified the presence of a novel herpesvirus associated with the lesions. Phylogenetic analysis of the deduced amino acid sequences of the herpesvirus DNA polymerase gene fragment showed it to align with alphaherpesvirus sequences from humans and domestic animals. Although clearly distinct, it was most closely related to two previously described alphaherpesviruses of dolphins. This case represents the first documentation of herpesvirus dermatitis in the Atlantic bottlenose dolphin.

Park, K.I., Paillard, C., LeChevalier, P., and Choi, K.S. **Report on the occurrence of brown ring disease (BRD) in Manila clam, *Ruditapes philippinarum*, on the west coast of Korea**. *Aquaculture* 255(1-4): 610-613, 2006.

Notes: This is the first report on the occurrence of *Vibrio tapetis*, the brown ring disease (BRD) agent in Manila clam, *Ruditapes philippinarum*, in Asian waters. Brown conchiolin deposits, a distinct sign of BRD, were observed on the inner shells of clams collected from Anmyeondo Island, on the west coast of Korea. The infection intensity, based on the appearance of conchiolin deposits, ranged from 1-2, indicating that BRD of clams is in the initial phase. There was a negative correlation between the level of BRD and the condition index of the clams ($P < 0.05$). Extrapallial fluid from infected clams was collected and incubated in marine broth at 18 C for 20 h to obtain genomic DNA of the BRD agent. *Vibrio tapetis*-specific 165 rRNA was amplified by polymerase chain reaction using a *V. tapetis*-specific primer pair. The DNA sequences of the BRD agent isolated in this study showed 99.0-99.3% similarity to *V. tapetis* reported from France and Norway, suggesting that the causative agent of BRD observed in this study was *V. tapetis* or taxonomically close to *V. tapetis* reported in Europe.

Altizer, S., Dobson, A., Hosseini, P., Hudson, P., Pascual, M., and Rohani, P. **Seasonality and the dynamics of infectious diseases**. *Ecology Letters* 9(4): 467-484, 2006.

Notes: Seasonal variations in temperature, rainfall and resource availability are ubiquitous and can exert strong pressures on population dynamics. Infectious diseases provide some of the best-studied examples of the role of seasonality in shaping population fluctuations. In this paper, we review examples from human and wildlife disease systems to illustrate the challenges inherent in understanding the mechanisms and impacts of seasonal environmental drivers. Empirical evidence points to several biologically distinct mechanisms by which seasonality can impact host-pathogen interactions, including seasonal changes in host social behaviour and contact rates, variation in encounters with infective stages in the environment, annual pulses of host births and deaths and changes in host immune defences. Mathematical models and field observations show that the strength and mechanisms of seasonality can alter the spread and persistence of infectious diseases, and that population-level responses can range from simple annual cycles to more complex multiyear fluctuations. From an applied perspective, understanding the timing and causes of seasonality offers important insights into how parasite-host systems operate, how and when parasite control measures should be applied, and how disease risks will respond to anthropogenic climate change and altered patterns of seasonality. Finally, by focusing on well-studied examples of infectious diseases, we hope to highlight general insights that are relevant to other ecological interactions.

Keesing, F., Holt, R.D., and Ostfeld, R.S. **Effects of species diversity on disease risk.** *Ecology Letters* 9(4): 485-498, 2006.

Notes: The transmission of infectious diseases is an inherently ecological process involving interactions among at least two, and often many, species. Not surprisingly, then, the species diversity of ecological communities can potentially affect the prevalence of infectious diseases. Although a number of studies have now identified effects of diversity on disease prevalence, the mechanisms underlying these effects remain unclear in many cases. Starting with simple epidemiological models, we describe a suite of mechanisms through which diversity could increase or decrease disease risk, and illustrate the potential applicability of these mechanisms for both vector-borne and non-vector-borne diseases, and for both specialist and generalist pathogens. We review examples of how these mechanisms may operate in specific disease systems. Because the effects of diversity on multi-host disease systems have been the subject of much recent research and controversy, we describe several recent efforts to delineate under what general conditions host diversity should increase or decrease disease prevalence, and illustrate these with examples. Both models and literature reviews suggest that high host diversity is more likely to decrease than increase disease risk. Reduced disease risk with increasing host diversity is especially likely when pathogen transmission is frequency-dependent, and when pathogen transmission is greater within species than between species, particularly when the most competent hosts are also relatively abundant and widespread. We conclude by identifying focal areas for future research, including (1) describing patterns of change in disease risk with changing diversity; (2) identifying the mechanisms responsible for observed changes in risk; (3) clarifying additional mechanisms in a wider range of epidemiological models; and (4) experimentally manipulating disease systems to assess the impact of proposed mechanisms.

Munn, C.B. **Viruses as pathogens of marine organisms - from bacteria to whales.** *Journal of the Marine Biological Association of the United Kingdom* 86(3): 453-467, 2006.

Notes: Viruses are the most abundant members of marine ecosystems and play an enormous role in ocean processes through their interactions with all types of marine organisms. This short review provides examples of the dramatic increase in our knowledge of the diversity of marine viruses as pathogens of bacteria, protists, molluscs, crustaceans, cnidaria, reptiles, fish and mammals. Several examples are provided showing evidence of evolution of new strains, changes in virulence, and transfer of viruses between ecosystems. The natural and anthropogenic causes of these shifts are discussed. Despite considerable advances in recent years, knowledge of the importance of viruses in many important groups of marine organisms is lacking or incomplete. Suggestions for future investigations necessary to understand the dynamics of biogeochemical processes and the impacts of disease in our oceans are proposed.

Nagasaki, K., Tomaru, Y., Shirai, Y., Takao, Y., and Mizumoto, H. **Dinoflagellate-infecting viruses.** *Journal of the Marine Biological Association of the United Kingdom* 86(3): 469-474, 2006.

Notes: Dinoflagellates (Dinophyceae) are considered to be one of the most abundant and diverse groups of phytoplankton; however, the viral impact on dinoflagellates was not studied until recently. This review shows the present information concerning the viruses infecting dinoflagellates and the ecology relationships between the host and the virus. So far, two

viruses have been isolated and characterized: a large DNA virus (HcV: *Heterocapsa circularisquama* virus) and a small RNA virus (HcRNAV: *H. circularisquama* RNA virus); both of which are infectious to the harmful bloom-forming dinoflagellate *H. circularisquama*. In the present we mainly discuss the relationship between HcRNAV and *H. circularisquama* from the viewpoint of physiology ecology and genetics. It will help clarify the viral impact on dinoflagellate populations in marine environments to understand the host/parasite ecology.

Dalton, S.J. and Smith, S.D.A. **Coral disease dynamics at a subtropical location, Solitary Islands Marine Park, eastern Australia.** *Coral Reefs* 25(1): 37-45, 2006.

Notes: Recent observations suggest that a spreading disease is increasingly contributing to hard coral mortality in the Solitary Islands Marine Park, NSW, Australia. This study determined coral disease prevalence and rate-of-spread through individual affected colonies and investigated the effect this epizootic had on coral populations at sites adjacent to South West Solitary Island. Quantitative data were collected between 2002 and 2004 using photographic and video methods, and visual census along radial arc belt transects. Disease similar to the reported white syndrome and white plague was apparent, spreading through hard coral species from the genera *Turbinaria*, *Acropora*, *Goniastrea*, *Pocillopora*, *Stylophora* and *Porites*. Coral disease prevalence varied between survey dates with mean prevalence increasing from 8.55% during March 2003 to 13.58% in June and declining to 7.75% in September and 6.21% during March 2004. There was a significant difference in mean prevalence between the affected species ($p < 0.001$) and an overall difference between survey dates ($p=0.001$). Additionally, the rate-of-spread of coral disease through coral colonies determined using repeated, seasonal, still photographs followed similar patterns, with disease progression differing between affected species ($p = 0.004$), and between survey dates ($p < 0.001$). Analysis of the video-transects indicated significant difference in disease prevalence over larger spatial scales (100s of m). However, disease frequency did not vary significantly between 2002 and 2003.

Roff, G., Hoegh-Guldberg, O., and Fine, M. **Intra-colonial response to Acroporid "white syndrome" lesions in tabular *Acropora* spp. (Scleractinia).** *Coral Reefs* 25(2): 255-264, 2006.

Notes: 'White syndrome' is considered to be the most prevalent coral disease on the Great Barrier Reef, characterised by rapid rates of lesion progression and high levels of colony mortality. This study investigated the production and translocation of photoassimilates towards white syndrome lesions (WSLs) and artificially inflicted lesions in healthy and diseased colonies of tabular *Acropora* spp. to determine the intra-colonial response to white syndrome using C-14 labelling. Translocation of C-14 labelled photoassimilates was preferentially orientated away from active WSLs, with minimal C-14 activity observed in the lesion borders, whilst artificial lesions (ALs) created directly opposite WSL borders showed significantly higher C-14 activity, suggesting active translocation of photoassimilates for tissue regeneration. Transport of photoassimilates in healthy coral colonies was preferentially oriented towards ALs with a higher perimeter-area ratio, although translocation towards WSL boundaries was minimal even though the lesion perimeter was often the width of the colony (> 200 cm). We suggest that the preferential orientation of photoassimilates away from WSLs may represent a deliberate strategy by the colony to induce a 'shutdown reaction' in order to preserve intra-colonial resources within areas of the colony that are more likely to survive and recover.
