

Marine Science Review - 197

Pathogens, diseases and syndromes



In this review:

- A. Recent articles – no abstract available
- B. Recent articles with abstracts

A. Recent articles – no abstract available

Smyth, J.A., Todd, D., Scott, A., Beckett, A., Twentyman, C.M., Brojer, C., Uhlhorn, H., and Gavier-Widen, D. **Identification of circovirus infection in three species of gull.** *Veterinary Record* 159(7): 212-214, 2006.

Macdonald, D.W. and Laurenson, M.K. **Infectious disease: Inextricable linkages between human and ecosystem health.** *Biological Conservation* 131(2): 143-150, 2006.

Kapan, D.D., Bennett, S.N., Ellis, B.N., Fox, J., Lewis, N.D., Spencer, J.H., Saksena, S., and Wilcox, B.A. **Avian influenza (H5N1) and the evolutionary and social ecology of infectious disease emergence.** *EcoHealth* 3(3): 187-194, 2006.

Cowart, J.D., Henkel, T.P., McMurray, S.E., and Pawlik, J.R. **Sponge orange band (SOB): a pathogenic-like condition of the giant barrel sponge, *Xestospongia muta*.** *Coral Reefs* 25(4): 513, 2006.

B. Recent articles with abstracts

Smolarek-Benson, K.A., Manire, C.A., Ewing, R.Y., Saliki, J.T., Townsend, F.I., Ehlers, B., and Romero, C.H. **Identification of novel alpha- and gammaherpesviruses from cutaneous and mucosal lesions of dolphins and whales.** *Journal of Virological Methods* 136: 261-266, 2006.

Notes: Total DNA extracted from mucosal and skin lesions of captive and stranded cetaceans was analyzed for herpesvirus DNA by nested and direct polymerase chain reactions (PCR). The targeted sequences corresponded to a region of the DNA polymerase gene containing multiple conserved amino acid motifs. Herpesvirus genomic DNA fragments (222-244 bp) were amplified from 11 lesions by nested PCR and from eight lesions (~730 bp) using direct PCR from US cetaceans. Fragments of various sizes were also amplified from skin, spleen and blood of a German dolphin. Sequencing and BLAST analysis of these DNA fragments indicated that alpha- or gammaherpesviruses were present in the cetacean lesions. Alphaherpesviruses were associated with skin lesions of three Atlantic bottlenose dolphins (*Tursiops truncatus*), while gammaherpesviruses were present in genital lesions of five Atlantic bottlenose dolphins, one Risso's dolphin (*Grampus griseus*), one dwarf sperm whale (*Kogia sima*) and one Blainville's beaked whale (*Mesoplodon densirostris*), as well as in one oral lesion from an Atlantic bottlenose dolphin. Phylogenetic analysis of deduced amino acid sequences showed that the cetacean alphaherpesviruses were most closely related to human alphaherpesviruses, namely, herpes simplex-1 and -2. On the other hand, cetacean gammaherpesviruses were most closely related to *Rhadinoviruses*. These novel cetacean herpesviruses appeared to be distinct from known herpesviruses of marine and terrestrial vertebrates. The sequencing data strongly suggest that these viruses are most likely cetacean specific and possibly have coevolved with their cetacean hosts.

Yang, W.C., Pang, V.F., Jeng, C.R., Chou, L.S., and Chueh, L.L. **Morbilliviral infection in a pygmy sperm whale (*Kogia breviceps*) from Taiwanese waters.** *Veterinary Microbiology* 116(1-3): 69-76, 2006.

Notes: Morbilliviral infection was diagnosed in an adult male pygmy sperm whale (*Kogia breviceps*) from southwestern Taiwan on the basis of pathological findings, immunohistochemical staining, and reverse transcription-polymerase chain reaction. The whale was found alive stranded on the beach and died after 5 days of medical care. It was thin and had dozens of nematode in the first stomach. The lungs were dark red and heavy. Histopathological examination revealed diffuse, moderate bronchointerstitial pneumonia. Intranuclear and intracytoplasmic inclusions with occasional syncytial cell formation were noted in the lungs, lymph nodes, and spleen. The RNA extracted from lung tissue was subjected to morbilliviral gene amplification. After priming with specific oligonucleotides, the cDNA covering the phosphoprotein (P) gene was copied and then amplified by PCR. The gene fragment amplified from the lung tissue was sequenced. Phylogenetic analysis of partial P gene revealed 97.6% sequence identity to the dolphin morbillivirus and 90.2% similarity to the pilot whale morbillivirus. Morbilliviral antigens were detected in the lungs, lymph nodes, and spleen by immunohistochemistry using polyclonal antibody against rinderpest virus. This is the first report of morbilliviral infection with genetic evidence in a pygmy sperm whale from the Western Pacific Ocean around Taiwan.

Dabritz, H.A., Atwill, E.R., Gardner, I.A., Miller, M.A., and Conrad, P.A. **Outdoor fecal deposition by free-roaming cats and attitudes of cat owners and nonowners toward stray pets, wildlife, and water pollution.** *Journal of the American Veterinary Medical Association* 229(1): 74-81, 2006.

Notes: *Objective* - To estimate cat population size, management, and outside fecal deposition and evaluate attitudes of cat owners and nonowners to stray animal control, water pollution, and wildlife protection. *Design* - Cross-sectional survey. *Sample Population* - 294 adult residents of Cayucos, Los Osos, and Morro Bay, Calif. *Procedures* - Telephone survey *Results* - The region's cat population was estimated at 7,284 owned and 2,046 feral cats, and 38% of surveyed households owned a mean of 1.9 cats/household. Forty-four percent of cats defecated outside > 75% of the time. Annual fecal deposition (wet weight) by owned cats in the 3 communities was estimated to be 77.6 tonnes (76.4 tons). Cat owners were more likely to oppose cat licensing and impounding stray cats and support trap-neuter-return for stray cats and less likely to be concerned about water pollution, than were noncat owners. *Conclusions and Clinical Relevance* - Feral cats represented a sizeable proportion (22%) of the free-roaming cats in this area and could be contributing 30.0 tonnes (29.5 tons) of feces to the environment per year. However, feral cats are not the principal source of fecal loading because owned cats defecating outdoors contribute an estimated 77.6 tonnes (76.4 tons) or 72% of the annual outdoor fecal deposition.

Sekar, R., Mills, D.K., Remily, E.R., Voss, J.D., and Richardson, L.L. **Microbial communities in the surface mucopolysaccharide layer and the black band microbial mat of black band-diseased *Siderastrea siderea*.** *Applied and Environmental Microbiology* 72(9): 5963-5973, 2006.

Notes: Microbial community profiles and species composition associated with two black band-diseased colonies of the coral *Siderastrea siderea* were studied by 16S rRNA-targeted gene cloning, sequencing, and amplicon-length heterogeneity PCR (LH-PCR). Bacterial communities associated with the surface mucopolysaccharide layer (SML) of apparently healthy tissues of the infected colonies, together with samples of the black band disease (BBD) infections, were analyzed using the same techniques for comparison. Gene sequences, ranging from 424 to 1,537 bp, were retrieved from all positive clones ($n = 43$ to 48) in each of the four clone libraries generated and used for comparative sequence analysis. In addition to LH-PCR community profiling, all of the clone sequences were aligned with LH-PCR primer sequences, and the theoretical lengths of the amplicons were determined. Results revealed that the community profiles were significantly different between BBD and SML samples. The SML samples were dominated by g-proteobacteria (53 to 64%), followed by b-proteobacteria (18 to 21%) and a-proteobacteria (5 to 11%). In contrast, both BBD clone libraries were dominated by a-proteobacteria (58 to 87%), followed by verrucomicrobia (2 to 10%) and 0 to 6% each of d-proteobacteria, bacteroidetes, firmicutes, and cyanobacteria. Alphaproteobacterial sequence types related to the bacteria associated with toxin-producing dinoflagellates were observed in BBD clone libraries but were not found in the SML libraries. Similarly, sequences affiliated with the family Desulfobacteraceae and toxin-producing cyanobacteria, both believed to be involved in BBD pathogenesis, were found only in BBD libraries. These data provide evidence for an association of numerous toxin-producing heterotrophic microorganisms with BBD of corals.

Rehtanz, M., Ghim, S., Rector, A., Van Ranst, M., Fair, P.A., Bossart, G.D., and Jenson, A.B. **Isolation and characterization of the first American bottlenose dolphin papillomavirus: *Tursiops truncatus* papillomavirus type 2.**

Notes: A novel papillomavirus (PV) was isolated from a genital condyloma of a free-ranging bottlenose dolphin inhabiting the coastal waters of Charleston Harbor, SC, USA: *Tursiops truncatus* papillomavirus type 2 (TtPV2). This novel virus represents the first isolated North American cetacean PV and the first American bottlenose dolphin PV. After the viral genome was cloned, sequenced and characterized genetically, phylogenetic analyses revealed that TtPV2 is most similar to the only published cetacean PV isolated and characterized thus far, *Phocoena spinipinnis* PV type 1 (PsPV1). A striking feature of the genome of TtPV2, as well as that of PsPV1, is the lack of an E7 open reading frame, which typically encodes one of the oncogenic proteins believed to be responsible for malignant transformation in the high-risk mucosotropic human papillomaviruses (HPVs). TtPV2 E6 contains a PDZ-binding motif that has been shown to be involved in transformation in the case of high-risk genital HPVs.

Virvilis, C. and Angelidis, P. **Presence of the parasite *Marteilia* sp. in the flat oyster (*Ostrea edulis* L) in Greece.** *Aquaculture* 259(1-4): 1-5, 2006.

Notes: Native oyster (*Ostrea edulis* L) beds of the gulf of Thessaloniki were totally extinct in the past 10 years. A cause for this extinction is the presence of the parasite *Marteilia* sp., as was proven by an earlier study conducted by the same workgroup. Furthermore, a parasite of the same species affects mussels (*Mytilus galloprovincialis* Lam) in the same gulf. To determine the degree of this infection throughout Greece, the present research was carried out. Oyster samples were collected from four different areas (Thessaloniki, Argos, Stilida, Igoumenitsa). Cytological procedures and histology were used to examine the samples. The parasite was detected only in the oysters originating from the Gulf of Thessaloniki, in a high prevalence (46%).

Miller, W.A., Miller, M.A., Gardner, I.A., Atwill, E.R., Byrne, B.A., Jang, S., Harris, M., Ames, J., Jessup, D., Paradies, D., Worcester, K., Melli, A., and Conrad, P.A. ***Salmonella* spp., *Vibrio* spp., *Clostridium perfringens*, and *Plesiomonas shigelloides* in marine and freshwater invertebrates from coastal California ecosystems.** *Microbial Ecology* 52(2): 198-206, 2006.

Notes: The coastal ecosystems of California are highly utilized by humans and animals, but the ecology of fecal bacteria at the land-sea interface is not well understood. This study evaluated the distribution of potentially pathogenic bacteria in invertebrates from linked marine, estuarine, and freshwater ecosystems in central California. A variety of filter-feeding clams, mussels, worms, and crab tissues were selectively cultured for *Salmonella* spp., *Campylobacter* spp., *Escherichia coli*-O157, *Clostridium perfringens*, *Plesiomonas shigelloides*, and *Vibrio* spp. A longitudinal study assessed environmental risk factors for detecting these bacterial species in sentinel mussel batches. Putative risk factors included mussel collection near higher risk areas for livestock or human sewage exposure, adjacent human population density, season, recent precipitation, water temperature, water type, bivalve type, and freshwater outflow exposure. Bacteria detected in invertebrates included *Salmonella* spp., *C. perfringens*, *P. shigelloides*, *Vibrio cholerae*, *Vibrio parahaemolyticus*, and *Vibrio alginolyticus*. Overall, 80% of mussel batches were culture positive for at least one of the bacterial species, although the pathogens *Campylobacter*, *E. coli*-O157, and *Salmonella* were not detected. Many of the same bacterial species were also cultured from upstream estuarine and riverine invertebrates. Exposure to human sewage sources, recent precipitation, and water temperature were significant risk factors for bacterial detection in sentinel mussel batches. These findings are consistent with the hypothesis that filter-feeding invertebrates along the coast concentrate fecal bacteria flowing from land to sea and show that the relationships between anthropogenic effects on coastal ecosystems and the environmental niches of fecal bacteria are complex and dynamic.

Lockwood, S.K., Chovan, J.L., and Gaydos, J.K. **Aerobic bacterial isolations from harbor seals (*Phoca vitulina*) stranded in Washington: 1992-2003.** *Journal of Zoo and Wildlife Medicine* 37(3): 281-291, 2006.

Notes: Bacterial cultures collected over 12 yr from stranded harbor seal (*Phoca vitulina*) pups and weanlings located in the North Puget Sound and San Juan Islands region of Washington were analyzed retrospectively to determine the most common pathogenic isolates and to describe their antimicrobial resistance patterns. Culture attempts ($n = 58$) from wounds, umbilici, ears, conjunctiva, nares, oral lesions, and feces yielded 134 pathogenic isolates that represented 17 genera. The majority of isolates were Gram-negative ($n = 87$; 65%) and of the tested isolates were most susceptible to amikacin ($n = 76$; 99%) and

gentamicin ($n = 76$; 97%) and least susceptible to ampicillin ($n = 76$; 26%). Of the Gram-positive isolates tested ($n = 29$), all were susceptible to amoxicillin/clavulanic acid. The most frequent isolates were *Escherichia coli* (17%), β -hemolytic *Streptococcus* spp. (15%), *Enterococcus* spp. (11%), and *Pseudomonas aeruginosa* (11%), with all four exhibiting resistance to more than 50% of the antimicrobials tested. The variety of organisms isolated, the variation in either Gram-negative or Gram-positive predominance, and the multiple drug resistance patterns observed suggest that when treating stranded harbor seals, culture and sensitivity testing are warranted and that antibiotic therapy should be based on results.

Kim, Y. and Powell, E.N. **Relationships among parasites and pathologies in sentinel bivalves: NOAA Status and Trends "Mussel Watch" Program.** *Bulletin of Marine Science* 79(1): 83-111, 2006.

Notes: NOAA's National Status and Trends "Mussel Watch" Program includes a comprehensive survey of the histopathology of sentinel bivalves from the east, west, Gulf, and Great Lakes coasts of the U.S. We analyzed the data for 1995-1998 to identify relationships between various parasites, various pathologies, and between parasite/pathology pairs with the goal of identifying consistencies and differences in these relationships between sentinel bivalves and between major geographic units of the U.S. coastline. The prevalences of parasite, pathology, and parasite-pathology pairs were significantly correlated more frequently for oysters than for mussels. The number of significant correlations within Gulf-coast oysters exceeded the number within east-coast oysters. Correlations were least frequent among east-coast mussels. The incidence of significant negative correlations in prevalence far exceeded the incidence of significant positive correlations in all species and bay regions. Significant relationships in infection intensity occurred much less frequently than for prevalence, but positive correlations occurred more frequently than they did for prevalence. Both trends reinforce the concept that environmental factors controlling transmission are likely distinct from those controlling proliferation. Only a few relationships between parasites were common to more than one sentinel bivalve or more than one coastal region. No single common relationship involved a pathology. However, though commonalities were few, consistent trends in prevalence between mussels and oysters and between coastal regions suggest potentially important large-scale trends among some important parasite groups, particularly gregarines and gut ciliates, gill gregarines and cestodes, prokaryotic inclusions and trematode metacercariae, and *Perkinsus marinus* (Mackin, Owen and Collier, 1950) and gregarines.

Wallensten, A., Munster, V.J., Osterhaus, A.D.M.E., Waldenstrom, J., Bonnedahl, J., Broman, T., Fouchier, R.A.M., and Olsen, B. **Mounting evidence for the presence of influenza A virus in the avifauna of the Antarctic region.** *Antarctic Science* 18(3): 353-356, 2006.

Notes: Penguin blood samples collected at Bird Island, sub-Antarctic South Georgia, and faecal samples taken from penguins at several localities along the Antarctic Peninsula were analysed in order to investigate if influenza A virus is present in penguin populations in the South Atlantic Antarctic region. Serology was performed on the blood samples while the faecal samples were screened by a RT-PCR method directed at the matrix protein gene for determining the presence of influenza A virus. All faecal samples were negative by PCR, but the blood samples gave serologic indications that influenza A virus is present amongst these penguin species, confirming previous studies, although the virus has still not been isolated from any bird in the Antarctic region.

Harakeh, S., Yassine, H., Hajjar, S., and El Fadel, M. **Isolates of *Staphylococcus aureus* and *saprophyticus* resistant to antimicrobials isolated from the Lebanese aquatic environment.** *Marine Pollution Bulletin* 52(8): 912-919, 2006.

Notes: The indiscriminate use of antimicrobials especially in developing countries has evoked serious bacterial resistance and led to the emergence of new and highly resistant strains of bacteria to commonly used antimicrobials. In Lebanon, pollution levels and bacterial infections are increasing at a high rate as a result of inadequate control measures to limit untreated effluent discharges into the sea or freshwater resources. The aim of this study was to isolate and molecularly characterize various *Staphylococcus* strains isolated from sea water, fresh water, sediments, and crab samples collected from representative communities along the coast of Lebanon. The results on the antimicrobial resistance indicated that the level of resistance of *Staphylococcus aureus* varied with various antimicrobials tested. The resistance patterns ranged between 45% in freshwater isolates and 54.8% in seawater ones. Fifty one percent of the tested isolates have shown resistance to at least one of the five tested antimicrobials; with seawater isolates exhibiting the highest rates of antimicrobial resistance.

Smith, K.E., Sax, D.F., and Lafferty, K.D. **Evidence for the role of infectious disease in species extinction and endangerment.** *Conservation Biology* 20(5): 1349-1357, 2006.

Notes: Infectious disease is listed among the top five causes of global species extinctions. However, the majority of available data supporting this contention is largely anecdotal. We used the IUCN Red List of Threatened and Endangered Species and literature indexed in the ISI Web of Science to assess the role of infectious disease in global species loss. Infectious disease was listed as a contributing factor in <4% of species extinctions known to have occurred since 1500 (833 plants and animals) and as contributing to a species' status as critically endangered in <8% of cases (2852 critically endangered plants and animals). Although infectious diseases appear to play a minor role in global species loss, our findings underscore two important limitations in the available evidence: uncertainty surrounding the threats to species survival and a temporal bias in the data. Several initiatives could help overcome these obstacles, including rigorous scientific tests to determine which infectious diseases present a significant threat at the species level, recognition of the limitations associated with the lack of baseline data for the role of infectious disease in species extinctions, combining data with theory to discern the circumstances under which infectious disease is most likely to serve as an agent of extinction, and improving surveillance programs for the detection of infectious disease. An evidence-based understanding of the role of infectious disease in species extinction and endangerment will help prioritize conservation initiatives and protect global biodiversity.

Nowak, B.F. and LaPatra, S.E. **Epitheliocystis in fish.** *Journal of Fish Diseases* 29(10): 573-588, 2006.

Notes: Epitheliocystis is a condition affecting the gills and skin of fish, which has been reported from more than 50 freshwater and marine species. It is caused by intracellular Gram-negative bacteria. Mortalities have been associated with epitheliocystis infections in cultured fish. This associated review provides an update of our current understanding of this condition, including characterization of the pathogen using immunohistochemical and molecular of studies. In most fish species the epitheliocystis agent was negative to an antibody specific for chlamydial genus-specific lipopolysaccharide antigen. Recently, four epitheliocystis agents from four different fish species have been characterized using molecular analysis. While they all belong to the order Chlamydiales, in a lineage separate from the Chlamydiaceae, they are distinct organisms and similarity analysis showed that they had highest similarity values with other chlamydia-like bacteria isolated from various sources, including humans or pig. This confirms the high diversity and host specificity of the pathogen. Further molecular analysis should result in an increased understanding of this condition. To date, the pathogen has not been cultured, making experimental studies difficult. High stocking densities, presence of nutrients, season, temperature and fish age have been identified as potential risk factors for the manifestation of this condition.

Newman, S.J. and Smith, S.A. **Marine mammal neoplasia: A review.** *Veterinary Pathology* 43(6): 865-880, 2006.

Notes: A review of the published literature indicates that marine mammal neoplasia includes the types and distributions of tumors seen in domestic species. A routine collection of samples from marine mammal species is hampered, and, hence, the literature is principally composed of reports from early whaling expeditions, captive zoo mammals, and epizootics that affect larger numbers of animals from a specific geographic location. The latter instances are most important, because many of these long-lived, free-ranging marine mammals may act as environmental sentinels for the health of the oceans. Examination of large numbers of mortalities reveals incidental proliferative and neoplastic conditions and, less commonly, identifies specific malignant cancers that can alter population dynamics. The best example of these is the presumptive herpesvirus-associated metastatic genital carcinomas found in California sea lions. Studies of tissues from St. Lawrence estuary beluga whales have demonstrated a high incidence of neoplasia and produced evidence that environmental contamination with high levels of polychlorinated biphenols and dichlorophenyl trichloroethane might be the cause. In addition, viruses are suspected to be the cause of gastric papillomas in belugas and cutaneous papillomas in Florida manatees and harbor porpoises. While experimental laboratory procedures can further elucidate mechanisms of neoplasia, continued pathologic examination of marine mammals will also be necessary to follow trends in wild populations.

Ford, S.E. and Chintala, M.M. **Northward expansion of a marine parasite: Testing the role of temperature adaptation.** *Journal of Experimental Marine Biology and Ecology* 339(2): 226-235, 2006.

Notes: The known range of the eastern oyster (*Crassostrea virginica*) parasite, *Perkinsus marinus*, expanded into the northeastern United States in the early 1990s. We used both in vitro and in vivo data to test the hypothesis that the northward expansion was associated with a low-temperature adapted strain of the parasite. In vitro proliferation of nine *P. marinus* isolates from three geographic sites, Massachusetts and New Jersey in the new range, and South Carolina in the historic southern range, was measured at seven temperatures (5 to 35°C) using a tetrazolium blue dye assay. We wanted to determine if there were between- and within-geographic location differences in the *P. marinus* proliferation rate, and if so, whether they were associated with temperature. We found no evidence of low-temperature adaptation based on the fact that net proliferation rates for isolates from all three geographic locations were similar at temperatures from 5 to 20°C. On the other hand, at temperatures of 25 to 35°C, the South Carolina isolates exhibited higher proliferation rates than the northern isolates suggesting possible high-temperature adaptation of parasite strains that are routinely exposed to higher temperatures. Although there was significant within-location variation among isolates, the data tended to group together by geographic location supporting the hypothesis that there is an important regional component to the proliferation rate of *P. marinus* isolates. A survey of published data showed that the temperature at which in vivo proliferation was first observed in oysters at sites from the Gulf of Mexico to Massachusetts was typically between 20 and 23°C with no evidence of a geographic cline. These results lend support to the hypothesis that the recent warming trend in the northeastern US is the most likely explanation for the *P. marinus* range extension.

Glenn, R.P. and Pugh, T.L. **Epizootic shell disease in American lobster (*Homarus americanus*) in Massachusetts coastal waters: Interactions of temperature, maturity, and intermolt duration.** *Journal of Crustacean Biology* 26(4): 639-645, 2006.

Notes: An outbreak of shell disease in American lobster (*Homarus americanus*) over the past several years has generated a great deal of attention and concern regarding its causes and spread into New England coastal waters. An examination of the disease within Massachusetts state waters was conducted from 2000 through 2004. The overall average incidence observed in our data was 3% males and 8% females. Female lobsters were more likely to exhibit disease symptoms than males, and larger lobsters were more likely to possess disease symptoms than smaller lobsters. Disease incidence was highest in May and June, immediately prior to the molting period, and decreased dramatically through the molting season. We detected a north to south latitudinal gradient of increasing shell disease prevalence along the Massachusetts coast. Over the course of our study period, we found relatively constant low levels of shell disease in both the Gulf of Maine and Outer Cape Cod regions. However, a significantly higher level of shell disease was recorded in the Buzzards Bay region, indicating important differences in regional prevalence of disease. Our data suggest that this gradient in shell disease may be related to an interaction between water temperature, sexual maturity, and intermolt duration. There is a significant correlation between disease incidence in Buzzards Bay and a series of warmer than average water temperatures from 1999 to 2003, which suggests that temperature may be a primary factor related to the recent outbreak of epizootic shell disease.

Castro, K.M., Factor, J.R., Angell, T., and Landers, D.F. **The conceptual approach to lobster shell disease revisited.** *Journal of Crustacean Biology* 26(4): 646-660, 2006.

Notes: A shell disease epizootic is described for the American clawed lobster (*Homarus americanus*) populations in southern New England. This paper presents a conceptual model for examination of shell disease and presents evidence to support three hypotheses. Hypothesis one proposes that epizootic shell disease prevalence has increased in wild lobster populations; hypothesis two proposes that there are population-level effects of shell disease and hypothesis three explores the relationship between shell disease, and environmental and anthropogenic disturbances. This conceptual model links environmental stressors to physiological upsets and disease to population level impacts and can serve as a general model of disease in the marine environment.

Aeby, G.S. and Santavy, D.L. **Factors affecting susceptibility of the coral *Montastraea faveolata* to black-band disease.** *Marine Ecology Progress Series* 318: 103-110, 2006.

Notes: Black-band disease affects many species of tropical reef-building corals, but it is unclear what factors contribute to the disease-susceptibility of individual corals or how the disease is transmitted between colonies. Studies have suggested that the ability of black-band disease to infect coral is enhanced by different stressors. We examined the effect of both water temperature and mechanical injury on the ability of this disease to infect the reef coral *Montastraea faveolata*, and investigated the possibility of an interaction between the 2 stressors. Under laboratory conditions, *Phormidium corallyticum* was able to successfully invade all injured fragments but no uninjured fragments of *M. faveolata*, irrespective of temperature regime. We also determined whether the local coral-feeding butterflyfish *Chaetodon capistratus* was involved in the inter-colony transfer of black-band disease. In aquaria, the presence of *C. capistratus* increased the rate at which the disease spread from infected to non-infected fragments of *M. faveolata*. Both corals that were protected from and those that were exposed to fish predation contracted the disease. Hence, either direct oral transmission of the pathogen from colony to colony and/or indirect fecal transmission could be occurring. Variables such as potential stressors and/or disease vectors on a reef could contribute to the patterns of black-band disease observed in the field.

Cervino, J.M., Winiarski-Cervino, K., Polson, S.W., Goreau, T., and Smith, G.W. **Identification of bacteria associated with a disease affecting the marine sponge *Ianthella basta* in New Britain, Papua New Guinea.** *Marine Ecology Progress Series* 324: 139-150, 2006.

Notes: *Ianthella basta* marine sponges in Kimbe Bay, west New Britain, Papua New Guinea were affected by a disease, and exhibited high mortality, between 1996 and 2000. These fan-shaped sponges were mottled with brown lesions, rotted tissue and large holes. The decayed tissue was surrounded by brown biofilm that smothered the ostia openings. Since 1996, *I. basta* suffered its highest mortality at 3 sites within 16-20 km of the shore of west New Britain. No mortality was observed at 3 other locations further from shore (between 27-41 km), nor at 10 sites located more than 41 km from shore outside of Kimbe Bay in deeper waters, nor at the site nearest to shore. Comparison of the carbon source utilization patterns of 99 bacterial isolates from all healthy and diseased sponges revealed 5 species of bacteria specifically present in diseased *I. basta*. These bacteria were not present in healthy sponge samples. Bacteria isolated from affected sponges and inoculated onto healthy sponges caused disease signs similar to those in field specimens. The 16S rRNA genes from these bacteria were sequenced and found to correspond with 2 species of *Bacillus* and 3 species of *Pseudomonas*. The closest relatives of these bacteria based on BLAST searches included many terrestrial pathogens and species that are used as pathogens against insects and fungi in integrated pest control management. The bacteria causing disease in *I. basta* may thus originate from pesticides applied to agricultural land, predominantly oil palm plantations, in west New Britain. The possibility that these bacteria can pass virulence factors to marine bacteria through horizontal gene transfer needs to be investigated, as this may have unexpected impacts on marine ecosystems.

Leotta, G.A., Chinen, I., Vigo, G.B., Pecoraro, M., and Rivas, M. **Outbreaks of avian cholera in Hope Bay, Antarctica.** *Journal of Wildlife Diseases* 42(2): 259-270, 2006.

Notes: During austral summers 1999-2000 and 2000-01, two outbreaks of avian cholera occurred in the Hope Bay area (63°24'S, 56°59'W), located on the tip of the Antarctic Peninsula. Eighty-six dead birds were found: five kelp gulls (*Larus dominicanus*), 36 skuas (*Stercorarius* sp.), and 45 Adelie penguins (*Pygoscelis adeliae*). The carcasses were studied using clinical, pathological, and microbiological criteria. Water samples from ponds where birds were settled and samples from 90 healthy birds also were analyzed during the second outbreak. *Pasteurella multocida* isolates were identified by biochemical tests, capsular type, somatic serotype, and susceptibility to nine antibiotics. Molecular subtyping was performed by ApaI and SmaI pulsed-field gel electrophoresis (PFGE) and enterobacterial repetitive intergenic consensus (ERIC-PCR). In February 2000, mortality in skuas was 16% and 2% in kelp gulls. In the 2000-01 breeding season, mortality in south polar skuas was 47%, 24% in brown skuas, 1.4% in kelp gulls, and 0.01% in Adelie penguins. All birds had lesions of avian cholera. In kelp gulls the presentation was chronic, whereas skuas and penguins suffered subacute and acute disease, respectively. Fifty-five isolates recovered from dead birds and one from water were identified as *P. multocida gallicida*, type A:1. The strains presented a unique molecular pattern by PFGE and ERIC-PCR. A possible hypothesis to explain the origin of the outbreaks was that nonbreeder kelp gulls carried *P. multocida gallicida* to Hope Bay, and avian cholera was transmitted through water to skuas and penguins.

This study reports avian cholera in new bird species, their potential role in the transmission of the disease, and the different responses of these species to the disease.

Tachibana, M., Watanabe, K., Kim, S., Omata, Y., Murata, K., Hammond, T., and Watarai, M. **Antibodies to *Brucella* spp. in Pacific bottlenose dolphins from the Solomon Islands.** *Journal of Wildlife Diseases* 42(2): 412-414, 2006.

Notes: *Brucella* spp. have been recently isolated from a variety of marine mammals. Serum samples from 58 Pacific bottlenose dolphins (*Tursiops aduncus*) from the Solomon Islands were tested for antibodies to *Brucella* spp. by the tube agglutination test (TAT), enzymed-linked immunosorbent assay (ELISA), and immunoblotting. Anti-*Brucella* spp. antibodies were detected by TAT and ELISA in 31 and 40 of 58 samples, respectively. These results suggest that Pacific bottlenose dolphins from the Solomon Islands are infected with *Brucella* spp. or a *Brucella*-like organism.

Domart-Coulon, I.J., Traylor-Knowles, N., Peters, E., Elbert, D., Downs, C.A., Price, K., Stubbs, J., McLaughlin, S., Cox, E., Aeby, G., Brown, P.R., and Ostrander, G.K. **Comprehensive characterization of skeletal tissue growth anomalies of the finger coral *Porites compressa*.** *Coral Reefs* 25(4): 531-543, 2006.

Notes: The scleractinian finger coral *Porites compressa* has been documented to develop raised growth anomalies of unknown origin, commonly referred to as "tumors". These skeletal tissue anomalies (STAs) are circumscribed nodule-like areas of enlarged skeleton and tissue with fewer polyps and zooxanthellae than adjacent tissue. A field survey of the STA prevalence in Oahu, Kaneohe Bay, Hawaii, was complemented by laboratory analysis to reveal biochemical, histological and skeletal differences between anomalous and reference tissue. MutY, Hsp90a1, GRP75 and metallothionein, proteins known to be up-regulated in hyperplastic tissues, were over expressed in the STAs compared to adjacent normal-appearing and reference tissues. Histological analysis was further accompanied by elemental and micro-structural analyses of skeleton. Anomalous skeleton was of similar aragonite composition to adjacent skeleton but more porous as evidenced by an increased rate of vertical extension without thickening. Polyp structure was retained throughout the lesion, but abnormal polyps were hypertrophied, with increased mass of aboral tissue lining the skeleton, and thickened areas of skeletogenic calcicoblastic epithelium along the basal floor. The latter were highly metabolically active and infiltrated with chromophore cells. These observations qualify the STAs as hyperplasia and are the first report in poritid corals of chromophore infiltration processes in active calcicoblastic epithelium areas.

Voss, J.D. and Richardson, L.L. **Nutrient enrichment enhances black band disease progression in corals.** *Coral Reefs* 25(4): 569-576, 2006.

Notes: Infectious diseases are recognized as significant contributors to the dramatic loss of corals observed worldwide. However, the causes of increased coral disease prevalence and severity are not well understood. One potential factor is elevated nutrient concentration related to localized anthropogenic activities such as inadequate waste water treatment or terrestrial runoff. In this study the effect of nutrient enrichment on the progression of black band disease (BBD) was investigated using both in situ and laboratory experiments. Experimental increases in localized nutrient availability using commercial time release fertilizer in situ resulted in doubling of BBD progression and coral tissue loss in the common reef framework coral *Siderastrea siderea*. Laboratory experiments in which artificially infected *S. siderea* colonies were exposed to increased nitrate concentrations (up to 3 μ M) demonstrated similar increases in BBD progression. These findings provide evidence that the impacts of this disease on coral populations are exacerbated by nutrient enrichment and that management to curtail excess nutrient loading may be important for reducing coral cover loss due to BBD.

Fine, M., Roff, G., Ainsworth, T.D., and Hoegh-Guldberg, O. **Phototrophic microendoliths bloom during coral "white syndrome".** *Coral Reefs* 25(4): 577-581, 2006.

Notes: Following rapid lesion progression of white syndrome in tabular *Acropora* spp., the white bare skeleton gradually changes to green, a result of endolithic algae blooms (primarily *Ostreobium* spp.). Endolithic algal biomass and chlorophyll

concentration were found to be an order of magnitude higher in the green zone compared with healthy appearing parts of each colony. Chl *b* to Chl *a* ratio increased from 1:1.6 in the healthy area to 1:2 and 1:3.5 in the white exposed skeleton and green zones, respectively. These observations together with pulse amplitude modulated (PAM) fluorometry suggest photoacclimation of the endoliths in the green zone. Histopathological microscopy revealed that the endolithic algal filaments penetrate the coral tissue. This study highlights the interaction of endolithic algae with both the skeleton and host tissue. This may have a critical role in the processes that accompany the post-disease state in reef-building corals.

Mijangos-Alquisires, Z., Quintero-Arredondo, N., Castro-Longoria, R., Grijalva-Chon, J.M., and Ramos-Paredes, J. **White spot syndrome virus (WSSV) in *Litopenaeus vannamei* captured from the Gulf of California near an area of extensive aquaculture activity.** *Diseases of Aquatic Organisms* 71(1): 87-90, 2006.

Notes: For the shrimp farming industry of Mexico, disease outbreaks caused by white spot syndrome virus (WSSV) are relatively recent. Efforts to control the virus are assisted by monitoring for its prevalence in aquaculture systems, but few attempts have been made to search for it in carriers from coastal waters. To search for WSSV carriers in the Gulf of California, we made surveys off the coast of Sinaloa, Mexico, in March 2001, November 2001, and September 2003 using polymerase chain reaction (PCR) assays and histopathology. WSSV-positive shrimp were detected only in November 2001, after hurricane Juliette. This suggested possible dispersal of WSSV to the marine environment from infected shrimp farms.

Olson, J.B., Gochfeld, D.J., and Slattery, M. ***Aplysina* red band syndrome: a new threat to Caribbean sponges.** *Diseases of Aquatic Organisms* 71(2): 163-168, 2006.

Notes: A substantial and increasing number of reports have documented dramatic changes and continuing declines in Caribbean coral reef communities over the past 2 decades. To date, the majority of disease reports have focused on scleractinian corals, whereas sponge diseases have been less frequently documented. In this study, we describe *Aplysina* red band syndrome (ARBS) affecting Caribbean rope sponges of the genus *Aplysina* observed on shallow reefs in the Bahamas. Visible signs of disease presence included 1 or more rust-colored leading edges, with or without a trailing area of necrotic tissue, such that the lesion forms a contiguous band around part or all of the sponge branch. Microscopic examination of the leading edge of the disease margin indicated that a cyanobacterium was consistently responsible for the coloration. Although the presence of this distinctive coloration was used to characterize the diseased state, it is not yet known whether this cyanobacterium is directly responsible for disease causation. The prevalence of ARBS declined significantly from July to October 2004 before increasing above July levels in January 2005. Transmission studies in the laboratory demonstrated that contact with the leading edge of an active lesion was sufficient to spread ARBS to a previously healthy sponge, suggesting that the etiologic agent, currently undescribed, is contagious. Studies to elucidate the etiologic agent of ARBS are ongoing. Sponges are an essential component of coral reef communities and emerging sponge diseases clearly have the potential to impact benthic community structure on coral reefs.

Maeno, Y., Yurimoto, T., Nasu, H., Ito, S., Aishima, N., Matsuyama, T., Kamaishi, T., Oseko, N., and Watanabe, Y. **Virus-like particles associated with mass mortalities of the pen shell *Atrina pectinata* in Japan.** *Diseases of Aquatic Organisms* 71(2): 169-173, 2006.

Notes: Mass mortalities of the pen shell *Atrina pectinata* occurred in the fishing grounds of Ariake Bay, in southwestern Japan, during late spring and summer in 2003 and 2004. Histological examination revealed extensive necrosis in the epithelial cells of the kidney and gill, and impairment of the endothelial cells of the mantle arteria. Although cestode larvae belonging to the genus *Tylocephalum* were found in the mantle, adductor muscle, kidney, and digestive gland, their prevalence and the intensity of infection were low. Examinations of moribund pen shells for *Haplosporidium* spp. infection using PCR analysis and for *Perkinsus* spp. infection using Ray's fluid thioglycollate medium were negative. Unenveloped virus-like particles were detected by transmission electron microscopy in the cytoplasm of affected kidney and gill cells of moribund pen shells. They were icosahedral spherical and 50 to 55 nm in diameter. These virus-like particles found in moribund pen shells are different from those described in other marine mollusks, and may be the causative agent of the mass mortalities of pen shells.

Rhodes, L.D., Durkin, C., Nance, S.L., and Rice, C.A. **Prevalence and analysis of *Renibacterium salmoninarum* infection among juvenile Chinook salmon *Oncorhynchus tshawytscha* in North Puget Sound.** *Diseases of Aquatic Organisms* 71(3): 179-190, 2006.

Notes: *Renibacterium salmoninarum* causes bacterial kidney disease (BKD), a chronic and sometimes fatal disease of salmon and trout that could lower fitness in populations with high prevalences of infection. Prevalence of *R. salmoninarum* infection among juvenile Chinook salmon *Oncorhynchus tshawytscha* inhabiting neritic marine habitats in North Puget Sound, Washington, USA, was assessed in 2002 and 2003. Fish were collected by monthly surface trawl at 32 sites within 4 bays, and kidney infections were detected by a quantitative fluorescent antibody technique (qFAT). The sensitivity of the qFAT was within an order of magnitude of the quantitative real-time PCR (qPCR) sensitivity. Prevalence of infection was classified by fish origin (marked/hatchery vs. unmarked/likely natural spawn), month of capture, capture location and stock origin. The highest percentages of infected fish (63.5 to 63.8 %) and the greatest infection severity were observed for fish collected in Bellingham Bay. The lowest percentages were found in Skagit Bay (11.4 to 13.5 %); however, there was no difference in prevalence between marked and unmarked fish among the capture locations. The optimal logistic regression model of infection probabilities identified the capture location of Bellingham Bay as the strongest effect, and analysis of coded wire tagged (CWT) fish revealed that prevalence of infection was associated with the capture location and not with the originating stock. These results suggest that infections can occur during the early marine life stages of Chinook salmon that may be due to common reservoirs of infection or horizontal transmission among fish stocks.

Avendano-Herrera, R., Toranzo, A.E., and Magarinos, B. **Tenacibaculosis infection in marine fish caused by *Tenacibaculum maritimum*: a review.** *Diseases of Aquatic Organisms* 71(3): 255-266, 2006.

Notes: *Tenacibaculum maritimum* is the aetiological agent of an ulcerative disease known as tenacibaculosis, which affects a large number of marine fish species in the world and is of considerable economic significance to aquaculture producers. Problems associated with epizootics include high mortality rates, increased susceptibility to other pathogens, high labour costs of treatment and enormous expenditures on chemotherapy. In the present article we review current knowledge on this bacterial pathogen, focusing on important aspects such as the phenotypic, serologic and genetic characterization of the bacterium, its geographical distribution and the host species affected. The epizootiology of the disease, the routes of transmission and the putative reservoirs of *T. maritimum* are also discussed. We include a summary of molecular diagnostic procedures, the current status of prevention and control strategies, the main virulence mechanisms of the pathogen, and we attempt to highlight fruitful areas for continued research.
