

Marine Science Review - 182

Pathogens and disease



In this review:

A. Recent articles with abstracts

A. Recent articles with abstracts

Graczyk, T.K., Girouard, A.S., Tamang, L., Napier, S.P., and Schwab, K.J. **Recovery, bioaccumulation, and inactivation of human waterborne pathogens by the Chesapeake Bay nonnative oyster, *Crassostrea ariakensis*.** *Applied and Environmental Microbiology* 72(5): 3390-3395, 2006.

Notes: The introduction of nonnative oysters (i.e., *Crassostrea ariakensis*) into the Chesapeake Bay has been proposed as necessary for the restoration of the oyster industry; however, nothing is known about the public health risks related to contamination of these oysters with human pathogens. Commercial market-size *C. ariakensis* triploids were maintained in large marine tanks with water of low (8-ppt), medium (12-ppt), and high (20-ppt) salinities spiked with 1.0×10^5 transmissive stages of the following human pathogens: *Cryptosporidium parvum* oocysts, *Giardia lamblia* cysts, and microsporidian spores (i.e., *Encephalitozoon intestinalis*, *Encephalitozoon hellem*, and *Enterocytozoon bieneusi*). Viable oocysts and spores were still detected in oysters on day 33 post-water inoculation (pwi), and cysts were detected on day 14 pwi. The recovery, bioaccumulation, depuration, and inactivation rates of human waterborne pathogens by *C. ariakensis* triploids were driven by salinity and were optimal in medium- and high-salinity water. The concentration of human pathogens from ambient water by *C. ariakensis* and the retention of these pathogens without (or with minimal) inactivation and a very low depuration rate provide evidence that these oysters may present a public health threat upon entering the human food chain, if harvested from polluted water. This conclusion is reinforced by the concentration of waterborne pathogens used in the present study, which was representative of levels of infectious agents in surface waters, including the Chesapeake Bay. Aquacultures of nonnative oysters in the Chesapeake Bay will provide excellent ecological services in regard to efficient cleaning of human-infectious agents from the estuarine waters.

Lehmann, T., Marcet, P.L., Graham, D.H., Dahl, E.R., and Dubey, J.P. **Globalization and the population structure of *Toxoplasma gondii*.** *Proceedings of the National Academy of Sciences [USA]* 103(30): 11423-11428, 2006.

Notes: *Toxoplasma gondii* is a protozoan parasite that infects nearly all mammal and bird species worldwide. Usually asymptomatic, toxoplasmosis can be severe and even fatal to many hosts, including people. Elucidating the contribution of genetic variation among parasites to patterns of disease transmission and manifestations has been the goal of many studies. Focusing on the geographic component of this variation, we show that most genotypes are locale-specific, but some are found across continents and are closely related to each other, indicating a recent radiation of a pandemic genotype. Furthermore, we show that the geographic structure of *T. gondii* is extraordinary in having one population that is found in all continents except South America, whereas other populations are generally confined to South America, and yet another population is found worldwide. Our evidence suggests that South American and Eurasian populations have evolved separately until recently, when ships populated by rats, mice, and cats provided *T. gondii* with unprecedented migration opportunities, probably during the transatlantic slave trade. Our results explain several enigmatic features of the population structure of *T. gondii* and demonstrate how pervasive, prompt, and elusive the impact of human globalization is on nature.

Remily, E.R. and Richardson, L.L. **Ecological physiology of a coral pathogen and the coral reef environment.** *Microbial Ecology* 51(3): 345-352, 2006.

Notes: Laboratory studies on the ecological physiology of a coral pathogen were carried out to investigate growth potential in terms of environmental factors that may control coral diseases on reefs. The disease chosen for this study, white plague type II, is considered to be one of the major diseases of Caribbean scleractinian corals, affecting a wide range of coral hosts and causing rapid and widespread tissue loss. It is caused by a single pathogen, the bacterium *Aurantimonas corallicida*. A series of laboratory experiments using a pure culture of the pathogen was carried out to examine the roles of temperature, pH, and O₂ concentration on growth rate. Results revealed optimal growth between 30 and 35°C, and between pH values of 6 and 8. There was a distinctive synergistic relationship between pH and temperature. Increasing temperature from 25 to 35°C expanded the range of pH tolerance from a minimum of 6.0 down to 5.0. O₂ concentration directly affected growth rate, which increased with increasing O₂. The combined effects of increasing O₂ and increasing temperature resulted in a synergistic effect of more rapid growth. These laboratory results are discussed in terms of the coral host and the range of the environmental factors that occur on coral reefs. We conclude that changing environmental conditions in the reef environment, in particular observed increases in water temperature, may be promoting coral diseases by allowing coral pathogens to expand their ecological niches. In the case of the white plague type II pathogen, elevated temperature would allow *A. corallicida* to colonize the low pH environment of the coral surface mucopolysaccharide layer as an initial stage of infection. The synergistic effect between temperature and oxygen concentration appeared to be less environmentally relevant for this coral pathogen.

Owen, J., Moore, F., Panella, N., Edwards, E., Bru, R., Hughes, M., and Komar, N. **Migrating birds as dispersal vehicles for West Nile virus.** *EcoHealth* 3(2): 79-85, 2006.

Notes: Whereas migrating birds have been implicated in the spread of West Nile virus (WNV), there is no direct evidence of birds actively migrating while infectious. The role of birds in WNV dispersal is difficult to assess in the field. However, this role can be evaluated experimentally because birds in migratory disposition display increased locomotor activity or restlessness under captive conditions. We tested the following hypotheses: (1) migrating passerine birds continue to exhibit migratory activity while infectious with WNV and (2) the migratory state of the individual affects the magnitude of viremia. We examined the migratory activity of two neoarctic-neotropical passerine migrants, Swainson's thrush (*Catharus ustulatus*) and gray catbird (*Dumetella carolinensis*), during acute WNV infection. All gray catbirds and six of nine Swainson's thrushes exhibited migratory activity while infectious. Moreover, migratory status did not appear to influence viremia titers, as might be expected if individuals were immunosuppressed during migration. Therefore, we demonstrate that migrating passerine birds are potential dispersal vehicles for WNV.

Austin, B. and Zhang, X.H. ***Vibrio harveyi*: a significant pathogen of marine vertebrates and invertebrates.** *Letters in Applied Microbiology* 43(2): 119-124, 2006.

Notes: *Vibrio harveyi*, which now includes *Vibrio carchariae* as a junior synonym, is a serious pathogen of marine fish and invertebrates, particularly penaeid shrimp. In fish, the diseases include vasculitis, gastro-enteritis and eye lesions. With shrimp, the pathogen is associated with luminous vibriosis and *Bolitas negricans*. Yet, the pathogenicity mechanisms are imprecisely understood, with likely mechanisms involving the ability to attach and form biofilms, quorum sensing, various extracellular products including proteases and haemolysins, lipopolysaccharide, and interaction with bacteriophage and bacteriocin-like substances.

Ackerman, P.A., Wicks, B.J., Iwama, G.K., and Randall, D.J. **Low levels of environmental ammonia increase susceptibility to disease in Chinook salmon smolts.** *Physiological and Biochemical Zoology* 79(4): 695-707, 2006.

Notes: Ammonia criteria are established using data from standardized toxicity tests involving healthy animals. Both intrinsic and extrinsic environmental changes affect the immune system, but few toxicity studies consider the overall impact on this system and potential changes in resistance to infection. To investigate the effects of subacute levels of ammonia in coastal waters on physiological and immunological systems of fish, juvenile Chinook salmon were maintained in seawater (10°C, pH 7.8) and exposed to two concentrations of ammonia, 2.5 and 10 mg/L total nitrogen. Both test levels resulted in increased

internal levels of ammonia in the fish. Neither treatment level affected feeding rates. Over a time course of 10 d, numerous significant effects were observed. White blood cell counts changed significantly, as did respiratory burst activity, plasma lysozyme activity, and plasma glucose concentration in both treatments compared to controls. In an experimental infection with *Vibrio anguillarum*, fish previously exposed to subacute levels of ammonia were more susceptible to pathogenic challenge. The findings of this study indicate that a more thorough investigation into the effects of environmental ammonia on fish populations in coastal waters should be undertaken and the current environmental standards reassessed.

Culley, A.I., Lang, A.S., and Suttle, C.A. **Metagenomic analysis of coastal RNA virus communities.** *Science* 312(5781): 1795-1798, 2006.

Notes: RNA viruses infect marine organisms from bacteria to whales, but RNA virus communities in the sea remain essentially unknown. Reverse-transcribed whole-genome shotgun sequencing was used to characterize the diversity of uncultivated marine RNA virus assemblages. A diverse assemblage of RNA viruses, including a broad group of marine picorna-like viruses, and distant relatives of viruses infecting arthropods and higher plants were found. Communities were dominated by distinct genotypes with small genome sizes, and we completely assembled the genomes of several hitherto undiscovered viruses. Our results show that the oceans are a reservoir of previously unknown RNA viruses.

Carnegie, R.B., Bureson, E.M., Hine, P.M., Stokes, N.A., Audemard, C., Bishop, M.J., and Peterson, C.H. ***Bonamia perspora* n. sp. (Haplosporidia), a parasite of the oyster *Ostreola equestris*, is the first *Bonamia* species known to produce spores.** *Journal of Eukaryotic Microbiology* 53(4): 232-245, 2006.

Notes: Examination of the oyster *Ostreola equestris* as a potential reservoir host for a species of *Bonamia* discovered in *Crassostrea ariakensis* in North Carolina (NC), USA, revealed a second novel *Bonamia* sp. Histopathology, electron microscopy, and molecular phylogenetic analysis support the designation of a new parasite species, *Bonamia perspora* n. sp., which is the first *Bonamia* species shown to produce a typical haplosporidian spore with an orifice and hinged operculum. Spores were confirmed to be from *B. perspora* by fluorescent in situ hybridization. *Bonamia perspora* was found at Morehead City and Wilmington, NC, with an overall prevalence of 1.4% (31/2,144). Uninucleate, plasmodial, and sporogonic stages occurred almost exclusively in connective tissues; uninucleate stages (2-6 µm) were rarely observed in hemocytes. Spores were 4.3-6.4 µm in length. Ultrastructurally, uninucleate, diplokaryotic, and plasmodial stages resembled those of other spore-forming haplosporidians, but few haplosporosomes were present, and plasmodia were small. Spore ornamentation consisted of spore wall-derived, thin, flat ribbons that emerged haphazardly around the spore, and which terminated in what appeared to be four-pronged caps. Number of ribbons per spore ranged from 15 to 30, and their length ranged from 1.0 to 3.4 µm. Parsimony analysis identified *B. perspora* as a sister species to *Bonamia ostreae*.

Kilpatrick, A.M., Daszak, P., Goodman, S.J., Rogg, H., Kramer, L.D., Cedenno, V., and Cunningham, A.A. **Predicting pathogen introduction: West Nile virus spread to Galapagos.** *Conservation Biology* 20(4): 1224-1231, 2006.

Notes: Emerging infectious diseases are a key threat to conservation and public health, yet predicting and preventing their emergence is notoriously difficult. We devised a predictive model for the introduction of a zoonotic vector-borne pathogen by considering each of the pathways by which it may be introduced to a new area and comparing the relative risk of each pathway. This framework is an adaptation of pest introduction models and estimates the number of infectious individuals arriving in a location and the duration of their infectivity. We used it to determine the most likely route for the introduction of West Nile virus to Galapagos and measures that can be taken to reduce the risk of introduction. The introduction of this highly pathogenic virus to this unique World Heritage Site could have devastating consequences, similar to those seen following introductions of pathogens into other endemic island faunas. Our model identified the transport of mosquitoes on airplanes as the highest risk for West Nile virus introduction. Pathogen dissemination through avian migration and the transportation of day-old chickens appeared to be less important pathways. Infected humans and mosquitoes transported in sea containers, in tires, or by wind all represented much lower risk. Our risk-assessment framework has broad applicability to other pathogens and other regions and depends only on the availability of data on the transport of goods and animals and the epidemiology of the pathogen.

Hall, S.R., Tessier, A.J., Duffy, M.A., Huebner, M., and Caceres, C.E. **Warmer does not have to mean sicker: Temperature and predators can jointly drive timing of epidemics.** *Ecology* 87(7): 1684-1695, 2006.

Notes: Ecologists and epidemiologists worry that global warming will increase disease prevalence. These fears arise because several direct and indirect mechanisms link warming to disease, and because parasite outbreaks are increasing in many taxa. However, this outcome is not a foregone conclusion, as physiological and community-interaction-based mechanisms may inhibit epidemics at warmer temperatures. Here, we explore this thermal-community-ecology-based mechanism, centering on fish predators that selectively prey upon *Daphnia* infected with a fungal parasite. We used an interplay between a simple model built around this system's biology and laboratory experiments designed to parameterize the model. Through this data-model interaction, we found that a given density of predators can inhibit epidemics as temperatures rise when thermal physiology of the predator scales more steeply than that of the host. This case is met in our fish-*Daphnia*-fungus system. Furthermore, the combination of steeply scaling parasite physiology and predation-induced mortality can inhibit epidemics at lower temperatures. This effect may terminate fungal epidemics of *Daphnia* as lakes cool in autumn. Thus, predation and physiology could constrain epidemics to intermediate temperatures (a pattern that we see in our system). More generally, these results accentuate the possibility that warmer temperatures might actually enhance predator control of parasites.

Savichtcheva, O. and Okabe, S. **Alternative indicators of fecal pollution: Relations with pathogens and conventional indicators, current methodologies for direct pathogen monitoring and future application perspectives.** *Water Research* 40(13): 2463-2476, 2006.

Notes: The ecological and survival characteristics of bacterial, viral and parasitic pathogens vary under environmental conditions, indicating that probably no single indicator organism can predict the presence of all enteric pathogens for all types of waters and different host-associated fecal pollution. If there are true correlations between indicator organisms and pathogens, it is necessary to find out to what extent and under which circumstances these organisms can be used as reliable indicators of fecal pollution. Application of conventional and alternative fecal indicators has greatly enhanced our abilities to predict and reduce health risk associated with the use of surface waters. New molecular-based techniques have shown that combined use of conventional and alternative indicators for fecal pollution increases both the detection sensitivity and specificity of fecal pollution and associated pathogens. In this review, we, therefore, summarize the advantages and limitations of conventional and alternative fecal indicators in terms of predicting pathogen presence as well as current and future methodologies for direct pathogen monitoring in environmental waters. This manuscript is mainly focused on the relationships between microbial fecal indicators and the presence of pathogens, which have not previously been summarized yet and could nicely supplement with recent literature reviews on microbial source tracking.

Costello, M.J. **Ecology of sea lice parasitic on farmed and wild fish.** *Trends in Parasitology* 22(10): 475-483, 2006.

Notes: Sea lice, especially *Lepeophtheirus salmonis* and *Caligus* spp., have the greatest economic impact of any parasite in salmonid fish farming and are also a threat to wild salmonids. Here, I review how the biology and ecology of various louse and host species influence their pathogenicity and epidemiology. Recent discoveries of new species and genotypes emphasize the need for more basic research on louse taxonomy and host preferences. Louse development rates are strongly dependent on temperature, and increasing mean sea temperatures are likely to increase infestation pressure on farms and wild fish, as well as affecting the geographical distribution of hosts and parasites. Despite progress in finding *L. salmonis* larvae in the plankton and in modelling louse production in several countries, more data on larval behaviour and distribution are required to develop dispersal and transmission models for both *L. salmonis* and *Caligus* spp. This knowledge could be used to take measures to reduce the risks of lice affecting farmed and wild fish.

Hall, A.J., Jepson, P.D., Goodman, S.J., and Harkonen, T. **Phocine distemper virus in the North and European Seas - Data and models, nature and nurture.** *Biological Conservation* 131(2): 221-229, 2006.

Notes: Two outbreaks of phocine distemper have severely affected harbour seal (*Phoca vitulina*) populations in European and UK waters. The first occurred in 1988 when the causative virus was identified as a new member of the genus morbillivirus. The second outbreak in 2002 was first detected on the same Danish Island of Anholt and involved similar populations and geographical locations. However, despite the obvious similarities between the epidemics, differences in viral transmission and case mortality were found. Harbour seals are highly susceptible to infection while sympatric grey seals (*Halichoerus grypus*) are resistant but could be important asymptomatic carriers of the disease. Arctic phocid seals remain the most likely source of the virus and grey seals could be the link between these primary hosts and the harbour seal populations further south. Future epidemiological models should therefore consider including multiple host species. The future conservation and management of harbour seal populations vulnerable to PDV relies on the ability to accurately predict the long-term impact on population abundance and distribution. Although knowledge about the behaviour and pathogenesis of the virus has increased substantially and data on host movements and contact rates are accumulating, studies into the determinants of the host range have lagged behind. The development of more realistic epidemiological models should be combined with studies into the factors controlling species and individual susceptibility. Assessing the risk of infection to endangered but currently unexposed potential host species (such as the Hawaiian monk seal, *Monachus schauinslandi*) is essential for guiding potential conservation management options, such as vaccination.

Leendertz, F.H., Pauli, G., Maetz-Rensing, K., Boardman, W., Nunn, C., Ellerbrok, H., Jensen, S. A., Junglen, S., and Boesch, C. **Pathogens as drivers of population declines: The importance of systematic monitoring in great apes and other threatened mammals.** *Biological Conservation* 131(2): 325-337, 2006.

Notes: Until recently, the focus of great ape behavioural and ecological research has been distinct from the focus of scientists working in medical and veterinary sciences. More scientists are calling for a connection between medical and field research due to recent disease outbreaks in great apes, including Ebola, and indications of cross-transmission of Ebola and other viruses between primates and humans. A major limitation to progress is the lack of information on infectious diseases and their transmission in wild primates. Here, we present examples of successful pathogen detection in wild great apes and describe approaches and techniques that can be used in the field, focusing in particular on investigation of deaths and non-invasive sample collection. This interdisciplinary approach is providing new insights to infectious diseases of great apes and is helping to protect the health of great ape populations. This framework can also be applied to other mammals under threat from infectious diseases, including African wild dogs, seals and Tasmanian devils. In addition to providing benefits for great ape conservation, research that integrates infectious disease with primate ecology provides insights to emerging diseases in humans and the role of disease in primate evolution.

Hui, E.K.W. **Reasons for the increase in emerging and re-emerging viral infectious diseases.** *Microbes and Infection* 8(3): 905-916, 2006.

Notes: In the past two decades, humans have faced many new viral infectious agents in emerging and re-emerging infectious diseases (EIDs). Many factors contribute to the appearance of EIDs. These factors are complex but can be classified into three different categories: virus factors, human factors, and ecological factors. The factors contributing to the cause of such viral infectious diseases will be systematically reviewed in this article.

Gozlan, R.E., Peeler, E.J., Longshaw, M., St-Hilaire, S., and Feist, S.W. **Effect of microbial pathogens on the diversity of aquatic populations, notably in Europe.** *Microbes and Infection* 8(5): 1358-1364, 2006.

Notes: The expansion of aquaculture and the demand for ornamental fish have resulted in the large-scale movements of aquatic animals and their pathogens. Here we review the most important non-native fish and shellfish pathogens in European waters and their global impacts on wild fish host populations. The role of theoretical models in the study of the impact of microbial pathogens is discussed, including its integration into risk assessments.

Hudson, P.J., Cattadori, M., Boag, B., and Dobson, A.P. **Climate disruption and parasite-host dynamics: patterns and processes associated with warming and the frequency of extreme climatic events.** *Journal of Helminthology* 80(2): 175-182, 2006.

Notes: Levels of parasitism and the dynamics of helminth systems is subject to the impact of environmental conditions such that we may expect long term increases in temperature will increase the force of infection and the parasite's basic reproduction number, R-0. We postulate that an increase in the force of infection will only lead to an increase in mean intensity of adults when adult parasite mortality is not determined by acquired immunity. Preliminary examination of long term trends of parasites of rabbits and grouse confirm these predictions. Parasite development rate increases with temperature and while laboratory studies indicate this is linear some recent studies indicate that this may be non-linear and would have an important impact on R-0. Warming would also reduce the selective pressure for the development of arrestment and this would increase R-0 so that in systems like the grouse and *Trichostrongylus tenuis* this would increase the instability and lead to larger disease outbreaks. Extreme climatic events that act across populations appear important in synchronizing transmission and disease outbreaks, so it is speculated that climate disruption will lead to increased frequency and intensity of disease outbreaks in parasite populations not regulated by acquired immunity.

Poulin, R. and Mouritsen, K.N. **Climate change, parasitism and the structure of intertidal ecosystems.** *Journal of Helminthology* 80(2): 183-191, 2006.

Notes: Evidence is accumulating rapidly showing that temperature and other climatic variables are driving many ecological processes. At the same time, recent research has highlighted the role of parasitism in the dynamics of animal populations and the structure of animal communities. Here, the likely interactions between climate change and parasitism are discussed in the context of intertidal ecosystems. Firstly, using the soft-sediment intertidal communities of Otago Harbour, New Zealand, as a case study, parasites are shown to be ubiquitous components of intertidal communities, found in practically all major animal species in the system. With the help of specific examples from Otago Harbour, it is demonstrated that parasites can regulate host population density, influence the diversity of the entire benthic community, and affect the structure of the intertidal food web. Secondly, we document the extreme sensitivity of cercarial production in parasitic trematodes to increases in temperature, and discuss how global warming could lead to enhanced trematode infections. Thirdly, the results of a simulation model are used to argue that parasite-mediated local extinctions of intertidal animals are a likely outcome of global warming. Specifically, the model predicts that following a temperature increase of less than 4°C, populations of the amphipod *Corophium volutator*, a hugely abundant tube-building amphipod on the mudflats of the Danish Wadden Sea, are likely to crash repeatedly due to mortality induced by microphallid trematodes. The available evidence indicates that climate-mediated changes in local parasite abundance will have significant repercussions for intertidal ecosystems. On the bright side, the marked effects of even slight increases in temperature on cercarial production in trematodes could form the basis for monitoring programmes, with these sensitive parasites providing early warning signals of the environmental impacts of global warming.

Khan, R.A. and Chandra, C.V. **Influence of climatic changes on the parasites of Atlantic cod *Gadus morhua* off coastal Labrador, Canada.** *Journal of Helminthology* 80(2): 193-197, 2006.

Notes: A study was conducted in 2000 and 2003, following the collapse of the commercial fishery in 1990, to compare metazoan parasites of Atlantic cod *Gadus morhua*, captured off coastal Labrador, with samples taken in 1980 and 1986. Fish were captured by otter trawl offshore in the North Atlantic Fish Organisation subarea 2J. Parasites were removed from the digestive tract, stained, identified and compared between the different groups. Both the prevalence and mean abundance of trematodes, larval nematodes and *E. gadi* were significantly lower in fish taken in 2000 and 2003 than in 1980. While mean values of trematodes and nematodes declined in 1986, those of *Echinorhynchus gadi* remained unchanged in 1986 and 1990. Four-year-old cod sampled in 1990 harboured significantly fewer *E. gadi* than older age groups. The most commonly occurring trematodes included *Podocotyle reflexa*, *Lepidapedon elongatum*, *Derogenes varicus* and *Hemiurus levinseni* while the larval nematode, *Anisakis* sp. was predominant. Comparison of offshore samples taken in 2000 and 2003 with others taken in previous years suggests an overall decline of parasites coincident with a change in climatic conditions, the absence of a major food source, namely capelin *Mallotus villosus*, of cod and ultimately the decline of the Labrador population.

Morley, N.J., Lewis, J.W., and Hoole, D. **Pollutant-induced effects on immunological and physiological interactions in aquatic host-trematode systems: implications for parasite transmission.** *Journal of Helminthology* 80(2): 137-149, 2006.

Notes: Under conditions of pollution both host and parasite are susceptible to the pathogenic effects of toxicants, which in turn may result in detrimental changes to their immunological and physiological processes. Digenetic trematodes, which encompass species of both medical and economic importance, possess complex life cycles and are common parasites of both vertebrates and molluscs. The combined stress induced by pollution and parasitism influences the physiology of the host which can have implications not only on host survival but also on the functional biology of resident parasite populations. The present paper reviews the effects of pollutants on the immunology and physiology in both vertebrate and molluscan host-trematode systems and the implications for parasite transmission.

Sures, B. **How parasitism and pollution affect the physiological homeostasis of aquatic hosts.** *Journal of Helminthology* 80(2): 151-157, 2006.

Notes: Parasitism poses a serious threat to hosts under certain circumstances, while the well-being of organisms is also negatively affected by environmental pollution. Little information is available on the simultaneous effects of parasites and pollutants on the physiological homeostasis of organisms. The present paper demonstrates that parasites: (i) may influence the metabolism of pollutants in infected hosts, (ii) interact with pollution in synergistic or antagonistic ways, and (iii) may induce physiological reactions in hosts which were thought to be pollutant-induced. Experimental studies on the uptake and accumulation of metals by fish reveal that fish infected with acanthocephalans have lower metal levels than uninfected hosts; e.g. *Pomphorhynchus laevis* reduces lead levels in fish bile, thereby diminishing or impeding the hepatic intestinal cycling of lead, which may reduce the quantity of metals available for fish. Alterations in pollutant uptake and accumulation in different intermediate and final hosts due to parasites are thus very important in the field of ecotoxicology. In addition to such alterations, there is a close interaction between the effects of pollutants and parasites which seems to be mediated at least partly by the endocrine system, which itself is closely related to the immune system in fish. Laboratory studies on eels experimentally infected with the swimbladder nematode *Anguillicola crassus* reveal that toxic chemicals such as polychlorinated biphenyls produce immunosuppressive effects which facilitate parasite infection. Similarly, an increase in serum cortisol concentration in eels due to chemical exposure and infection is correlated with decreasing levels of anti-*A. Crassus* antibodies. Furthermore, parasites are able to elicit physiological changes which are attributed to chemicals with endocrine disrupting activity, e.g. the cestode *Ligula intestinalis* is known to suppress gonad development in roach. The most thoroughly documented examples of endocrine disruption in wild fish are in roach, and it is conceivable that this disruption is not only due to chemical activity but also to parasites such as *L. intestinalis* or species of the phylum Microspora.

Weil, E., Smith, G., and Gil-Agudelo, D.L. **Status and progress in coral reef disease research.** *Diseases of Aquatic Organisms* 69(1): 1-7, 2006.

Notes: Recent findings on the ecology, etiology and pathology of coral pathogens, host resistance mechanisms, previously unknown disease/syndromes and the global nature of coral reef diseases have increased our concern about the health and future of coral reef communities. Much of what has been discovered in the past 4 years is presented in this special issue. Among the significant findings, the role that various *Vibrio* species play in coral disease and health, the composition of the 'normal microbiota' of corals, and the possible role of viruses in the disease process are important additions to our knowledge. New information concerning disease resistance and vectors, variation in pathogen composition for both fungal diseases of gorgonians and black band disease across oceans, environmental effects on disease susceptibility and resistance, and temporal and spatial disease variations among different coral species is presented in a number of papers. While the Caribbean may still be the 'disease hot spot' for coral reefs, it is now clear that diseases of coral reef organisms have become a global threat to coral reefs and a major cause of reef deterioration.

Kaczmarzsky, L.T. **Coral disease dynamics in the central Philippines.** *Diseases of Aquatic Organisms* 69(1): 9-21, 2006.

Notes: Limited quantitative research has been conducted on coral disease in the Philippines and baseline data are much needed. Field surveys for prevalence and distribution patterns were conducted from November 2002 to August 2003. Sites

included the islands of Negros, Cebu, Siquijor, Panglao, Olango, Sumilon, Bantayan, Pescador, Balicassag and Palawan. In 154 belt transects, 10 026 *Porites* colonies were examined at 28 sites covering 3080 m². Two syndromes, *Porites* ulcerative white spot (PUWS) and coral tumors, occurred at high prevalence. Tumors as high as 39.1% occurred among massive *Porites*, and PUWS was as high as 53.7% among massive and branching *Porites*. In 8 mo, 116 tagged colonies showed slow progression and low mortality. Along a 41 km human impact gradient centered on Dumaguete City (Negros), 15 sites were examined. Correlation analyses linked higher disease prevalence to anthropogenic influence (Spearman's rank correlation coefficient [$r(s)$] = -0.54, $p = 0.04$ for tumors and $r(s) = -0.69$, $p = 0.005$ for PUWS). In most sites disease prevalence was lower than in the sites near Dumaguete. High PUWS prevalence near uninhabited Sumilon Island appeared to be linked to the highly diseased reefs near Dumaguete City due to transmission of disease along a cross-shelf front formed between the Tahon Strait and Bohol Sea. Other observations included 12 potential new host species for PUWS (4 new genera and 1 octocorallia) and 5 likely new hosts for black band disease (BBD) in the Philippines, and a relatively high prevalence (7.8%) of BBD in 1 site in western Palawan.

Ward, J.R., Rypien, K.L., Bruno, J.F., Harvell, C.D., Jordan-Dahlgren, E., Mullen, K.M., Rodriguez-Martinez, R.E., Sanchez, J., and Smith, G. **Coral diversity and disease in Mexico.** *Diseases of Aquatic Organisms* 69(1): 23-31, 2006.

Notes: Field studies and empirical tests of the 'diversity-disease hypothesis' demonstrate the effects of species richness on disease transmission and severity in plant systems. Yet the converse, i.e. effects of disease on diversity, is rarely considered in either relatively well-studied plant systems or marine ecosystems. We investigated these effects along the Mexican Yucatan Peninsula to (1) quantify the relationship between disease prevalence and coral diversity, (2) test the hypothesis that octocoral and scleractinian disease prevalence are associated with one another, and (3) establish a long-term dataset. Aspergillosis of sea fans and 6 scleractinian diseases were documented. Prevalence of aspergillosis declined from 12.85% in 2002 to 5.26% in 2004, while prevalence of scleractinian diseases remained relatively constant at 5.7 +/- 0.8% in 2002 and 7.96 +/- 0.7% in 2004. Sites were relatively rich (71 species of octocoral and scleractinian corals) and even ($E5 > 0.5$). Sea fan disease prevalence was not associated with scleractinian disease prevalence, nor were there consistent associations between disease and measures of diversity. However, the most abundant octocoral and scleractinian species are susceptible to infection with several diseases, and disease may alter coral diversity in complex ways. These data represent the first in what will become a long-term dataset monitoring disease prevalence and associated changes in coral diversity.

Voss, J.D. and Richardson, L.L. **Coral diseases near Lee Stocking Island, Bahamas: Patterns and potential drivers.** *Diseases of Aquatic Organisms* 69(1): 33-40, 2006.

Notes: The number of coral diseases, coral species they infect, number of reported cases, and range over which these diseases are distributed have all increased dramatically in the past 3 decades, posing a serious threat to coral reef ecosystems worldwide. While some published studies provide data on the distribution of coral diseases at local and regional levels, few studies have addressed the factors that may drive these distributions. We recorded coral disease occurrence, prevalence, and severity along with temperature, sedimentation, and coral population data (species abundance and colony size) over 2 consecutive summers on reefs near Lee Stocking Island (LSI) in the Bahamas' Exuma Chain. In 2002 a total of 11 092 coral colonies (all species present) were examined within a survey area of 9420 m², and 13 973 colonies within 10 362 m² in 2003. Similar to other reports, relatively large, framework species including *Siderastrea siderea*, *Colpophyllia natans*, and *Montastraea annularis*, along with the smaller *Dichocoenia stokesi*, were the species most susceptible to coral disease. Recurring infections were observed on individual colonies from 2002 to 2003, and were more likely for black band disease (BBD) than for either white plague (WP) or dark spots syndrome (DS). In 2002, WP and DS demonstrated clumped distributions, while BBD was randomly distributed. However, in 2003 BBD and WP were clumped. This is the first study, to our knowledge, that quantitatively documents coral disease dynamics on reefs surrounding LSI.

Page, C. and Willis, B. **Distribution, host range and large-scale spatial variability in black band disease prevalence on the Great Barrier Reef, Australia.** *Diseases of Aquatic Organisms* 69(1): 41-51, 2006.

Notes: The prevalence and host range of black band disease (BBD) was determined from surveys of 19 reefs within the Great Barrier Reef Marine Park, Australia. Prevalence of BBD was compared among reefs distributed across large-scale cross-shelf

and long-shelf gradients of terrestrial or anthropogenic influence. We found that BBD was widespread throughout the Great Barrier Reef (GBR) and was present on 73.7% of the 19 reefs surveyed in 3 latitudinal sectors and 3 cross-shelf positions in the summer of 2004. Although BBD occurred on all mid-shelf reefs and all but one outer-shelf reefs, overall prevalence was low, infecting on average 0.09% of sessile cnidarians and 0.1% of scleractinian corals surveyed. BBD affected similar to 7% of scleractinian taxa (25 of approximately 350 GBR hard coral species) and 1 soft coral family, although most cases of BBD were recorded on branching *Acropora* species. Prevalence of BBD did not correlate with distance from terrestrial influences, being highest on mid-shelf reefs and lowest on inshore reefs (absent from 66%, n = 6, of these reefs). BBD prevalence was consistently higher in all shelf positions in the northern (Cooktown/Lizard Island) sector, which is adjacent to relatively pristine catchments compared to the central (Townsville) sector, which is adjacent to a more developed catchment. BBD cases were clustered within reefs and transects, which was consistent with local dispersal of pathogens via currents, although the spread of BBD was not dependent on the density or cover of any of the coral taxa examined. In combination, these results suggest that BBD is part of the natural ecology of coral assemblages of the GBR, and its prevalence is relatively unaffected by terrestrial influences on the scales characteristic of cross-shelf gradients.

Bruckner, A.W. and Bruckner, R.J. **Consequences of yellow band disease (YBD) on *Montastraea annularis* (species complex) populations on remote reefs off Mona Island, Puerto Rico.** *Diseases of Aquatic Organisms* 69(1): 67-73, 2006.

Notes: The rate and extent of mortality from yellow band disease (YBD) to *Montastraea annularis* (species complex) on reefs off Mona Island, Puerto Rico, was evaluated over 8 yr. Isolated YBD infections were first observed in 1996. Prevalence of YBD increased dramatically in 1999, with a maximum of 52% of all *M. annularis* colonies infected in 1 shallow site. YBD continued to spread among adjacent, previously uninfected corals over the next 4 yr, and disease prevalence progressively increased in deeper sites. Linear rates of disease advance and tissue mortality have been slow (5 to 15 cm yr⁻¹), although colonies with single YBD lesions have become infected in multiple locations. Most (85%) colonies identified with YBD in 1999 and 2000 were still affected in 2003, and these corals have lost a mean of 60% of their living tissue. Mortality from YBD is being compounded by black band disease, white plague and other syndromes; bioeroding sponges, macroalgae, cyanobacteria and other competitors have colonized tissue-denuded skeleton, minimizing the likelihood of resheeting. The deteriorating health of *M. annularis* is of particular concern, as these are the dominant corals on these reefs, the largest (2 to 3 m diameter and height) and presumably oldest colonies were infected with YBD more frequently than small colonies, and no recruitment has been observed. YBD is causing extensive mortality to key reef-building taxa in a remote location where anthropogenic stressors are minimal. Additional research on causes of YBD, mechanisms of infection, and strategies to mitigate YBD is needed; otherwise, *M. annularis* may suffer a fate similar to that of the Atlantic acroporids.

Croquer, A., Bastidas, C., and Lipscomb, D. **Folliculinid ciliates: a new threat to Caribbean corals?** *Diseases of Aquatic Organisms* 69(1): 75-78, 2006.

Notes: This is the first report of a putative pathogenic ciliate protozoan that has been associated with Caribbean corals. Previously, only 2 species of the phylum Ciliophora had been linked to coral diseases, and they were exclusive to the Indo-Pacific region. In this study, a ciliate of the genus *Halofolliculina* was found on 10 hard coral species at the National Parks of Los Roques and Morrocoy, Venezuela. The general morphology of this ciliate is very similar to that of *Halofolliculina corallasia* from the Indo-Pacific, which is known to cause skeletal eroding band. None of the other 31 genera in the family Folliculinidae are known to cause diseases in corals or in any other animal species. The presence of this ciliate, which shows a prevalence comparable to that of other epizootics in the Caribbean, suggests it could be a new threat to the coral reefs of this region.

Pantos, O. and Bythell, J.C. **Bacterial community structure associated with white band disease in the elkhorn coral *Acropora palmata* determined using culture-independent 16S rRNA techniques.** *Diseases of Aquatic Organisms* 69(1): 79-88, 2006.

Notes: Culture-independent molecular (16S ribosomal RNA) techniques showed distinct differences in bacterial communities associated with white band disease (WBD) Type I and healthy elkhorn coral *Acropora palmata*. Differences were apparent at all levels, with a greater diversity present in tissues of diseased colonies. The bacterial community associated with remote, non-diseased coral was distinct from the apparently healthy tissues of infected corals several cm from the disease lesion. This

demonstrates a whole-organism effect from what appears to be a localised disease lesion, an effect that has also been recently demonstrated in white plague-like disease in star coral *Montastraea annularis*. The pattern of bacterial community structure changes was similar to that recently demonstrated for white plague-like disease and black band disease. Some of the changes are likely to be explained by the colonisation of dead and degrading tissues by a micro-heterotroph community adapted to the decomposition of coral tissues. However, specific ribosomal types that are absent from healthy tissues appear consistently in all samples of each of the diseases. These ribotypes are closely related members of a group of alpha-proteobacteria that cause disease, notably juvenile oyster disease, in other marine organisms. It is clearly important that members of this group are isolated for challenge experiments to determine their role in the diseases.

Gil-Agudelo, D.L., Myers, C., Smith, G.W., and Kim, K. **Changes in the microbial communities associated with *Gorgonia ventalina* during aspergillosis infection.** *Diseases of Aquatic Organisms* 69(1): 89-94, 2006.

Notes: The surface mucopolysaccharide layer (SML) secreted by corals is a rich environment where bacteria live and proliferate, with population levels often being several orders of magnitude higher than in the surrounding waters (at least for culturable microbes). Some studies have suggested that these communities play an important role in energy and nutrient flux in marine environments. We hypothesize that the microbial community structure of the SML also plays a role in protection against disease. This hypothesis is based on studies that have shown differences in the bacterial composition of the mucus of healthy and diseased corals. In this study we tested the differences in the microbial communities living in association with the SML of healthy and diseased *Gorgonia ventalina* by comparing their metabolic profiles using Biolog EcoPlates. Overall, metabolic profiles of the coral surface microbiota were significantly different to those in the water column based on stepwise canonical discriminant analyses (CDAs). Furthermore, differences between communities living in healthy and diseased corals were also found. Changes were observed between affected and unaffected areas of the same colony, although these changes were not as obvious as between individual healthy and diseased colonies. Results suggest that the microbial communities living in the SML of *G. ventalina* are affected by the presence of aspergillosis, even if the area is not in direct contact with the infection. This suggests the possibility of changes in the composition of the SML throughout the colony as a response to aspergillosis infection.

Kim, K., Alker, A.P., Shuster, K., Quirolo, C., and Harvell, C.D. **Longitudinal study of aspergillosis in sea fan corals.** *Diseases of Aquatic Organisms* 69(1): 95-99, 2006.

Notes: Aspergillosis (a fungal disease) is affecting sea fan corals *Gorgonia* spp. throughout the Caribbean. To measure the impact of this disease, we established longitudinal, or in other words individual-based, monitoring studies on 3 reefs in the Florida Keys, USA, to obtain estimates of incidence, rates of disease progress, recovery, and mortality. At Western Dry Rocks (near Key West), 40 *Gorgonia ventalina* colonies (20 initially healthy and 20 initially diseased) were photo-monitored between June 1996 and May 1998. Additional sea fans were visually monitored during 2 localized outbreaks at Conch (May 1998 to September 1999) and Carysfort (July 2000 to May 2001) reefs located in the Upper Keys. Data from Western Dry Rocks showed that over a 2 yr period, the incidence rate was 0.58 sea fans yr⁻¹ and that tissue purpling can lead to tissue loss and subsequently to mortality, albeit at low frequencies. Most sea fans, once infected, maintained a low level of damage over time. Only 3 fans recovered from the disease; however 2 were subsequently re-infected. Case fatality rate was 10% (2 of 20 initially infected died), which is equivalent to 5% yr⁻¹. However, mortality can increase during localized outbreaks. At Conch, mortality was 46% yr⁻¹ among infected sea fans (compared to 8% yr⁻¹ at Carysfort, a less impacted site, during the same period). During an outbreak at Carysfort, mortality was 95% yr⁻¹ among diseased sea fans. These data clearly demonstrate the significant role aspergillosis plays in the population ecology of sea fan corals.

Davy, S.K., Burchett, S.G., Dale, A.L., Davies, P., Davy, J.E., Muncke, C., Hoegh-Guldberg, O., and Wilson, W.H. **Viruses: agents of coral disease?** *Diseases of Aquatic Organisms* 69(1): 101-110, 2006.

Notes: The potential role of viruses in coral disease has only recently begun to receive attention. Here we describe our attempts to determine whether viruses are present in thermally stressed corals *Pavona danai*, *Acropora formosa* and *Stylophora pistillata* and zoanths *Zoanthus* sp., and their zooxanthellae. Heat-shocked *P. danai*, *A. formosa* and *Zoanthus* sp. all produced numerous virus-like particles (VLPs) that were evident in the animal tissue, zooxanthellae and the surrounding seawater; VLPs

were also seen around heat-shocked freshly isolated zooxanthellae (FIZ) from *P. danai* and *S. pistillata*. The most commonly seen VLPs were tail-less, hexagonal and about 40 to 50 nm in diameter, though a diverse range of other VLP morphotypes (e.g. rounded, rod-shaped, droplet-shaped, filamentous) were also present around corals. When VLPs around heat-shocked FIZ from *S. pistillata* were added to non-stressed FIZ from this coral, they resulted in cell lysis, suggesting that an infectious agent was present; however, analysis with transmission electron microscopy provided no clear evidence of viral infection. The release of diverse VLPs was again apparent when flow cytometry was used to enumerate release by heat-stressed *A. formosa* nubbins. Our data support the infection of reef corals by viruses, though we cannot yet determine the precise origin (i.e. coral, zooxanthellae and/or surface microbes) of the VLPs seen. Furthermore, genome sequence data are required to establish the presence of viruses unequivocally.

Sussman, M., Bourne, D.G., and Willis, B.L. **A single cyanobacterial ribotype is associated with both red and black bands on diseased corals from Palau.** *Diseases of Aquatic Organisms* 69(1): 111-118, 2006.

Notes: Filamentous cyanobacteria forming red and black bands (black band disease, BBD) on 3 scleractinian corals from Palau were molecularly identified as belonging to a single ribotype. Red cyanobacterial mats sampled from infections on *Pachyseris speciosa* and a massive *Porites* sp. yielded red strains RMS1 and RMS2 respectively; the black cyanobacterial mat sampled from an infection on *Montipora* sp. yielded black strain BMS1. Following trials of a range of specialized media and culture conditions, 2 media, Grund and ASN-III, were identified as the best for successful isolation and culturing. Cultured cyanobacteria were examined under a light microscope to establish purity, color and morphological appearance. DNA extraction and partial sequencing of the 16S rDNA gene of both red and black cyanobacterial isolates demonstrated 100% sequence identity. These isolated strains were also found to have 99% sequence identity with an uncultured cyanobacterial strain previously identified by molecular techniques as belonging to a cyanobacterial ribotype associated with BBD-infected corals in the Caribbean. This is the first report of the successful isolation and culture of cyanobacterial strains derived from both red bands and BBD. Based on these findings, it is suggested that the classification of these 2 syndromes as separate coral diseases be postponed until further evidence is collected.

Viehman, S., Mills, D.K., Meichel, G.W., and Richardson, L.L. **Culture and identification of *Desulfovibrio* spp. from corals infected by black band disease on Dominican and Florida Keys reefs.** *Diseases of Aquatic Organisms* 69(1): 119-127, 2006.

Notes: Black band disease (BBD) of corals is characterized as a pathogenic microbial consortium composed of a wide variety of microorganisms. Together, many of these microorganisms contribute to an active sulfur cycle that produces anoxia and high levels of sulfide adjacent to the coral surface, conditions that are lethal to coral tissue. Sulfate-reducing bacteria, as sulfide producers, are an important component of the sulfur cycle and the black band community. Previous molecular survey studies have shown multiple *Desulfovibrio* species present in BBD but with limited consistency between bacterial species and infections. In this study we compared 16S rRNA gene sequences of sulfate-reducing bacteria selectively cultured from 6 BBD bands on 4 coral species, *Diploria clivosa*, *D. strigosa*, *D. labyrinthiformes*, and *Siderastrea siderea*, in the Florida Keys and Dominica. The 16S rRNA gene sequences were obtained through direct sequencing of PCR products or by cloning. A BLAST search revealed that 8 out of 10 cultures sequenced were highly homologous to *Desulfovibrio* sp. strain TBP-1, a strain originally isolated from marine sediment. Although the remaining 2 sequences were less homologous to *Desulfovibrio* sp. strain TBP-1, they did not match any other sulfate-reducing (or other) species in GenBank.
