# An introduction to Ecology of Infectious Diseases – Oysters and Estuaries

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Infectious diseases are recognized as an important factor regulating marine ecosystems (Harvell *et al.*, 1999, 2002, 2004; Porter *et al.*, 2001; McCallum *et al.*, 2004; Ward and Lafferty, 2004; Stewart *et al.*, 2008; Bienfang *et al.*, 2011). Many of the organisms affected by marine diseases have important ecological roles in estuarine and coastal environments and some are also commercially important. Outbreaks of infectious diseases in these environments, referred to as epizootics, can produce significant population declines and extinctions, both of which threaten biodiversity, food web interactions, and ecosystem productivity (Harvell *et al.*, 2002, 2004).

The incidence of marine infectious diseases has been increasing over the past three decades and climate change, especially warming temperatures, has been suggested as a contributing cause (Harvell *et al.*, 2004). Warmer temperatures can increase pathogen proliferation rates and modify host physiology, as well as support disease range expansion by altering the suitability of the environment (Harvell *et al.*, 2004; Pascual and Bouma, 2009). Salinity also provides an important control on the prevalence, intensity and distribution of marine infectious diseases, especially in estuarine environments, which provide a transitional region between freshwater and ocean environments. Salinity is projected to change in response to sea level rise and to alterations in the timing and amount of freshwater delivery (e.g., Scavia *et al.*, 2002). The consequences of modified salinity environments in estuarine and coastal systems for disease epizootics and pathogen transmission (via altered circulation) are unknown.

The implication of climate change as a factor for increasing marine infectious diseases is mostly based on short-term data sets or inferred from experimental efforts (e.g., Harvell *et al.*, 2002, 2004). Long-term baseline data supplemented by controlled experiments that allow definitive cause and effect to be determined are lacking for most marine infectious diseases. Also the infectious agent and mode of transmission for many marine infectious

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diseases are unknown, which makes it difficult to identify trends in prevalence and intensity, and to relate cause and effect.

Climate cycles, such as the El Niño-Southern Oscillation (ENSO) and the North Atlantic Oscillation (NAO), influence marine infectious diseases by modifying local and regional temperature and salinity conditions (Harvell *et al.*, 2002, 2004; Cook *et al.*, 1998; Soniat *et al.*, 2009). For example, dermo disease prevalence and intensity in eastern oyster (*Crassostrea virginica*) populations along the Gulf of Mexico increases during La Niña events, which produce warm and dry conditions (Powell *et al.*, 1992). Outbreaks of coral diseases in the Caribbean have been associated with ENSO and NAO cycles (Harvell *et al.*, 2002, 2004). Understanding the linkages between large-scale climate cycles and marine infectious diseases and possible consequences of climate change requires long-term studies of the host, pathogen, host-pathogen interactions and the environment.

Oysters are a particularly good model organism for understanding marine diseases, the environmental drivers that influence them and their impact on host populations – and consequently for predicting the likely impact of climate change on the diseases and the populations affected. Oysters are commercially important and are considered a "keystone" species because oyster reefs provide habitat, refuge and food for a myriad of other organisms. Consequently, basic biological, physiological and ecological aspects of oysters and oyster communities are well known. In addition, over the last half century, a number of catastrophic diseases have affected oysters in many areas, and they, too, have been well studied. As a result, long-term data sets exist that describe oyster-parasite interactions under different environmental conditions. These data have supported analyses that provide insights into the controls on oyster disease and have also supported the development of models of the host-pathogen interactions.

Delaware Bay, on the mid-Atlantic coast of the United States (see Fig. 1 in Ford and Bushek, this issue), is a good model system. It is a relatively simple estuary dominated by a single freshwater input that creates a strong salinity gradient along which oysters grow. Oyster reefs along this gradient have been monitored annually since 1953. Two diseases, both caused by introduced protozoan pathogens, have been the principal factors influencing oyster populations in Delaware Bay for most of this time. MSX disease, caused by *Haplosporidium nelsoni* (Haskin *et al.*, 1966), was first recognized as the cause of epizootic mortalities in 1957 and dermo disease, caused by *Perkinsus marinus* (Mackin *et al.*, 1950), began causing important mortalities in 1990. These diseases have been monitored since the epizootics began and the oyster population responses have been documented.

An important outcome of these long-term surveillance programs has been the ability to document whether or not resistance to the diseases has developed in the oyster population. In 1985–86 a particularly severe and widespread MSX disease epizootic, associated with drought, caused extensive oyster mortalities throughout Delaware Bay. This widespread natural selection event built upon the moderate resistance that had developed after the initial epizootic and has resulted in a population of oysters over much of the bay that is highly resistant to MSX disease. This natural disease selection experiment provided the

basis for a National Science Foundation-supported Ecology of Infectious Diseases (EID) program that is focused on host-parasite relationships in eastern oyster populations affected by MSX and dermo diseases and how these might be altered by climate change. The science goals of the EID project are to determine the:

- time scales of selection pressure toward alleles conferring disease resistance,
- role of disease refugia in modulating population genetic structure,
- interplay between range contraction (resulting from epizootics) and disease resistance in preventing local extinction of host populations, and
- effects of a warming climate on oyster generation time, parasite transmission and proliferation, fecundity, and consequences for shifts in the genetic structure of the host population.

The Delaware Bay EID project uses the extensive long-term data sets on Delaware Bay oyster populations and their diseases, and the system-wide oyster-disease experiment that resulted in disease resistance, to investigate the science questions related to these goals. The results presented in the papers in this issue address aspects of each of the project science goals.

The first two papers in this collection use long-term data sets to provide a historical perspective on MSX and dermo diseases, which have affected oysters in Delaware Bay over nearly all of the past 6 decades. They show how climate cycles drive disease and how climate extremes can lead to the development of resistance to disease by altering the genetic structure of the affected population. Ford and Bushek (this issue) document the role of selective forces that led to development of resistance to MSX disease, a natural selection process that occurred in two steps separated by nearly 30 years. The first resulted from the initial epizootic in 1957–59, which conferred a moderate level of resistance. The second was associated with a severe drought that allowed high salinity conditions, and hence the pathogen, to spread farther up-estuary where it produced extreme mortality of oysters in 1985–86 in regions that had been largely free of the disease. The surviving oysters were resistant to MSX disease and their offspring repopulated the bay. Bushek *et al.* (this issue) provide the historical perspective for dermo disease, which became epizootic in Delaware Bay in 1990. Their study shows that both local environmental factors (temperature and river flow) and larger scale (NAO) climatic signals influenced spatial and temporal disease patterns over a multiyear period. An important outcome of this analysis is that, in contrast to MSX disease, oysters have not developed resistance to dermo disease despite continuing disease pressure and mortality. Both papers highlight how critical long-term data sets are to understanding the impact of normal and extreme environmental fluctuations, and large-scale climate cycles, on marine diseases and their host populations. Such studies provide the data needed to forecast the likely impact of climate change on the interaction between host and parasite in an estuarine system.

The next two papers deal specifically with the role of local water properties and circulation patterns in establishing and maintaining zones of refuge from disease in an estuary. Both

MSX and dermo parasites are sensitive to low salinity. Ford *et al.* (this issue) use traditional and molecular detection assays to follow both the MSX and dermo parasites in known disease-affected regions and putative refuge areas of the estuary, as determined by salinity regimes. The results show that refuges do occur in the upper low-salinity reaches of the estuary and its tributaries, but that they are transient and not always linked to short-term salinity variation. Further, the parasites may be present in the refuges, but not cause disease or mortality. The authors discuss the role of refuges from disease selection and point out that they are likely to retard the development of resistance in an estuarine population if the genetic contribution from the refuge populations is substantial. Wang *et al.* (this issue) describe a hydrodynamic model, based on the Regional Ocean Model System (ROMS) configured for Delaware Bay, which they used to examine water properties and their relationship to MSX disease. They simulate multiyear periods when the MSX disease was present or absent in upper bay areas and confirm, using rigorous statistical analyses, the influence of low river flow (and hence high salinity), and the co-occurrence of high salinity and high temperature in the appearance of MSX disease outbreaks in these regions. Their simulations also suggest that periods of enhanced upbay transport might be at least partially responsible for movement of the MSX parasite into refuge areas from lower bay regions where the disease is prevalent, thus providing a mechanism other than salinity itself for the appearance of disease agents in the upper estuary.

Major improvement in resistance to MSX disease followed an extreme selection event associated with drought, but other mechanisms may also influence the rate at which resistance develops. Powell *et al.* (this issue (b)) and He *et al.* (this issue) examine two potential means for accelerating or retarding the development of resistance in a marine population. Using a newly developed gene-based population dynamics model, Powell *et al.* (this issue (b)) investigate a possible explanation for the observed failure of oysters in Delaware Bay to develop resistance to dermo disease. Their simulations show that the cyclic nature of epizootics, such as those associated with the NAO, moderates the overall effect of the disease on selection. Although selective mortality is strong during disease peaks, which are associated with high salinity, survival of the more susceptible genotypes is enhanced when disease pressure is low, during periods of reduced salinity. Further, the alleles that confer disease resistance are likely to drift and become less frequent in the population when selective pressure relaxes. Simulations suggest that the destiny of oyster populations affected by dermo disease and also under the influence of large-scale climate cycles is likely to include a lengthy period of persistent mortality and low abundance while resistance develops only incrementally. He *et al.* (this issue) examine another potential mechanism for influencing the rate at which resistance might develop in an oyster population: a phenomenon known as sweepstake reproductive success (SRS). A SRS event would occur if a very small proportion of the overall population were successful in providing recruits for the subsequent generation. Such an occurrence might amplify resistance if the successful parents were highly selected, but it might also slow its development if those parents had experienced little or no selection. He *et al.* (this issue) use a variety of genetic assays to estimate the size of the population of

Delaware Bay oysters that produced newly set and adult oysters in different regions of the bay in different years. While estimates for each individual collection were extremely small relative to the estimated total oyster population size, values for adults pooled over all sites and years, and representing an accumulation of many years of recruitment, had values very similar to the total population size estimates. Thus, it is unlikely that SRS events, which might have followed major epizootics, contributed to the development of resistance to MSX disease in Delaware Bay.

The question of how oyster genotypes conferring disease resistance or susceptibility are moved around the estuary is explored in a series of three modeling papers. Narváez *et al.* (this issue (a)) examine larval transport in Delaware Bay using the ROMS-based hydrodynamic model combined with a model of oyster larvae growth and behavior. Their simulations indicate a general downbay drift of larvae, but that larvae produced by upper bay populations have much lower survival rates than those produced by mid and lower bay oysters, which themselves have high rates of self-recruitment. Success rates are further diminished during periods of high river flow that reduce salinity. This pattern would enhance the rate of development of resistance to both MSX and dermo diseases by limiting the genetic contribution of susceptible oysters in the upper bay refuge areas and enhancing that of the highly selected midbay populations. The tendency to self-recruit on the midbay reefs helps preserve these central locations when either disease or heavy freshwater flow kills oysters at the upper and lower extremes, respectively.

If larval survival from upper bay oysters is relatively low and if most of those that do survive are transported down bay, how do up-estuary reefs maintain themselves? Narváez *et al.* (this issue (b)) simulate larval release at different phases of the tide and show that those released at spring tides are transported mostly down-estuary; whereas, those released on neap tides are likely to be transported up-estuary, thus replenishing the upper bay populations. High river discharge, however, can overwhelm this upbay–downbay transport pattern, driving larvae farther downbay and potentially out of the estuary, again minimizing the genetic impact of upbay refuge populations.

To further investigate how different genotypes are exchanged within an estuarine metapopulation, Munroe *et al.* (this issue) use an individual-based model to simulate the genetic connectivity among oyster reefs in Delaware Bay. By varying factors such as mortality, oyster abundance and growth rates, they show that although larval dispersal is the mechanism for gene transfer among oyster reefs, the characteristics of adult populations, especially mortality rates, exert a controlling influence on dispersal of genotypes, with implications for the transfer of resistance alleles within the estuary depending on the abundance of adult oysters, as well as their genotypes, in the source population. This modeling study and the experimentally-based studies of disease refuges (Ford *et al.*, this issue) and oyster population genetics (He *et al.*, this issue) illustrate the complex interactions that occur among environmental conditions, the adult oyster population, disease mortality (i.e., range contraction from epizootics), and disease resistance that prevent local extinction of oyster populations in Delaware Bay.

Modeling of disease in oyster populations suggests that under suitable food conditions, oysters infected with the dermo parasite can survive by adding somatic tissue at a rate that is faster than the rate at which the mass of the parasites increases. Thus food supply is a critical element of these models, as well as of other models of larval and adult oyster growth. Using food values calculated from water samples collected over a 2-year period in Delaware Bay, Powell *et al.* (this issue (c)) evaluate the adequacy of using environmental parameters, including salinity, as a predictor of food supply. Food supply did not follow the upbay-downbay pattern anticipated by the salinity gradient. Rather values tended to be depressed on the eastern side of the bay where the majority of oysters reside, suggesting that oyster feeding itself might be influencing food supply and that food values cannot not be predicted using environmental variables or those generated by a hydrodynamic model.

The final paper in our series, by Powell *et al.* (this issue (a)), discusses the impact of disease on the sustainability of oyster reefs and the implication that this has for restoration and management. Simulations suggested that reef accretion in mid-Atlantic estuaries is not possible when dermo disease limits the addition of shell to the reef surface. Under these conditions, reef stasis, when it is neither accreting nor eroding, is the only realistically achievable restoration goal, and only when annual exploitation rates do not exceed about 5% of the fishable stock. In contrast, higher growth and recruitment rates of oysters in the Gulf of Mexico may allow for both reef accretion and an enhanced fishery.

The Delaware Bay EID project results described in this issue demonstrate that using long-term ecological, environmental, population and disease data as a starting point, followed by a combination of field experiments, genetic and disease analyses, and modeling has allowed us to quantify the effect of environmental variations on a model estuarine population and has provided a basis that can be used to project the likely impact of climate change on host-parasite interactions. The interrelated approaches used in the Delaware Bay EID project allowed identification of independent and interactive factors that control marine diseases and as such may provide a model for future studies designed to understand direct and indirect effects of climate change on marine infectious diseases.

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