



Understanding the ecology of disease in Great Lakes fish populations

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Disease may be an important factor affecting wild fish population dynamics in the Great Lakes, but a lack of information on the ecology of fish disease currently precludes the prediction of risks to fish populations. Here we propose a conceptual framework for conducting ecologically-oriented fish health research that addresses the inter-relationships among fish health, fish populations, and ecosystem dysfunction in the Great Lakes. The conceptual framework describes potential ways in which disease processes and the population-level impacts of disease may relate to ecosystem function, and suggests that functional ecosystems are more likely to be resilient with respect to disease events than dysfunctional ecosystems. We suggest that ecosystem- or population-level research on the ecology of fish disease is necessary to understand the relationships between ecosystem function and fish health, and to improve prediction of population-level effects of diseases on wild fish populations in the Great Lakes. Examples of how the framework can be used to generate research questions are provided using three disease models of current interest in the Great Lakes: thiamine deficiency complex, botulism, and bacterial kidney disease.

Keywords: disease ecology, population dynamics, fish health

Introduction

A great deal of research has been conducted in the U. S. on fish disease over the past century (Mitchell, 2001), but a limited understanding still exists about the risks of disease to natural fish populations (Moffitt et al., 1998). Although disease outbreaks have apparently resulted in significant mortality of wild fish in the Great Lakes (Van Oosten, 1944; Nepszy et al., 1978; Holey et al., 1998; Elsayed et al., 2006; Getchell et al., 2006), the effects on Great Lakes fish populations are difficult to measure and predict. We suggest that this is a result of a lack of research directed at the ecology

of fish disease. Understanding the ecology of disease is crucial to long-term sustainability of wildlife populations (Friend et al., 2001), including diverse natural fish populations in the Great Lakes.

The purpose of this paper is to describe a conceptual framework that proposes relationships between ecosystem function and fish health in the Great Lakes. This description is intended to challenge investigators to disprove the framework and its assumptions, and thereby stimulate research on the topic and ultimately improve the understanding and prediction of the effects of diseases on wild fish populations in the Great Lakes. Examples of how this framework can be used to generate research

questions are provided using three diseases of recent interest in the Great Lakes: thiamine deficiency complex, botulism, and bacterial kidney disease. We adopt a broad definition of fish health as a state characterized by anatomical integrity; the ability to perform individual-, population- and community-level roles; the ability to be resistant and resilient to physical, biological and social stresses; and the freedom from risk of disease and untimely death (Stephen and Thorburn, 2002). We define diseases as threats to fish health which may include communicable diseases, parasites, nutrient deficiencies, and trophically accumulated toxins (e.g., botulism), but not contaminants.

Conceptual framework

The conceptual framework presented here was developed using several assumptions about the nature of Great Lakes ecosystems and disease processes. First, the biosphere is always changing, and these changes have affected and will continue to affect Great Lakes aquatic ecosystems. Second, pathogens are natural components of ecosystems; therefore, pathogens and hosts evolve in response to each other and to ecosystem conditions. As a result, pathogens may occur in the absence of disease. Third, the prevalence and severity of disease vary temporally and spatially, within which normative conditions can be defined, and are influenced by interactions among hosts, pathogens, and the environment, all of which are controlled by a combination of forcing by natural and anthropogenic variables. Fourth, we suggest that although diseases may have population-level impacts and can exert a regulating force under some conditions, most pathogens do not exert long-term population-level effects, although some individuals may be severely affected. It is our contention that fish health and disease in wild fish populations can be better understood if evaluated in an ecosystem framework than in pathogen-centric or host-centric frameworks, which by their nature focus on individual fish.

A central premise of this framework is that functioning healthy ecosystems are more likely to be resilient to disease events than dysfunctional ecosystems (e.g. Folke et al., 2004). The importance of ecosystem stability and function is consistent with epidemiological principles that suggest that the frequency and severity of disease events are governed in part by the state of the ecosystem (Hedrick, 1998). For example, variables influencing disease

transmission include temperature, host-immune response, pathogen density, and host-population density. These variables in turn are influenced by many ecosystem elements such as climate change, chemical contaminants (which influence host susceptibility and infectivity of pathogens), fishery management actions (harvest and stocking alter host population density), predators (which may selectively cull infected individuals from the population), and exotic species (which have the potential to alter host population density and transmission pathways, and may carry new pathogens that are frequently more pathogenic in naïve hosts).

Definitions of ecosystem health and ecosystem dysfunction are currently under debate by ecologists (Rapport et al., 1998) and a complete discussion of these topics is beyond the scope of this paper. We offer a broad definition of ecosystem dysfunction as a state in which ecosystems have been sufficiently disrupted to reduce vigor, organization, or resilience (cf. Rapport et al., 1998). For example, dysfunctional ecosystems may be characterized by major changes in community structure or in pathways of energy flow which may result in diminished ecosystem services (e.g. Holmlund and Hammer, 1999). We hypothesize that functional ecosystems with high resilience (e.g. McCann, 2000) and few disruptions will experience relatively few or small changes to variables that influence the expression of disease. A functional ecosystem should have a narrower natural range of temporal and spatial variability for the variables which influence disease transmission than a dysfunctional ecosystem. Likewise, variables that influence disease transmission may show a wider range of variability in dysfunctional ecosystems, thereby increasing the likelihood that the threshold required for epizootics will be exceeded.

The prevalence and severity of disease in wild populations are functions of interactions among pathogens, hosts, and the environment, and the latter is the least understood (Hedrick, 1998). Most pathogens and other disease agents are natural components of ecosystems and may cause disease events only under certain environmental conditions. We present a conceptual framework (Fig. 1) derived from a more simplified version by Hedrick (1998) that represents potential linkages among environmental factors and fish disease. This model outlines specific hypothesized ways in which physical and biological factors may interact with pathogens to cause individual-level effects on fish, which may ultimately lead to population-level effects.

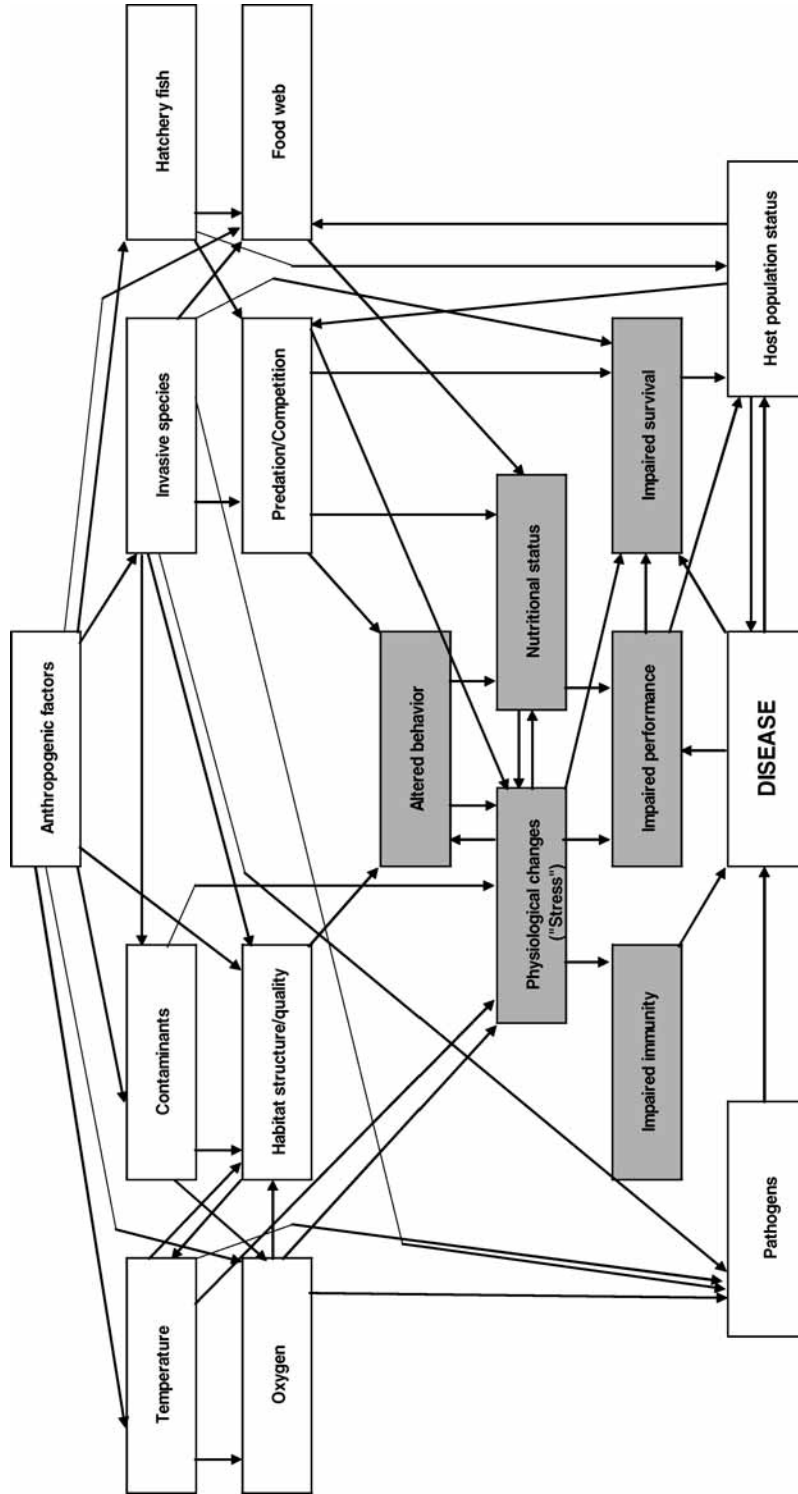


Figure 1. Conceptual framework representing a hypothetical web of causation for the manifestation of disease in a population of fish. Physical (top left) and biological (top right) factors interact with pathogens to cause individual-level effects (shaded) that may cause population-level effects. Diagram after Hedrick (1998).

The conceptual framework suggests that disease processes must be considered in an ecosystem context to predict the impact of disease on wild fish populations, and that the maintenance of ecosystem function may be one way to minimize disease events in natural systems (Fig. 1). The purpose of presenting this framework is to promote the development of specific, process-related hypotheses that may be tested using a variety of research methods and disease models with the goal of supporting or revising the framework.

Fish health in the Great Lakes

Extensive mortality events of alewives *Alosa pseudoharengus*, thought to be caused by disease, were reported from Lake Ontario as early as the 1890s (Smith, 1892; Rathbun, 1893), but published reports of disease-related mortality of fishes in the Great Lakes are rare and sporadic. A number of diseases have been reported from Great Lakes fish populations during the past few decades, including epizootic epitheliotropic disease (EED; Bradley et al., 1989), bacterial kidney disease (BKD; Beyerle and Hnath, 2002), whirling disease (Beyerle and Hnath, 2002), infectious pancreatic necrosis (IPN; Beyerle and Hnath, 2002), viral hemorrhagic septicemia (VHS; USDA, 2006; Elsayed et al., 2006), heterosporis (Duggan et al., 2003), furunculosis (Beyerle and Hnath, 2002), piscirickettsia (MDNR, 2004), thiamine deficiency complex (TDC, also known as early mortality syndrome, or EMS; Honeyfield et al., 1998) and botulism (Klindt and Town, 2005; Getchell et al., 2006). Over 200 species of pathogens have been isolated from Great Lakes fish populations in recent years, including protozoa, bacteria, fungi, and viruses (M. Faisal, Michigan State University, Lansing, MI, USA, pers. comm.). Several of these were pathogens described for the first time in the Great Lakes basin, but a number of viral isolates, bacteria, and protozoa could not be identified and are believed to be new pathogens of fishes. These unidentified pathogens were isolated from a variety of species, including lake whitefish *Coregonus clupeaformis*, Pacific salmon *Oncorhynchus* spp., brown trout *Salmo trutta*, largemouth bass *Micropterus salmoides*, muskellunge *Esox masquinongy*, and northern pike *Esox lucius*. Ongoing research suggests that a large proportion of individuals in lake whitefish populations from lakes Huron and Michigan may show symptoms of disease, and many may die as a result, but the

ultimate effects of disease on these populations are unknown (M. Faisal, Michigan State University, Lansing, MI, USA, pers. comm.). The incidence of several diseases of Great Lakes fish populations appears to have increased in recent decades, including TDC (Honeyfield et al., 1998) and botulism (NYSDEC, 2006), while emerging diseases such as VHS have recently resulted in large fish kills in the Great Lakes (NYSDEC, 2006; USDA, 2006).

Although the frequency of disease events in aquatic ecosystems has seemingly increased in recent decades (Harvell et al., 1999; Ward and Lafferty, 2004), a lack of baseline data makes confirmation of this trend difficult (Lafferty et al., 2004). The ability to detect disease has improved with advancing technology, which could lead to the appearance of an increasing rate of disease events. Whether an apparent increase in frequency of disease events is real or due to a combination of better detection abilities and increased observational intensity is unknown (Lafferty et al., 2004). Extensive fish kills caused by disease have been noted for centuries in the U. S. (Mitchell, 2003), but reliable data on the frequency of occurrence of mass mortality events are lacking. Baseline data on the incidence of disease events in fish populations or the conditions that have led to disease outbreaks do not exist for the Great Lakes.

A number of fish disease outbreaks have occurred recently in the Great Lakes, causing concern among fish management agencies and the public. For example, VHS, an international reportable disease which is considered to be the most serious viral disease of freshwater salmonids in Europe, was detected in the Great Lakes in 2005 (Elsayed et al., 2006; NYSDEC, 2006; USDA, 2006). During 2005–2006, VHS caused large fish kills of freshwater drum *Aplodinotus grunniens*, muskellunge, round gobies *Neogobius melanostomus*, and yellow perch *Perca flavescens* in lakes Erie, Ontario, and St. Clair, and was confirmed as the cause of smaller mortality events in smallmouth bass *Micropterus dolomieu*, freshwater drum, black crappie *Pomoxis nigromaculatus*, and bluegill *Lepomis macrochirus* in Lake St. Clair (USDA, 2006). VHS was also found in Lake Huron in 2006 (MDNR, 2007a) and Lake Michigan in 2007. These fish kills, along with others believed to be caused by botulism, have caused great concern among the public in the Great Lakes region. Although the fish kills were described by the media as large, it is unknown whether the actual number of dead fish was large relative to population size and

whether this source of mortality was ecologically significant.

Because of the discovery of VHS in the Great Lakes, the United States Department of Agriculture's Animal and Plant Health Inspection Service (USDA-APHIS) issued an emergency Federal Order in late 2006 prohibiting the interstate movement of live VHS-susceptible fish species from all eight Great Lakes states and the importation of live VHS-susceptible fish species into the U.S. from the provinces of Ontario and Quebec. The province of Ontario also prohibited the movement of susceptible species within the province. The state of Michigan halted all stocking of walleye *Sander vitreus*, northern pike, and muskellunge in Michigan waters in 2007 because of the threat of VHS to state hatcheries (MDNR, 2007b). All of the Great Lakes states and the province of Ontario have since enacted measures designed to reduce the probability of spreading the virus, although specific measures vary by state. These restrictions have resulted in hardships for state, federal and private aquaculture operations, as well as economic losses for the baitfish industry. The VHS example illustrates that fish disease in the Great Lakes may result in serious economic consequences for aquaculture operations as well as lost tourism and fishery opportunities.

A lack of information exists on the ecology of disease in Great Lakes fish populations, but it is not clear how to best collect this information (Stephen and Thorburn, 2002). It is not feasible to develop monitoring programs for all potential diseases in all fish species in all of the Great Lakes. If, however, consideration of disease in an ecosystem context reveals that the maintenance of ecosystem function is one way to minimize disease events in natural systems, monitoring for all potential diseases in all fish species may not be necessary. We suggest that ecosystem- or population-level research focused on interactions between environmental variables and the occurrence of disease events will aid in understanding and predicting the effects of disease on fish populations in the Great Lakes. We propose that an increased ability to predict the effects of disease will allow development of focused monitoring programs for diseases of concern under specific conditions in which outbreaks are likely. Furthermore, we propose that the maintenance of ecosystem function may be one viable management strategy to minimize disease events in natural systems. Maintenance of ecosystem function in the Great Lakes might involve such strategies as preventing invasions of

exotic species, managing exotic species abundance (e.g., sea lamprey control), promoting natural recruitment of native species, pollution control, and habitat protection.

Anthropogenic factors and fish disease

Although anthropogenic factors may have profound effects on disease in Great Lakes ecosystems, relatively little research has focused on the effects of anthropogenic changes to the environment on the incidence of disease in natural populations (Daszak et al., 2001). The ecology of disease in Great Lakes ecosystems is complex due to the large number of potential disease-causing pathogens and vectors and the variety of environmental variables that affect the incidence of disease (e.g. Fig. 1). The incidence and impacts of disease in natural populations may be affected by pollution (Arkoosh et al., 1998; Lafferty and Gerber, 2002), habitat structure (Cáceres et al., 2006), habitat alteration (Real, 1996; Lafferty and Gerber, 2002), food availability (Marty et al., 2003), outbreeding (Goldberg et al., 2005), temperature or climate warming (Harvell et al., 1999; Cairns et al., 2005; Lester et al., 2007), water quality (Snieszko, 1974; Inendino et al., 2005), predators (Duffy et al., 2005), introduced species (Lafferty et al., 2004), and the size, age, or life stage of the host (LaPatra, 1998). These variables, many of which are affected by human activities, may interact in complex ways (e.g. Johnson et al., 2006; Hall et al., 2006; see Fig. 1) to affect disease dynamics in Great Lakes fish populations.

Human activities may have affected the rate at which new pathogens are introduced into ecosystems in recent years. The rate of introduction of new pathogens to ecosystems has apparently increased in recent decades (Daszak et al., 2000; Lafferty et al., 2004; Gozlan et al., 2006), and some new pathogens may have devastating effects on recipient ecosystems (e.g., Gozlan et al., 2005). When a well-established population is severely affected by an epizootic, the cause is often a newly introduced pathogen (Lafferty and Gerber, 2002). Introduced pathogens that are successful typically have a broad host range and are more pathogenic in new naïve hosts than in the original host (Lafferty et al., 2004). When a new pathogen is introduced along with an invasive species, the rate at which it spreads may be affected by the colonization dynamics of the host (Bar-David et al., 2006).

Although laboratory experiments suggest that anthropogenic factors such as chemical contaminants and hypoxia may impair immune function, potentially leading to increased susceptibility to disease, few studies have demonstrated this in the field (Mydlarz et al., 2006). Increases in anthropogenic stressors (e.g. contaminants, climate warming, habitat change) are often assumed to lead to increased disease in populations (Snieszko, 1974; Lafferty et al., 2004) because stressors may increase an individual's susceptibility to disease. However, an increase in susceptibility at the individual level does not always translate directly to an increased effect at the population level. For example, some stressors may have more negative impacts on parasites than on hosts, thereby resulting in increased recovery rates of infected individuals and mitigation of the impacts of disease on the host population. If this effect is compounded by differential mortality of diseased individuals, the spread of an epizootic through the population may actually be decreased by the stressor, despite an increased impact of the disease on infected individuals (Lafferty et al., 2004). Thus, the population-level effect of a disease is difficult to discern from the effect of the disease on individuals (Lafferty and Holt, 2003).

Not all pathogens respond to stressors or environmental change in the same way, and recognizing that stressors can increase or decrease disease is important for a full understanding of the population-level effects of diseases (Lafferty et al., 2004). For example, stressors tend to have mitigating effects on infectious diseases when transmission is mainly between members of the same population and host specificity is high. Stressors are more likely to aggravate the effects of infectious diseases when pathogens are generalists and/or persist in a resistant reservoir population (Lafferty and Holt, 2003).

Some stressors affect population dynamics through mechanisms that decrease host density or through behavioral effects that decrease the probability of contact among hosts, and in these cases, stressors will reduce the chance of an epizootic through decreased probability of transmission (Lafferty et al., 2004). Population density may have significant effects on disease transmission in wild populations, because denser populations are more likely to promote transmission (Reno, 1998; Ögüt, 2001). Relatively small populations are less likely to transmit disease between individuals because epidemiological principles suggest that the spread of infectious disease increases with host density (Lafferty

and Gerber, 2002). Because dense populations tend to have more parasites (Lafferty et al., 2004), epizootics could result from increases in host density rather than increased susceptibility due to external stressors. Environmental variables and fishery management practices that affect fish population size may therefore also affect disease transmission and fish health. We contend that the ecology of fish disease in the Great Lakes must be studied from an ecosystem perspective in order to understand the potential effects of anthropogenic stressors on fish disease at the population level.

Disease ecology from an ecosystem perspective

Epidemiology and disease dynamics have been studied extensively in human and some wild animal populations (Anderson and May, 1979), but not in wild fish populations (Gozlan et al., 2006). Investigations of the ecology of natural fish populations have paid little attention to disease (Real, 1996; Lafferty and Gerber, 2002), and ecological aspects of disease in wild fish populations have received particularly little study (Hedrick, 1998; Reno, 1998). Even for Atlantic salmon *Salmo salar*, one of the best-studied fish species, disease in wild populations has been little studied (Bakke and Harris, 1998). Although population models show that the abundance and recruitment of herring *Clupea* spp. can be affected by disease (Patterson, 1996; Marty et al., 2003), little related work has been conducted in the Great Lakes, and disease effects on dynamics of Great Lakes fish populations are poorly understood.

Epidemiological techniques and tools from other disciplines (e.g., human health, conservation biology) should be applied to understanding diseases in aquatic ecosystems, and integrated epidemiological and ecological models may prove useful in studying the ecology of fish disease in the Great Lakes (e.g., Rapport, 1999). For example, epidemiological models have proven useful in estimating the role of disease in population processes and comparing disease management strategies in wildlife populations (McCarty and Miller, 1998), although it is unclear how epidemiological models derived primarily for terrestrial animal populations will translate to aquatic systems (McCallum et al., 2004). These models can be combined with geospatial analysis and geographic information systems to estimate disease risk at large scales (Nicholson and Mather,

1996). Models that elucidate the scales over which population processes (demography, movement) operate to govern the distribution of disease may also be useful in understanding host-pathogen dynamics (e.g., Farnsworth et al., 2006).

The focus of much fish health research has been at the individual level (Stephen and Thorburn, 2002) and the results have been particularly useful for hatchery and aquaculture fish health management. However, examining the effects of disease at population, community, or ecosystem levels may be more appropriate and useful for fishery management of wild populations (Power, 2002). Fish population status provides an integrative indicator of environmental conditions (Munkittrick and Dixon, 1989) and may provide a cost-effective way of assessing fish health and the potential for disease outbreaks. Population-level indices of the health of fish populations are based on the assessment of population characteristics such as size and age distributions, fecundity, age at maturity, or average body condition (Shuter, 1990; Munkittrick et al., 2000; Power, 2002). Stephen and Thorburn (2002) suggest that a population-based approach to fish health is necessary to understand fish disease ecology in the Great Lakes.

Whether or not diseases commonly have regulating effects on wild fish populations is unknown (Stephen and Thorburn, 2002) and little field data exist that quantify the effects of disease on fish populations, particularly over large temporal scales (Bakke and Harris, 1998; Stephen and Thorburn, 2002). Although reductions in vertebrate abundance (e.g. Sinderman, 1987; Whittington et al., 1997; Hochachka and Dhondt, 2000; Lafferty and Gerber, 2002; Gozlan et al., 2005) and even extinction (Cunningham and Daszak, 1998; Smith et al., 2005) have been caused by pathogens, disease-related mortality may invoke compensatory mechanisms and in many cases may be non-regulating. For example, the parasite that causes whirling disease (*Myxobolus cerebralis*) has occurred in Pennsylvania trout populations for at least 30 years with no conspicuous population declines or mass mortality events associated with it (Kaeser et al., 2006). Some pathogens may play positive roles in promoting biodiversity and maintaining ecosystems (Lafferty et al., 2004), and some, perhaps most, infectious agents have no detectable effects on host populations. However, some pathogens may cause mortality, reduce growth, lower fecundity, alter behavior, or change social status (Lafferty et al., 2004). Moreover, the ef-

fects of disease on wild fish populations may be difficult to detect because diseased or dead animals may be difficult to directly observe (e.g., Davis, 1944; Ricker, 1945; Schneider, 1998), and because sub-clinical carriers of a pathogen may not be systematically surveyed (Gozlan et al., 2006).

Disease in wild fish populations results from complex interactions among pathogens, hosts, and the environment (Hedrick, 1998; Reno, 1998; see Fig. 1). Many variables affect disease transmissibility, including temperature, host-immune response, and host-population density. Because these and other variables interact to determine the effect of a pathogen at the population level, understanding fish disease ecology and population-level impacts on fishes in the Great Lakes requires an integrated ecosystem perspective that accounts for variables affecting host resistance, pathogens, and the environment. Understanding the population-level impact of diseases and the conditions under which diseases are most likely to regulate fish populations is essential because this is the level at which managers and the public are concerned. For example, management biologists are more concerned about a disease with population-level effects than they are with a disease that affects a few individuals severely, but not the population as a whole.

We hypothesize that population-level effects of disease will be fewer in functional (healthy) than in dysfunctional ecosystems. Recent environmental changes in the Great Lakes may be affecting the relative importance of disease as a variable regulating fish populations. The Great Lakes have been substantially disrupted in the past century, and largely have not achieved a stable state of dynamic equilibrium. Great Lakes ecosystems are dysfunctional due to altered land-use, increasing human populations, introduced species, and pollution, among other factors (Bogue, 2000). However, the effects of these variables on the prevalence, severity, and population-level impact of disease are unknown. A goal of research and management in the Great Lakes should be to understand how these variables affect ecosystems, including consideration of fish health and the ecology of disease.

Examples of fish disease problems in the Great Lakes

Great Lakes ecosystems have been seriously affected by habitat alteration, water quality

degradation, and the invasion of exotic species, among other factors. For example, the invasion of the Great Lakes by multiple exotic fish and invertebrate species has caused perturbations that may cascade through the entire ecosystem. The invasion of the Great Lakes by zebra and quagga mussels (*Dreissena* spp.) has been implicated in changes in water chemistry (Nicholls et al., 1999), water clarity (Fahnenstiel et al., 1995), nutrient and energy flow (Hecky et al., 2004), benthic invertebrate density (Lozano et al., 2001; Mayer et al., 2002), algal community composition (Pillsbury et al., 2002), and the proliferation of blue-green algae (Bierman et al., 2005). The combined effects of invasive species and other anthropogenic stressors on Great Lakes ecosystems may be significant but are difficult to predict (Vanderploeg et al., 2002), and may include serious impacts on fish health, which have the potential to undermine restoration efforts for native species.

We propose that an integrated, multi-species, ecosystem-level approach to research is necessary to understand the ecology and potential population-level effects of fish disease in the Great Lakes. Examples of how the proposed conceptual framework can be applied to research are provided below using current fish health concerns in the Great Lakes. We suggest that research is needed to determine the relationship between ecosystem function and fish health; to understand what variables affect fish health and disease transmission; and to understand and quantify how and why these variables differ between functional and dysfunctional ecosystems. Determining the mechanisms by which environmental variables affect disease processes at the population-level, understanding how environmental variables interact to affect fish health, and defining a “normative” condition for fish pathogens in functional ecosystems are critical steps in advancing our understanding of the relationship between ecosystem function and fish health.

Thiamine Deficiency Complex

Thiamine Deficiency Complex (TDC—also known as Early Mortality Syndrome, or EMS) results in high levels of early life stage mortality of salmonines in the Great Lakes and may affect adult behavior and survival (Brown et al., 2005b). TDC may be a significant impediment to restoration of lake trout and Atlantic salmon and has the potential to severely restrict salmonine production in the

Great Lakes (Fisher et al., 1996). TDC results from low egg thiamine concentrations that are caused by thiaminolytic enzymes (i.e. thiaminase) present in the diet (Tillitt et al., 2005) rather than low thiamine levels in the diet (Fitzsimons et al., 1998). TDC was present in the Great Lakes as early as the 1960s, but mortality rates from TDC rose dramatically in the 1990s (Honeyfield et al., 1998), coincident with the most recent wave of invasive species, including Dreissenid mussels and round gobies.

In terms of our conceptual framework (Fig. 1), the ecological variables regulating the presence, intensity, and consequences of TDC are not fully understood. Specifically, the sources and pathways of thiaminase in Great Lakes food webs have not been identified, and the physical and biological variables that affect the availability of thiaminase in the food web are not understood. Thiaminase may be produced by bacteria in the gut of forage fishes, although thiaminase-producing bacteria were found in only 25% of alewife stomachs in one study (Honeyfield et al., 2002). Other hypothesized sources of thiaminase include blue-green algae (Honeyfield et al., 2002; Tillitt et al., 2005), zooplankton (Zajicek et al., 2005), and de novo production by fish (Bos and Kozik, 2000), but little evidence exists to identify sources of thiaminase in Great Lakes fishes. To fully understand the ecology of the disease, research is needed to identify sources and trophic pathways of thiaminase in Great Lakes food webs, and to determine how and by what mechanisms they are affected by environmental variables.

The thiaminase activity of fish species varies widely among sampling locations (Ji and Adelman, 1998; Fitzsimons et al., 2005; Tillitt et al., 2005), indicating that environmental variables may affect the incidence of TDC. Analysis of historical data suggests that the occurrence of TDC may be correlated with the presence of certain zooplankton and phytoplankton species (Hinterkopf et al., 1999). Thiaminase levels in salmonids are correlated with dietary factors (Brown et al., 2005a), so nutritional status or food web structure may be associated with thiaminase activity. Recent changes in the species composition of Great Lakes food webs may have resulted in increases in the abundance of lower trophic species that contain thiaminase, which may have affected the diet of fish species and may have increased the incidence or severity of TDC in some areas. Alternatively, changes in environmental variables including species composition of Great Lakes food webs may have altered the physiology of fishes

that produce thiaminase (if they exist), resulting in changes in thiaminase activity and concomitant increases in the incidence or severity of TDC. Determining how trophic transfer of thiaminase is affected by environmental variables and food-web structure is necessary to understand and predict the occurrence of TDC in Great Lakes ecosystems. Research is needed to determine how and why the incidence and severity of TDC varies between functional and dysfunctional ecosystems, to determine the effects of TDC at the population level, and to identify potential management strategies to mitigate TDC.

Botulism

Botulism is caused by a potent neurotoxin produced by the bacterium *Clostridium botulinum*. Botulism toxin impacts neuromuscular function and may cause paralysis and death of infected animals. *C. botulinum* is classified into seven types (A–G) based on the characteristics of the toxin produced; types C and E are most often associated with outbreaks of disease in fish and fish-eating birds. Periodic outbreaks of botulism have resulted in extensive die-offs of multiple species of fish and fish-eating birds in the Great Lakes since at least the 1960s (Brand et al. 1983), but outbreaks have apparently become more common and widespread in recent years, particularly in lakes Michigan, Huron, and Erie. Botulism has been implicated in the recent deaths of lake sturgeon in lakes Ontario and Erie coincident with bird die-offs (Klindt and Town, 2005; Getchell et al., 2006) and may therefore be a serious impediment to lake sturgeon restoration. Further research is necessary to determine the conditions that lead to botulism-related disease outbreaks and the population-level effects of botulism on Great Lakes fish populations.

Spores of *C. botulinum* are widely distributed in the environment and may occur in soil, surface waters, aquatic sediments, and the tissues of fish and other animals (Jensen and Allen, 1960; Bott et al., 1968; Sayler et al., 1976; Reed and Rocke, 1992; Kadlec, 2002). *C. botulinum* was found in the digestive tracts of less than 10% of fish from the open waters of the Great Lakes, but was present in over 50% of apparently otherwise healthy fish from Green Bay (Lake Michigan), which suggests that the relative occurrence of bacterial spores varies among locations and may be related to local environmental or limnological conditions (Bott et al., 1966).

Although *C. botulinum* spores are ubiquitous in the environment, the toxin is produced only when the bacteria encounter suitable conditions for growth. The bacteria require anoxic conditions within specific temperature ($>10^{\circ}\text{C}$) and pH (>5) ranges for germination, but the environmental variables required for toxins to accumulate to levels sufficient to cause die-offs are unclear (Rocke and Samuel, 1999). Decaying organic matter, particularly plants or animal carcasses, may provide anaerobic conditions necessary for *C. botulinum* to grow (Reed and Rocke, 1992; Barras and Kadlec, 2000), and abundant populations of invertebrates that consume bacteria, or their predators, may also contribute to bioaccumulation of botulism toxin (Jensen and Allen, 1960; Rocke et al., 1999; Kadlec, 2002). Research is necessary to determine the mechanisms by which environmental variables control spatial and temporal variation in botulism toxin production and accumulation and the occurrence of botulism outbreaks.

The presence of invasive species, particularly Dreissenid mussels and round gobies, has been hypothesized to play a role in the increased occurrence of botulism in Great Lakes fish and birds (Klindt and Town, 2005; Perez-Fuentetaja et al., 2006). The invasion of the Great Lakes by Dreissenid mussels has been implicated in enhanced nearshore benthic algal growth (Hecky et al., 2004), which may help create the anoxic conditions required by *C. botulinum* through the biological oxygen demand caused by decomposing algae. Dreissenid mussels may accumulate botulism toxin, which may be passed on to fish predators (e.g. round gobies, lake sturgeon). With respect to Fig. 1, we suggest that the effects of exotic species on the food web and the effects of physical and biological variables on the distribution of toxin-producing *C. botulinum* are poorly understood. Research is necessary to identify the trophic pathways by which fish and birds acquire botulism toxin from Great Lakes food webs and how trophic transfer is affected by environmental variables and food web structure.

Bacterial kidney disease

Bacterial kidney disease (BKD) is a serious and often fatal disease caused by *Renibacterium salmoninarum*, and is common in wild and hatchery-reared salmonids worldwide (Fryer and Sanders, 1981; Arkoosh et al., 2004). Pacific salmon in the Great Lakes have been infected with *R. salmoninarum* since they were first introduced in the late

1960s (Holey et al., 1998), and the bacterium continues to be found in wild and hatchery-reared salmon in the Great Lakes (Beyerle and Hnath, 2002). BKD is characterized by kidney lesions, or in advanced stages, enlarged and necrotic kidneys (Beacham and Evelyn, 1992). Although *R. salmoninarum* occurs naturally in wild salmonids, many infected fish show no clinical signs of disease (Jónsdóttir et al., 1998; Arkoosh et al., 2004). BKD may affect the behavior and survival of salmonids (Sanders et al., 1992; Price and Schreck, 2003) and may increase susceptibility to predation of juveniles (Mesa et al., 1998).

The epidemiology of BKD may be affected by ecological features of the environment such as the abundance of food (Jónsdóttir et al., 1998). The occurrence of a BKD epizootic in Lake Michigan Chinook salmon *Oncorhynchus tshawytscha* in the late 1980s and early 1990s may have been due to a decline in alewife abundance, which may have caused sufficient nutritional stress to make salmon susceptible to *R. salmoninarum* (Holey et al., 1998). Rapid fluctuations in the abundance of an exotic fish species like alewife may be a symptom of ecosystem dysfunction and may cause changes in the food web that lead to changes in nutritional status of individuals that may have population-level consequences (Fig. 1). *R. salmoninarum* continues to be routinely isolated from wild and hatchery salmon in the Great Lakes (Beyerle and Hnath, 2002); thus, the potential for future outbreaks of BKD exists. The mechanisms by which environmental variables control spatial and temporal variation in the occurrence and severity of BKD epizootics are unknown, and research is necessary to determine the population-level effects of BKD and to predict the occurrence of epizootics.

Conclusions

Ecosystem changes will continue to result in new pathogen introductions and environmental changes that may affect the incidence and severity of fish disease outbreaks in the Great Lakes. In this paper, we suggest that directed ecosystem or population-level research on the ecology of fish disease in the Great Lakes is necessary to better understand and predict the effects of disease on wild fish populations. We contend that optimal management strategies for minimizing disease outbreaks in wild fish populations should focus not on pathogen detection at the individual level, but rather on maintaining a functioning and stable ecosystem; and that an evolutionary and ecosystem perspective on wild fish

health is necessary to understand the types and advantages of management practices available to control the effects of diseases in the wild.

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