Modeling fish health to inform research and management: Renibacterium salmoninarum dynamics in Lake Michigan

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Abstract. Little is known about the interaction between fish pathogens and managed freshwater fish populations. We develop a model of chinook salmon (Oncorhynchus tschawytscha)–Renibacterium salmoninarum (Rs) dynamics based on free-swimming Lake Michigan fish by synthesizing population and epidemiological theory. Using the model, we expose critical uncertainties about the system, identify opportunities for efficient and insightful data collection, and pose testable hypotheses. Our simulation results suggest that hatcheries potentially play an important role in Lake Michigan Rs dynamics, and understanding vertical transmission will be critical for quantifying this role. Our results also show that disease-mediated responses to chinook salmon density need to be considered when evaluating management actions. Related to this, a better understanding of the stock–recruitment relationship and natural mortality rates for wild-spawned fish and the impact of hatchery stocking on recruitment is required. Finally, to further develop models capable of assisting fishery management, fish health surveys ought to be integrated with stock assessment. This is the first time a host–pathogen modeling framework has been applied to managed, freshwater ecosystems, and we suggest that such an approach should be used more frequently to inform other emerging and chronic fish health issues.

Key words: bacterial kidney disease; chinook salmon; epidemiology; fish health; Great Lakes, Lake Michigan, USA; host–pathogen model; multiple hosts; Oncorhynchus tschawytscha; Renibacterium salmoninarum; SIR models.

INTRODUCTION

Fishery managers are increasingly concerned about fish health, but little is known about the dynamics and effects of pathogens in fish populations outside of laboratory, aquaculture, and hatchery facilities (Harvell et al. 2004, Faisal 2007). Quantitative modeling has provided a useful approach to organize and improve understanding of host–pathogen dynamics in wild populations, but such efforts have been largely limited to terrestrial ecosystems (Reno 1998, McCallum et al. 2004). Dobson and May (1987) developed an early theoretical model of pathogens in fish, but most work that followed focused on captive populations (Ogut et al. 2005, Scheel et al. 2007) and marine systems (Murray et al. 2001). Furthermore, these studies did not directly model management actions. The development of models that incorporate management is essential to managing aquatic animal health (Harvell et al. 2004, Peeler et al. 2007, Chambers et al. 2008).

The presence of Renibacterium salmoninarum (Rs), the causative agent for bacterial kidney disease (BKD), is well-established in the Great Lakes of the United States, a large intensively managed freshwater ecosystem. Benjamin and Bence (2003b) estimated a substantial increase in salmonid mortality in Lake Michigan associated with increased prevalence of Rs (Holey et al. 1998). Rs is also believed to be “one of the most important bacterial diseases affecting wild and propagated anadromous salmonid stocks” (Wiens and Kaat-tari 1999) in the Pacific Northwest, but little is known about the pathogen’s dynamics in the wild.

Here we develop a model of chinook salmon (Oncorhynchus tschawytscha)–Rs dynamics based on free-swimming fish populations and explicitly include management actions. Models like ours can help synthesize and interpret complex data sets and thereby aid managers in making inferences about the possible consequences of management strategies. Patterson (1996) used a complex data set to estimate disease-induced mortality caused by the phycomycete fungal parasite Ichthyophonus hoferi in North Sea herring (Clupea harengus) from catch-at-age data combined with prevalence data, but did not evaluate how alternative management strategies may affect this parameter. Patterson (1996) noted that failing to account for disease effects can lead to an overestimation...
of fishing mortality, which may have implications for harvest policy. In a terrestrial example, Barlow (1991, 1996) and Smith and Cheeseman (2002) employed host-pathogen models to evaluate alternative control strategies for bovine tuberculosis (Mycobacterium bovis) in New Zealand possums (Trichosurus vulpecula) and English badgers (Meles meles), respectively.

Host–pathogen models such as ours can also be used to develop and evaluate hypotheses about system dynamics, thereby exposing critical uncertainties and identifying opportunities for efficient and insightful data collection. A lack of data on disease transmission does not pose an insurmountable barrier for fulfilling these objectives (Caley and Hone 2004). For example, Murray et al. (2001) developed a model of herpes virus transmission in pilchards to examine assumptions about transmission processes. Ogut et al. (2005) demonstrated how host–pathogen models can be used to gain insight into the disease dynamics, explore uncertainties, and estimate parameters for a captive chinook salmon population infected with Aeromonas salmonicida (the etiologic agent of furunculosis).

Following terrestrial investigations, previous fish-pathogen modeling efforts have focused on single fish populations and ignore the influence of management activities on the system. However, the ability of pathogens to influence ecological relationships among species is receiving increased attention (Hatcher et al. 2006). Moreover, many freshwater systems, such as Lake Michigan, are highly influenced by human activities (e.g., stocking of salmonids) that affect host community dynamics, and thus the risk of a disease event is in part determined by human behaviors. Finally, there is increasing concern about, and evidence for, pathogen transmission among farmed, stocked, and wild fish (Krkosek et al. 2005, Chambers et al. 2008).

We use a multiple-host disease framework to incorporate management features into a model of Rs in Lake Michigan in order to qualitatively explore the implications of modeling assumptions, model sensitivity, and management actions on host–pathogen dynamics. Two host stocks were included in the model: chinook salmon resulting from wild spawning (“wild” chinook) and chinook salmon resulting from collection of feral gametes and hatchery production (“hatchery” chinook).

**System background**

Chinook salmon have been stocked into Lake Michigan in large numbers since 1967. Age-0 smolts are released into selected rivers throughout the lake during the spring; some of these rivers now contain populations of naturally produced age-0 salmon. Recent estimates of wild chinook salmon production in Lake Michigan approach or even exceed 50% of total production (R. Claramunt, personal communication). The hatchery and wild chinook salmon emigrate from these rivers during their first summer and feed in Lake Michigan for multiple years, returning primarily as age-3 or age-4 adults. There is no evidence that hatchery and wild chinook salmon occupy different habitats during their lake-resident period and most salmon home to their natal stream. For hatchery fish this will be the river into which they were stocked as age-0 smolts.

In 1987, chinook salmon in Lake Michigan suffered a large increase in mortality (Benjamin and Bence 2003a) associated with a widely observed outbreak of bacterial kidney disease (BKD) and a high prevalence of Rs, first documented in the spring of 1988 (Holey et al. 1998). Subsequently, Rs has been documented in other Lake Michigan salmonines and in sea lampreys (Petromyzon marinus; Eissa et al. 2006). Since 1970, fish collected for eggs and hatcheries have been inspected for pathogens including Rs, but techniques and protocols have changed substantially over time (J. G. Hnath and M. Faisal, unpublished manuscript).

Knowledge of Rs/BKD dynamics in Lake Michigan is extremely limited, despite evidence of the importance of this disease for salmonid dynamics (Holey et al. 1998, Benjamin and Bence 2003a, b). Most knowledge about fish-borne disease comes from observations and studies conducted in hatcheries or fish production facilities (Stephen and Thorburn 2002), and the dynamics of BKD are no exception (Wiens and Kaattari 1999). From such experiments it is known that Rs can be transmitted horizontally (i.e., directly) among juvenile and adult salmonids (Mitchum and Sherman 1981, Balfry et al. 1996), as well as vertically from adult females to eggs (summarized in Wiens and Kaattari [1999] and in Chambers et al. [2008]). Further research has shown that fish may become infected when the pathogen is present in sufficiently high levels in the surrounding water (summarized in Hamel 2005). But it is unclear which transmission processes drive pathogen dynamics among free-swimming fish populations or which are important for pathogen maintenance.

**METHODS**

**Model development**

Host–pathogen models are population models that track how the host population is distributed among health classes (e.g., susceptible and infected), and pathogen dynamics are tracked based on the proportion of the population in each health class. We use a susceptible-exposed-infected-exposed (SEIE) host–pathogen framework (Fig. 1).

The SEIE model is a modification of the standard susceptible-infected-recovered (SIR) framework for modeling host–pathogen relationships (Anderson and May 1991, Reno 1998). The health classes S, E, and I, represent three subpopulations; susceptible, exposed, and infectious, respectively. Susceptible individuals do not host the pathogen currently (i.e., are healthy with respect to the pathogen of interest), but may do so in the future. Infectious individuals are infectious and subject to disease-induced mortality (infectious is used to mean infected and infectious). The slow development of
bacterial kidney disease in exposed hosts motivates the inclusion of a latent/exposed (E) stage (Heesterbeek and Roberts 1995, Murray et al. 2001). Exposed fish in health class E harbor $R_s$, and host the pathogen; however, they are not yet infectious, nor are they subject to disease-induced mortality. In our model, infection may abate, and individuals in class I may return to class E. This can be thought of as an infection in remission.

The number of individuals in a given health class depends on rates of transition among the different classes, including the rates at which individuals become exposed to the pathogen, become infectious, die due to disease, or go into remission. Taking host population dynamics into account is important for a chronic disease like BKD because the disease course occurs on a comparable timescale with that of the host’s lifespan. Thus, the number of individuals among different health classes also depends on birth and disease-independent death rates, which may be density dependent. In these systems, the pathogen can persist in the population for multiple generations (i.e., is endemic; see Barlow [1991, 1996] for examples). In contrast, for highly transmissible and virulent pathogens, host dynamics are often ignored because pathogen dynamics occur on much shorter timescales than the lifespan of the host. In the pilchard example of Murray et al. (2001), the pathogen infects a large number of fish and then dies out within one generation (i.e., is epidemic) because the lack of susceptible individuals in the population leads to local extinction of the pathogen (fish that survive develop immunity and therefore are not susceptible in the example of Murray et al. [2001]). This can lead to cycles of disease outbreaks if a pathogen is continually reintroduced.

Our host–pathogen model is a system of population models for two fish host types, wild chinook (w) and hatchery chinook salmon (h). We used an age-structured model with five age classes (age 0 to age 4) for each chinook salmon type (Fig. 2). Each age of each host type is treated as an individual host type.

Given this general framework for integrating fish population and pathogen dynamics, we can now explain our model in detail. The model operates on an annual time step, and within each year there are five sequential steps (Fig. 3): (1) recruitment and aging, (2) pretransmission mortality, (3) pathogen transmission, (4) disease progression/remission, and (5) post-transmission mortality. In the following section, these steps are discussed in detail.

**Step 1.**—At the beginning of each time step, the age composition of each host group is updated. All fish of age $a$ at time $t$ that survive the year become age $a + 1$ at time $t + 1$. Recruitment of wild chinook salmon is calculated from a Ricker (1954) stock–recruitment relationship, $r = \alpha A e^{-\gamma A'}$, where $A$ and $A'$ are related to mature host abundance (explained in detail in the next paragraph), $r$ is recruitment, and $\alpha$ and $\gamma$ are
parameters. Recruitment is simply the number of fish stocked for hatchery chinook salmon.

All mature wild and hatchery chinook salmon produce wild offspring (Fig. 2), but the proportion of fish in an age class that spawn and the fecundity of spawners varies by age class. The Ricker function includes a density-independent term \( a \) related to the average maximum production of offspring per adult. The Ricker function also has a density-dependent term \( \left( e^{-\gamma A_0} \right) \) that accounts for limitations on recruitment due to competition or similar processes. We assume that the magnitude of density dependence is determined by the entire spawning population for wild chinook salmon. Hence,

\[
A' = \eta_w = \sum_i \sum_a \psi_{i,a} N_{i,a}
\]

where \( \psi \) is a measure of the relative fecundity and spawner proportion for each age class, and where \( N_{i,a} \) is the population of host type \( i \) (\( i = \{w, h\} \)) at age \( a \) (assume that \( \psi_a = \alpha_a/\alpha_4 \), where age 4 has the largest value of \( \alpha \), though more general specifications are possible). In contrast, we assume that the density-independent term is scaled only by the spawning adults in the specified cohort. Thus, in our model \( A \neq A' \). This gives the following system of equations:

\[
N_{h,0} = s_t
\]

\[
N_{w,0} = \sum_i \sum_a \alpha_i \beta N_{i,a} e^{-\gamma N_{i,a}} \quad i = \{w, h\}
\]

where \( s_t \) is the number of hatchery salmon that are stocked.

In addition to determining how many progeny are produced, we must also index progeny by health class, because their distribution across health classes affects the total mortality rate they experience during the next step of the model. \( R_s \) can be transmitted vertically from mother to egg through reproduction (summarized in Wiens and Kaattari 1999). To model vertical transmission we modify the density-independent component of recruitment in Eq. 1 to distinguish the contribution of infectious and non-infectious adults to infectious and susceptible offspring. We assume that spawners in class E (exposed) do not transmit pathogen to their progeny, and any offspring that contract the pathogen from vertical transmission are placed in class I (infectious),

\[
\frac{N_{w,0}}{N_{h,0}} = \sum_i \sum_a \alpha_i \beta N_{i,a} e^{-\gamma N_{i,a}} \quad i = \{w, h\}
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though we examine this assumption below. The parameter \( v \) is introduced to account for the proportion of infectious progeny produced from class I spawners (i.e., the vertical transmission rate). We assumed a 10% rate of vertical transmission, which is within the observed range (1%–14%) found in laboratory experiments for coho salmon (Oncorhynchus kisutch; summarized in Hamel 2005). For wild chinook salmon recruitment the resulting equations are

\[
S_{w,0} = \sum_i \sum_a \alpha_{ia} \left[ N_{i,a} - I_{i,a} \right] e^{-\gamma_i t_i} \\
I_{w,0} = \sum_i \sum_a \alpha_{ia} \left( v I_{i,a} \right) e^{-\gamma_i t_i},
\]

(2)

where \( S_{w,0} \) and \( I_{w,0} \) represent recruits of susceptible fish from uninfected and infectious parents, and infectious fish from infectious parents, respectively.

Step 2 (and 5).—instantaneous mortality is applied twice during the year (Fig. 3), before pathogen transmission and after disease advancement. Let the proportion of the year represented by the solid line on the left side of Fig. 3 be \( \tau \) (in our simulations we assume \( \tau = 0.5 \)). The standard equation for applying instantaneous mortality is

\[
N_{i,a,t+\tau} = N_{i,a,t} e^{-z_{i,a} \tau}
\]

which assumes that the total mortality rate, \( z_{i,a} \) (for host type \( i \) and age \( a \)), is constant. In a host–pathogen model even if the component instantaneous mortality rates (i.e., natural, non-BKD mortality, \( m \), fishing mortality, \( f \), and BKD-induced mortality, \( d \)) are constant, the value of \( z \) in this model could not be constant throughout the year because the proportion of \( N \) that experiences disease-induced mortality, \( d \), changes as a result of disease transmission and progression (steps 3 and 4). Therefore, we model the mortality of each health class separately:

\[
S_{i,a,t+\tau} = S_{i,a,t} e^{-(m_i+f_i) \tau} \\
E_{i,a,t+\tau} = E_{i,a,t} e^{-(m_i+f_i) \tau} \\
I_{i,a,t+\tau} = I_{i,a,t} e^{-(m_i+f_i+d_i) \tau}.
\]

(4)

For the second application of mortality (right solid line in Fig. 3), \( \tau \) is replaced with \( 1 - \tau \) and \( t \) is replaced with \( t + \tau \) on the right-hand side, and \( t + \tau \) is replaced with \( t + 1 \) on the left-hand side. This approach implicitly assumes that disease transmission and progression occur over a relatively short period of time during the year. We assumed that the instantaneous rate of BKD-induced mortality, \( d \), is 0.64. This value is based on mortality rates reported in Benjamin and Bence (2003b) that are associated with the epizootic of the late 1980s.

Step 3.—Once fish are established in an age class, susceptible fish can transition into the exposed class via contact with infectious fish. Fish are assumed to mix randomly with density-dependent transmission, so that contacts between susceptible and healthy individuals occur proportionally to density with a constant probability that a susceptible individual becomes exposed given a contact with an infectious individual. The proportionality coefficient and the conditional transmission rate are collapsed into a single parameter, \( \beta \). This is the most common transmission function used for non-sexually transmitted wildlife pathogens; but see McCallum et al. (2001) for a discussion of other possible transmission functions. During each time step fish move from health class S (susceptible) to E (exposed) at time \( t \) according to horizontal transmission function \( H_{i,a}(S_i, I_j) \), which is specific to host type and age. Horizontal transmission generally follows Dobson (2004):

\[
S_{(i,a),t+\Delta} = -H_{(i,a)(S_i,I_j)}(S_{(i,a),t}) \\
= S_{(i,a),t} - S_{(i,a),t} \sum_j \sum_k \beta_{(i,a),(j,k)} f_{j,k,t} \\
E_{(i,a),t+\Delta} = H_{(i,a)(S_i,I_j)}(S_{(i,a),t}) \\
= E_{(i,a),t} + S_{(i,a),t} \sum_j \sum_k \beta_{(i,a),(j,k)} f_{j,k,t}
\]

(5)

where \( \beta \) is the per capita rate of pathogen transmission from host \( j \) cohort \( k \) to host \( i \) cohort \( a \), where \( i \) and \( j \) index all potential host types and \( a \) and \( k \) index their age, and \( \Delta \) represents a small change in time.

Step 4.—Immediately following the recruitment of susceptible individuals to the exposed class, the advancement process between the exposed and infectious classes occurs. Traditionally, exposed individuals are included to model a fixed latency period, and advancement is simply determined by a delay parameter that represents the inverse of the average latency period (Heesterbeek and Roberts 1995). However, researchers do not know what the average latency period is for \( R_i \)/BKD. Moreover, the BKD epidemic in Lake Michigan coincided with a period of reduced chinook salmon growth rates, suggesting that nutritional stress may play an important role in triggering clinical disease (Holey et al. 1998). Thus, we make advancement a consequence of nutritional stress. We assume that nutritional stress is a function of intraspecific competition and that increased host densities approximate reduced food resources per individual (implicitly assuming that the prey resource is fixed), thus making advancement a function of

\[
\sum_i \sum_a N_{i,a,t+\Delta}.
\]

As the density of the host population increases, ceteris paribus, so does the rate at which exposed individuals become infectious. Conversely, low host densities result in increased food resources per individual, and thus result in a net recovery from the infectious to the exposed class. In other words, infectious fish return to the exposed class at a greater rate than exposed fish transition to the infectious class. We define the advancement function \( Q \) as the process by which
exposed fish advance to the infectious class (negative advancement implies remission to the exposed class):

$$\Delta E_{i+2\Delta t} = E_{i+\Delta t} - Q[Y(\Lambda),E_{i,a,t+\Delta},I_{i,a,t+\Delta}]$$

$$\Delta I_{i+2\Delta t} = I_{i+\Delta t} + Q[Y(\Lambda),E_{i,a,t+\Delta},I_{i,a,t+\Delta}]$$

where

$$\Lambda = \sum_{i} \sum_{a} N_{i,a,t+\Delta}$$

and where $Y$ is a function that defines the rate of movement between classes $E$ and $I$ and must have two qualities. First, $|Y| \leq 1$, and second, there must be some $\Lambda = \bar{N}$ where $Y(\bar{N}) = 0$ (i.e., there is no net movement from exposed to infectious). Function $Y$ takes the form

$$Y(\Lambda) = \frac{(\Lambda - q_{eq})}{(\Lambda - q_{eq}) + q_{50\%}}$$

where $q_{50\%}$ is the population density at which 50% of the exposed (infectious) individuals become infectious (exposed) and $q_{eq} = \bar{N}$. The parameter $q_{eq}$ also determines the direction of movement:

$$Q[Y(\Lambda),E_{i,a,t+\Delta},I_{i,a,t+\Delta}] = \begin{cases} Y(\Lambda)E_{i,a,t+\Delta}, & \text{if } \Lambda > q_{eq} \\ -Y(\Lambda)I_{i,a,t+\Delta}, & \text{if } \Lambda < q_{eq} \end{cases}$$

Simulations

Two modeling workshops and numerous correspondences with fish health specialists and Great Lakes fishery biologists were conducted to solicit expert opinion on model processes and parameter values for calibration of the model (parameter values used are listed in Table 1). Realistic values were used for recruitment. Mortality parameters were based on Benjamin and Bence (2003b). There are no estimates for important parameters in the model such as transmission rates, which inherently are difficult to obtain for wild populations (Tompkins et al. 2002). Transmission and advancement parameters, therefore, where chosen so that equilibrium prevalence in age-4 hatchery fish approximated observed prevalence (J. G. Hnath and M. Faisal, unpublished manuscript). Quantitative enzyme-linked immunoassay (QELISA) results were used to approximate a total prevalence $(E + I) at 37% for age-4 hatchery fish. Prevalence of clinical signs, 4.7%, was used to calibrate the prevalence of age-4 infectious (class I) hatchery fish.

When all age classes are considered, the term

$$\sum_{i} \sum_{a} \beta_{(i,a),(j,k)}$$

in Eq. 5 can be expressed as a transmission matrix $\beta$. One may expect unique values for each element of $\beta$. This, however, would lead to a large number of parameters. To maintain tractability we investigate two structures for the matrix $\beta$: (1) where all the elements of $\beta$ are equal (full transmission) except for elements relating transmission to age 0, which can only occur from age 0 or via vertical transmission, and (2) where all off-diagonal elements are zero, implying that transmission only occurs within age classes (age-based transmission). One may also expect unique values by age of $q_{eq}$ and $q_{50\%}$, but for tractability we constrain these to be equal across all ages.

We conducted a series of simulations to identify emergent properties resulting from the combination of population and host–pathogen theories. The model has a large number of parameters, and in the absence of data, a detailed sensitivity analysis for each parameter may be less illuminating than the other analyses discussed in the latter parts of the Results section. Therefore, we focused on examining changes in the parameters that ecological and epidemiological theory suggests would have the greatest affect on model
outcome. Analyses were conducted across age classes (e.g., all natural mortality parameters were increased by 5% simultaneously to examine the elasticity with respect to natural mortality).

To assess sensitivity, we employed the concept of arc elasticity, and calculated the percentage change in the density of exposed and infectious wild and hatchery chinook salmon at equilibrium with respect to a 5% increase in the model parameter. If the \( |\text{arc elasticity}| > 1 \), then the model was deemed to be elastic and sensitive to changes in the parameter; likewise, if the \( |\text{arc elasticity}| < 1 \), then the model was deemed to be insensitive to changes to the parameter. To explore the robustness of the arc elasticity measures we also computed arc elasticities with respect to a 20% change.

We then used the simulation model to investigate the consequences of various management actions. We explored the effects of stocking level and hatchery biosecurity practices, and the interactions between stocking rates and hatchery biosecurity practices. Stocking is the primary chinook salmon management tool and directly affects density. There are two components to a stocking program that could influence \( R_s \) prevalence in the lake: the total number of fish stocked and the infection prevalence of stocked fish. We simulated three different stocking levels: 2, 5, and \( 8 \times 10^6 \) fish per year, which correspond to recent levels of chinook salmon stocking into Lake Michigan (\( 5 \times 10^6 \)), historic high stocking levels (\( 8 \times 10^6 \)), and a substantial decrease in stocking (\( 2 \times 10^6 \)). We also examined five hatchery biosecurity management scenarios that span a plausible range of prevalence of infectious, stocked fish. One of these mimics vertical transmission from wild reproduction. The other four were modeled as the percentage of infectious fish that hatcheries produced: 0%, 5%, 15%, and 95%.

Finally, we characterized conditions that could lead to an outbreak of bacterial kidney disease (BKD) like that observed in Lake Michigan in the mid to late 1980s. To do this we simulated stocking \( 5 \times 10^6 \) fish with 5% prevalence for 100 years, and then applied either a deterioration in hatchery biosecurity to stocking 95% infectious fish or an increase in stocking to \( 8 \times 10^6 \) fish for three years to determine which was more likely to create a die-off.

The model was simulated for a sufficiently long time period that transient dynamics subsided and the system appeared to arrive at equilibrium (where changes in the state variables were close to zero). Most simulations ran for 100 years, but 200-yr simulations were used when the system was deliberately perturbed during the first 100 years. The initial source of \( R_s \) is assumed to be hatchery fish. We implemented the model in Microsoft Visual Basic interfaced through a Microsoft Excel workbook (Microsoft, Redmond, Washington, USA).

Results

Three model specifications and sensitivity

We began by exploring two model specification questions: (1) the assignment of offspring that receive infection via vertical transmission to the I class vs. the E class, and (2) the nature of horizontal transmission, full vs. age-based transmission. Taking the assignment of vertical transmission to health class I, and allowing for the full transmission matrix, we calibrated the model so that at equilibrium, age-4 hatchery fish approximated the observations of J. G. Hnath and M. Faisal (unpublished manuscript; Fig. 4B). Fig. 4 illustrates that a model with full transmission and offspring subject to vertical transmission assigned to the I class could be considered the most conservative. This is because larger transmission parameters or larger values for \( Q \) would be required to create realistic prevalence levels for other model structures. Moreover, different assumptions about the structure of the model affect the pattern of equilibrium prevalence. A full transmission matrix and vertical transmission resulting in I offspring showed a pattern that is consistent between hatchery and wild fish.

The alternative models yielded different equilibrium exposed and infectious patterns across age classes and between hatchery and wild fish. When vertical transmission results in class E offspring, exposed prevalence was relatively constant across ages in hatchery fish, but was increasing with age in wild fish. Exposed prevalence in hatchery fish was greater than in wild fish. Infection prevalence decreased with age in hatchery fish, but increased with age in wild fish with age-based transmission.

We used the full matrix transmission model with vertical transmission assigned to class I for the remaining analysis. The equilibrium densities of exposed and infectious wild and hatchery chinook salmon showed greatest sensitivity to the natural mortality rate (Table 2). Equilibrium densities of exposed and infectious wild chinook salmon were also sensitive to the stock–recruitment parameters. Infectious classes were generally sensitive to disease-induced mortality, but exposed classes were generally insensitive to this parameter. Most age, health, and origin classes were slightly sensitive to the transmission coefficient, but not as sensitive as they were to standard demographic parameters. Finally, all classes were generally insensitive to disease advancement parameters, with the exception of wild infectious fish, which were only slightly sensitive to \( q_{50\%} \). The effect of an increase in any parameter always had the same sign across all categories of host. The patterns of sensitivity were similar for the other model specifications and are not reported here.

We also investigated arc elasticities for larger changes in the parameter values (20%; see Appendix). The ordering of the arc elasticities was qualitatively unchanged from the results reported previously. Generally, arc elasticities decreased in absolute value, though a few increased slightly. A change in the arc elasticity when the percentage change in the parameter was increased indicates higher order effects resulting from nonlinearities. The arc elasticities associated with changes in the advance parameters declined the most in absolute value.
The arc elasticities associated with changes in the natural mortality rate and the density-dependent stock recruitment parameter were also sensitive to the magnitude of the change.

The effects of management on prevalence

First, we examined the effects of stocking on prevalence at equilibrium for cases where stocking did not directly contribute infectious fish (hatcheries produced 0% infectious fish) over the broadest range of stocking levels. In this case, the pathogen could not be sustained in the system (Fig. 5). Hatchery biosecurity practices mimicking vertical transmission in wild-spawned fish also failed to allow the pathogen to persist (Fig. 5), even at the highest stocking levels. When there were initially infectious fish in the system, higher stocking levels lead to longer pathogen persistence. The pathogen also persisted longer in the system when hatchery biosecurity practices mimicked vertical transmission levels in wild-spawned fish.

Deterioration in hatchery biosecurity practices, leading to more infectious hatchery releases, resulted in sustained prevalence of exposed and infectious chinook salmon in both wild and hatchery salmon. Even small deteriorations in hatchery biosecurity practices, such as increasing the infection prevalence of released infectious fish from 0% to 5%, resulted in sustained prevalence of exposed or infectious fish (Fig. 6). This suggests that hatchery biosecurity measures play a critical role in managing fish health.

The effects of management on population density

Previous results showed that increased biosecurity measures in hatcheries can lead to lower prevalence of the pathogen in the wild. Prevalence of a pathogen could be argued to be an indicator of fish health, and fish
Table 2. Arc elasticity results for wild (w) and hatchery (h) chinook salmon by age class (0–4 yr) and health class (exposed to or infectious with *Renibacterium salmoninarum*) with the full transmission and vertical infection going to the infectious health class.

<table>
<thead>
<tr>
<th>Parameter</th>
<th>Health class</th>
<th>Salmon type (wild or hatchery) and age class</th>
</tr>
</thead>
<tbody>
<tr>
<td></td>
<td></td>
<td>w0  h0  w1  h1  w2  h2  w3  h3  w4  h4</td>
</tr>
<tr>
<td>Ricker density-dependent parameter, γ</td>
<td>E</td>
<td>−1.10 −0.73 −1.40 −0.62 −1.40 −0.53 −1.36 −0.45 −1.30 −0.38</td>
</tr>
<tr>
<td></td>
<td>I</td>
<td>−1.92 −0.29 −2.57 −0.71 −2.21 −1.00 −2.12 −1.12 −2.07 −1.13</td>
</tr>
<tr>
<td>Ricker density-independent parameter, α</td>
<td>E</td>
<td>1.21 0.85 1.59 0.72 1.58 0.62 1.53 0.52 1.46 0.43</td>
</tr>
<tr>
<td></td>
<td>I</td>
<td>2.20 0.33 3.02 0.82 2.59 1.14 2.48 1.24 2.40 1.27</td>
</tr>
<tr>
<td>Disease transmission parameter, β</td>
<td>E</td>
<td>1.15 1.61 1.39 1.49 1.36 1.39 1.30 1.29 1.30 1.29</td>
</tr>
<tr>
<td></td>
<td>I</td>
<td>1.19 0.31 1.30 0.77 1.34 1.07 1.34 1.18 1.30 1.18</td>
</tr>
<tr>
<td>Advancement parameter, q_{50%/v}</td>
<td>E</td>
<td>−0.04 −0.42 −0.29 −0.34 −0.26 −0.26 −0.20 −0.19 −0.14 −0.12</td>
</tr>
<tr>
<td></td>
<td>I</td>
<td>−1.04 −0.26 −1.14 −0.65 −1.18 −0.92 −1.15 −1.03 −1.11 −1.04</td>
</tr>
<tr>
<td>Advancement (equilibrium) parameter, q_{eq}</td>
<td>E</td>
<td>−0.02 −0.19 −0.07 −0.16 −0.09 −0.14 −0.09 −0.12 −0.07 −0.09</td>
</tr>
<tr>
<td></td>
<td>I</td>
<td>−0.32 −0.09 −1.23 −0.22 −0.53 −0.31 −0.41 −0.34 −0.36 −0.35</td>
</tr>
<tr>
<td>Vertical transmission parameter, v</td>
<td>E</td>
<td>0.11 0.10 0.06 0.07 0.05 0.06 0.05 0.05 0.04 0.05</td>
</tr>
<tr>
<td></td>
<td>I</td>
<td>0.47 0.02 0.21 0.04 0.08 0.05 0.06 0.05 0.05 0.05</td>
</tr>
<tr>
<td>Disease-induced mortality, d</td>
<td>E</td>
<td>−0.48 −1.09 −0.86 −1.01 −0.88 −0.95 −0.86 −0.89 −0.82 −0.83</td>
</tr>
<tr>
<td></td>
<td>I</td>
<td>−1.29 −0.78 −1.43 −1.36 −1.35 −1.60 −1.43 −1.65 −1.49 −1.65</td>
</tr>
<tr>
<td>Natural mortality, m</td>
<td>E</td>
<td>−1.37 −2.47 −2.38 −2.58 −2.67 −2.69 −2.86 −2.82 −3.03 −2.94</td>
</tr>
<tr>
<td></td>
<td>I</td>
<td>−2.69 −1.26 −3.93 −2.33 −3.75 −3.13 −3.88 −3.60 −4.04 −3.87</td>
</tr>
<tr>
<td>Fishing mortality, f</td>
<td>E</td>
<td>−0.03 −0.15 −0.13 −0.15 −0.20 −0.20 −0.37 −0.37 −0.61 −0.60</td>
</tr>
<tr>
<td></td>
<td>I</td>
<td>−0.15 −0.04 −0.24 −0.12 −0.28 −0.23 −0.45 −0.43 −0.69 −0.67</td>
</tr>
</tbody>
</table>

Notes: Arc elasticity is the percentage change in the prevalence of a given health class at age, divided by 5% (the amount by which the parameter value was increased). If \( |\text{arc elasticity}| > 1 \), then the model is deemed to be elastic and sensitive to changes in the parameter, likewise, if \( |\text{arc elasticity}| < 1 \), then the model is deemed to be insensitive to changes in the parameter.

health status may explain sources of non-fishing mortality. Managers, however, may ultimately be more interested in the population of fish available to anglers. Accordingly, there may be tradeoffs between hatchery practices that create greater biosecurity and stocking levels that create more fish. Therefore, we examined how the interaction of stocking, hatchery practices, and disease dynamics affected fish density (Table 3). From these simulations, we can make two important observations about the interaction among population size, stocking level, hatchery practices, and disease dynamics.

First, assuming that the fishing mortality rate is not affected by fish density, large increases in the number of fish stocked did not result in proportional increases in the fish population. This is true even in the case where stocking did not contribute infectious fish to the population. Due to density dependence in the stock–recruitment relationship, there is a clear pattern of diminishing survival and reproduction with increased stocking.

Second, increasing stocking at the expense of increasing the contribution of pathogen from the hatchery can result in more available older fish, up to some level of hatchery contribution to infection. Increased stocking from \( 2 \times 10^6 \) fish with 0% prevalence to \( 5 \times 10^6 \) fish increased the stock size at age 4 for all but the worst

Fig. 5. Simulated time series of a bacterial kidney disease (BKD) outbreak in wild age-4 fish. Dotted and solid lines represent exposed and infectious fish, respectively. (A) The situation when hatchery fish are the initial source of infection, but after the introduction of the pathogen to the system, hatcheries do not produce infectious fish. Black and gray lines illustrate the time course of infection when \( 8 \times 10^6 \) and \( 2 \times 10^6 \) fish are stocked, respectively. (B) The situation when \( 8 \times 10^6 \) fish are stocked. Hatchery fish are the initial source of infection. Black and gray lines represent the time course when hatcheries do not produce infected fish and when hatcheries mimic wild vertical transmission, respectively. The black lines are the same in both panels.
hatchery biosecurity practices (Table 3). However, this pattern did not hold for increased stocking from $5 \times 10^6$ fish with 0% prevalence to stocking $8 \times 10^6$ fish with 15% prevalence.

Recreating a fish kill

A decline in the stock size or density due to disease could be triggered by increased stocking or declines in hatchery biosecurity as both are capable of increasing pathogen prevalence. A decline in hatchery biosecurity causes the density of fish in the lake to decline (Fig. 7B). In the model simulations, this resulted in just over a 40% decline in the available age-4 fish in the years in which the stocked infectious fish mature. There was a second decrease in age-0 fish even after hatchery practices had been restored to stocking only 5% infectious fish. This results from vertical transmission in the wild. The prevalence of Rs in wild spawners was increased so there were more offspring infected via vertical transmission. This resulted in continued losses of juvenile fish. The same qualitative result occurs when hatchery biosecurity practices only declined to stocking 15% infectious fish, though the numerical response in such a case is less severe.

Increases in stocking to $8 \times 10^6$ fish initially increased the density of the population of young fish (Fig. 7A). There was, however, a slight decrease in the density of older fish initially due to horizontal transmission. There was also additional mortality due to disease upon return to the previous stocking level, but this too was relatively small. This was not surprising, since increases in stocking when only 5% infectious fish are stocked provided positive gains at equilibrium (Table 3). Declines in hatchery biosecurity were more likely to cause declines in population than disease-related mortality associated with increased stocking.

**DISCUSSION**

Models enable the organization of information that allows formulation of meaningful hypotheses and identification of priority research. The development of models of fish–pathogen systems is critical to managing fish health (Peeler et al. 2007). In the absence of empirical data upon which to base parameter estimates,
it is best to emphasize the qualitative behavior of the models and their sensitivity to plausible parameter values. Such qualitative conclusions are useful in providing a basis for determining critical areas of uncertainty and priorities for future research. Such modeling results should not be viewed as prescriptions for future management; and as more information and data become available, the model results may change, at least quantitatively. The value of these models is that they provide a way to formalize and explore the consequences of expert opinions about the dynamics of these systems and to understand how complementary bodies of theory (i.e., population dynamics and disease ecology) interact. A number of useful inferences can be drawn from this work about relationships among different components of the Lake Michigan *Renibacterium salmoninarum* (*Rs*) system. These inferences can help prioritize future research and inform management surveillance and experiments.

Our modeling results suggest, perhaps not surprisingly, that hatcheries may play an important role in Lake Michigan *Rs* dynamics, and that density management of chinook salmon can be important to pathogen dynamics. But the role of hatcheries is not independent of natural recruitment. An understanding of the interaction between wild recruitment and stocking is needed to better understand how the stocking of chinook salmon affects disease dynamics.

Holey et al. (1998) and J. G. Hnath and M. Faisal (*unpublished manuscript*) have expressed concern that hatchery biosecurity practices can affect *Rs* dynamics and outbreaks of bacterial kidney disease (BKD) in Lake Michigan. J. G. Hnath and M. Faisal (*unpublished manuscript*) state that practices such as using Heath-type stacking incubators can contribute to the spread of *Rs* among eggs. This effectively increases the rate of vertical transmission in hatcheries. The role of vertical transmission (or horizontal transmission among eggs) may not have been fully appreciated. Our results indicate that there are two effects of increased rates of infection in eggs. The first effect is clear: an increase in the number of infected eggs will lead to an increase in the number of infectious fish. The less obvious second effect is that age-0 fish that are born infectious (either due to vertical transmission or hatchery induced egg-to-egg transmission) represent an additional source of pathogen exposure for susceptible wild and hatchery age-0 fish. Our model also suggests that even short-term failures in hatchery procedures that result in releases of a high proportion of infectious fish can lead to a drastic increase in prevalence and potential decreases in stock size of both wild and hatchery salmon. Finally, increasing stocking rates do not necessarily overcome poor hatchery biosecurity with respect to density of older chinook salmon, due to disease-induced mortality and density-dependent compensation in wild recruitment (Table 3). To explicitly evaluate tradeoffs between hatchery practices that reduce prevalence and hatchery practices that produce more fish, one must also consider the relative costs of improving biosecurity and increasing output. Furthermore, managers need to consider the marginal benefits from having more fish, weighed against other possible spillover effects from introducing more pathogen. However, it does appear that there will be some level of hatchery-contributed prevalence that should be acceptable.

Increasing natural production of chinook salmon in Lake Michigan complicates management of *Rs*, and managers would benefit from a better understanding of the recruitment dynamics of Lake Michigan wild chinook salmon. Specifically, it would be useful to know if stocking of chinook salmon leads to compensation in wild production at current abundance levels as we assumed in our models. The density of chinook salmon also affects *Rs*-host dynamics. Thus, managers need to account for the response of wild chinook salmon when making stocking decisions both for disease and production objectives. Because of compensatory pro-

Fig. 7. Simulation results where the system is allowed to reach equilibrium, then shocked and allowed to return to equilibrium. Response is measured as the proportional deviation from the equilibrium population size for a given age class. (A) Effect of a three-year increase in stocking from $5 \times 10^6$ to $8 \times 10^6$ fish, assuming 5% infected stocked fish. (B) Effect of a three-year hatchery biosecurity breakdown so that the prevalence of stocked infectious fish goes from 5% to 95%, assuming $5 \times 10^6$ fish stocked.
cesses, it is possible that a reduction in stocking may not reduce the number of fish in the lake and may free resources to improve hatchery conditions. Table 3 shows that under certain conditions reductions in stocking coupled with improvements in hatchery biosecurity can lead to a greater number of older fish. Finally, under certain conditions, wild spawning fish may be less likely to create infected eggs than hatcheries.

Models that integrate population and epidemiological theory have been applied to fish (e.g., Des Clerrs and Wootten 1990, Murray et al. 2001), but seldom have been used to improve understanding and management of wild fish populations; but see Krocke et al. (2005) for an exception. Pathogen and disease models have not been explicitly considered in the leading fish population dynamics texts (Hilborn and Walters 1992, Quinn and Deriso 1999). These texts acknowledge the importance of disease in shaping mortality, but simply lump disease-induced mortality into unmanageable natural mortality. Moreover, such natural mortality estimates are applied to the entire population (combining health classes), which implies that the proportion of fish in a specific health class does not change. For some populations, mortality may change substantially as a result of host–pathogen dynamics. This is especially a concern in systems where a substantial number of fish are stocked and where invading species may simultaneously introduce new pathogens. More careful consideration of the role of host–pathogen dynamics is merited in these cases, and the development of models is critical to “building an ecological approach to fish health management” (Stephen and Thorburn 2002). In this paper we have introduced a mechanistic approach for modeling the role pathogens play in shaping fish population dynamics.

In developing our model of the Rs–salmon system in Lake Michigan we have included realistic yet simple assumptions about the system. Extensions that include more complex assumptions are left for future research. These include more explicit modeling of the interaction between nutrition and disease advancement to infection and the effects of selection against disease-susceptible salmon strains.

The disease ecology literature generally includes latency only as time delay (Heesterbeek and Roberts 1995, Murray et al. 2001). We have provided a first attempt to include additional ecological realism. We assume that the probability that a fish becomes infectious given that it is exposed is a function of ecological conditions (i.e., the probability of an exposed fish becoming infectious increases with density, a proxy for stress). This relationship was emphasized in our expert workshops. Stress, however, can have complex interactions with pathogen virulence (Lafferty and Holt 2003). While decreased food resources are believed to have been important in the Rs outbreak in Lake Michigan in the late 1980s (Holey et al. 1998), a similar Rs outbreak has not been observed in association with more recent alewife declines in Lakes Michigan or Huron, suggesting the possibility of increased infection resistance in Great Lakes chinook salmon. So, while our model may help explain past events, and provide general insight into fish health management, it cannot necessarily predict future disease events.

The hypothesis that chinook salmon in Lake Michigan went through a genetic bottleneck imposed by Rs, and that the surviving salmon are genetically predisposed to resist BKD was discussed in our workshops. Such a possibility should be considered when exploring the long-run dynamics of an endemic pathogen. Our model cannot provide evidence for or against this hypothesis. A simpler explanation, supported by our model, is that hatchery biosecurity practices have substantially improved. A more comprehensive and model-based Rs assessment program could help discriminate among these alternative explanations.

We recommend five priorities for improving understanding of Rs dynamics in Lake Michigan. We suspect that these recommendations would be applicable to other fishery–pathogen systems, particularly where hatcheries supplement fish stocks.

First, it is imperative that researchers have good understanding of standard demographic parameters (i.e., the natural mortality rate and the stock–recruitment relationship of wild spawning chinook salmon in Lake Michigan). The prevalence at equilibrium for wild-spawned chinook salmon was more sensitive to these parameters than to the disease-related parameters. It is important for managers to have better understanding of the interactions among natural mortality, wild recruitment, stocking, and disease transmission. Understanding the stock–recruitment relationship is a critical element to understanding vertical transmission, which is the next research recommendation.

Second, the role of vertical transmission should be further examined. Fenichel and Horan (2007) have shown that vertical transmission can have important management implications in terrestrial systems. Assessing size of runs of wild-spawning chinook salmon and testing resulting eggs would provide information both about wild recruitment and vertical transmission in the wild. Alternatively, wild-spawned smolts could be collected and examined for Rs, and then prevalence rates could be compared to those being released from hatcheries. Ultimately, prevalence goals for hatcheries will need to consider vertical transmission rates in the wild.

Third, the model we used to represent the hypothesized link between nutritional stress and the advancement (function Q) of chinook salmon hosts from exposed to infectious states (Holey et al. 1998) needs to be further investigated. Rs dynamics are relatively insensitive to parameters in the Q function, but little is known about this relationship. The predator–prey dynamics of Lake Michigan salmonines have been the subject of considerable study (Szalai 2003, Madenjian et al. 2005).
al. 2005), but this needs to be coupled with a better mechanistic understanding of how nutritional stress affects R0 dynamics.

Fourth, we urge a more structured approach to assessing fish health at the population level. It is imperative that sampling be designed to estimate epidemiological parameters (see Williams and Moffitt [2001] for a discussion of this topic), and managers should not rely on opportunistic sampling or only on testing fish contributing gametes to hatchery facilities. Fig. 4 illustrates alternative hypotheses about model structure. Given a statistically robust sampling design, for wild and hatchery fish, one of these hypotheses is likely to find greater support from the data. Stocks that are regularly assessed may have sampling designs adequate for fish health assessment already in place. Additionally, statistical approaches that integrate stock and health assessment should be the subject of future research, but improved health assessment sampling designs can yield a wealth of information prior to the development of methods for full integration of stock and health assessment.

Finally, more explicit consideration should be given to the tradeoffs associated with increasing fish production in hatcheries and increasing fish production in the fishery and the contribution to angler welfare (see Horan et al. [2008] for an example of such a study with deer and livestock). While fish populations provide valuable ecosystem services, their production in hatcheries may create externalities in the form of disease that merit explicit consideration.

Alone, models cannot resolve all fishery management questions. However, models are a necessary component of fishery management and research. Models play a major role in stock assessment and harvest policy (Hilborn and Walters 1992, Quinn and Deriso 1999), but have played virtually no role in wild fish health management. In the future, we hope that the same analytical and quantitative rigor that has been applied to other areas of fisheries management is applied to fish health. In this paper, we have developed such a model to address the effects of a pathogen on a fishery. We hope that this model can serve as an example for addressing other emerging and chronic fish health issues.

Acknowledgments

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Literature Cited


**APPENDIX**

Elasticity results for wild and hatchery chinook salmon by age and health class with the full transmission and vertical infection going to the infectious health class (*Ecological Archives* A019-031-A1).