Journal of Aquatic Animal Health 10:160–171, 1998

Factors Involved in the Dissemination of Disease in Fish Populations

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Abstract.—Infectious diseases have been observed in both human and animal populations for millenia. Unlike diseases of ''higher'' animals, the dispersal of disease in fish populations rarely has been studied quantitatively. However, the principles that govern the spread of diseases of humans and other mammals should, with modification, be applicable to the study of infectious diseases in fishes. Disease in populations is a dynamic phenomenon; fluctuations in prevalence and impact are dependent on the interactions among host, pathogen, and environment. Models of the dynamics of infectious diseases in salmon and other fishes can be constructed and refined to reflect the characteristics of diseases by integrating the most important factors in the process. Among the factors that have been shown to be important in other systems are the ''contagiousness'' of the pathogen (transmission coefficient, β), duration of infection, host population density, development of immunity, and efficacy of therapeutants.

Microbial pathogens have preyed on fish for eons and have coevolved with them. These cohabitants have, in a general way, established an overall equilibrium with their hosts in their natural habitat. However, this equilibrium is unstable and, when viewed at a regional or local rather than at a global level, may result in epizootic disease. With the advent of fish culture and the development of the science of microbiology in the 19th century, more attention was paid to the occurrence of epizootic diseases in cultured fishes. The development of aquaculture has shifted the focus from the health of fishes in ecosystems (which is indirectly affected by anthropogenic involvement) to direct oversight and manipulation of captive populations. The artificial rearing of fishes has led to the exacerbation of diseases that previously existed in wild populations. Currently, a contentious issue is the question of whether cultured fish are the source of diseases inimical to wild, especially endangered, populations of fish (most notably salmonids). Similarly, those in the aquaculture community are concerned about the converse: are wild fish transmitting disease to cultured fishes? These are among the plethora of unanswered questions about dissemination of disease in fish populations.

Fortunately, the intricate complexities of ecosystems and the somewhat less complex culture environment, intimidating as they are, may yield some answers if approached rationally. The objective of this paper is to review some of the most important factors that determine the establishment and course of infectious diseases in fish populations. It has been long understood that intercalations of host, agent, and environmental factors determine, to a large extent, the course of disease in wild or cultured fish. The relationships among these variables have been analyzed empirically; it is apparent that mathematical methods can be applied to the study of diseases caused by a variety of pathogens in a variety of host population structures. In this sense, fish are no different from humans and other terrestrial animals when we address the factors which affect how diseases impinge on a population; they are simply wetter.

Mathematical models are used commonly for the estimation of the dynamics of fish populations (e.g., Weatherly and Gill 1987), especially commercially exploited species. There have been few similar studies for the diseases of fishes and their impacts on specific populations. Disease dynamics have been studied extensively in humans and to a lesser extent in other animals, including populations of some wild animals (reviewed in Anderson and May 1979, 1982; May and Anderson 1979; Grenfell and Dobson 1995). Models derived from mathematical simulations, however, vary in their ability to emulate real world situations, in part because they are dependent on the accuracy of the data used to construct the models. Simple deterministic models (those based on preselected variable values) can generally predict the course of disease; more complex deterministic and stochastic models (those which incorporate probabilities

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of parameter values) incorporating myriad variables are closer to reality. For fishes, there have been a few mathematical treatments of the disease processes in feral populations of Atlantic herring *Clupea harengus* affected by *Ichthyophonus hoferi* in the North Sea (Patterson 1996) as well as of lymphocystis in European flounder *Platichthys flesus* in the same region (Lorenzen et al. 1991). Laboratory experiments have been carried out to define parameters of disease dynamics for infectious pancreatic necrosis disease in cultured trout (Bebak 1996) and for *Gyrodactylus* in guppies *Poecilia reticulata* (Scott and Anderson 1984). Thus, some preliminary work has been done in developing sophisticated models of disease for fish. However, even with some rudimentary experimental work and conservative assumptions, basic models of diseases can be constructed which may reflect the process of a wide variety of diseases in fish. More complex models can then be refined from these preliminary efforts.

Types of Pathogens

As a convenient dichotomy, infectious pathogens have been classified into two groups according to their inherent characteristics. Anderson and May (1979) classified those microscopic pathogens that replicate to high numbers in the host, have a short replication cycle relative to the life span of the host, and generate a significant protective immune response as microparasites. This group includes viruses, bacteria, chlamydia and rickettsia, and protoctistans (protozoans). These pathogens also require only a single host during their life cycle, although the hosts affected may belong to more than one species. The second group of pathogens is the macroparasites, which are larger in size (often visible with the unaided eye), do not multiply to large numbers while in the host but rather infect the host at a variable level during contact–transmission, and then mature rather than replicate within the host. These pathogens also generally fail to induce a protective immune response, so reinfection is commonplace. In addition, macroparasites often have complex life cycles involving multiple hosts and significant morphological metamorphoses. This group includes the monogeneans and digeneans, nematodes, cestodes, copepods, et cetera. In terms of developing models of disease, the pathogens affecting single hosts tend to be simpler to model; models derived for pathogens with multiple hosts, such as *Myxobolus cerebralis*, are inherently more complex (Roberts 1986).

Major Factors Involved in the Process of Disease

One of the basic tenets of epidemiologic modeling of disease is that the factors which determine the progress of disease interact in a multiplicative rather than an additive manner. Some essential relationships between pathogen and population are based on the law of mass action originally promulgated for chemical reactions of molecules (Anderson and May 1979). Therefore, the mathematical constructs deal, in large measure, with the density of individuals per unit area (or volume for fish). Consequently, the models are based on density parameters, although other approaches dealing with life spans and duration of infectiousness have been established (Mollison 1995b).

When whole populations are examined to determine if and how a disease develops, the ''natural'' population flux dictates the framework of the model to be developed. If one examines a single episode of disease, the assumption is made that there will be no influx of animals due to birth or immigration and no efflux of animals due to emigration. When acute or subacute diseases are considered this assumption is appropriate because during the short time of epizootic disease, the core population changes little, except for disease-related mortality. On the other hand, when dealing with chronic or recurring diseases that span year-classes and extend to time periods that include a new susceptible generation of animals, this assumption is not valid. This is also the case when one considers long-term population trends with the objective of estimating the impact of disease over many years. Incremental reduction of spawning productivity can be magnified over generations and can lead to an accumulated impact more serious than disease on a single generation.

For the short-term, single epizootic situation, the following equation holds:

$$N_t = S_t + I_t + R_t; \qquad (1)$$

N = the population, S = the number of uninfected animals susceptible to the disease, I = the number of infected individuals, and R = the number of ''removed'' individuals—those that are immune and no longer susceptible or have died. At any given time t, during the course of an invasion by a pathogen, this dynamic relationship will hold true. This type of model is termed a deterministic *S–I–R* model (Anderson and May 1979). Under special circumstances where the host never becomes immune and no disease-specific mortalities

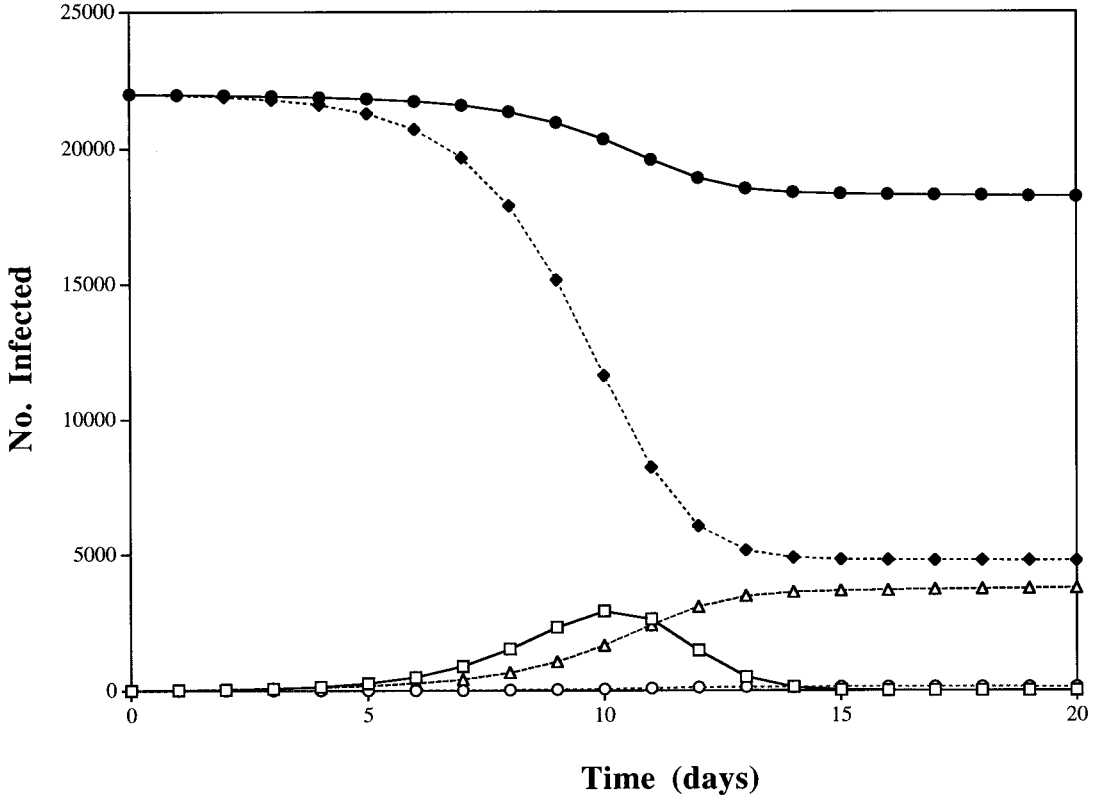

FIGURE 1.—Effects of disease on populations and relative composition of susceptible (♦), infected (□), dead (△), and recovered (○) classes within the total population (●). The initial susceptible population is 22,000; $\beta = 1.5$ effective contacts/d; natural mortality is 0.2/d; disease mortality = 50%; rate of immunity/recovery = 49.8%. Ten infectious individuals were added at time 0.

occur, the equation reduces to a simplified *S–I* model. A general graphic representation of the components of the *S–I–R* model is indicated in Figure 1.

Factors that can affect the subsets of individuals in the population are elements of the environment, characteristics of the host, or characteristics of the pathogen (Snieszko 1978). Characteristics of the pathogen include the ability to infect a particular species of animal, invasiveness (pathogenicity), and virulence factors. Descriptions of these characteristics are detailed in several textbooks on fish diseases (e.g., Roberts 1986; Austin and Austin 1987; Wolf 1988). Similarly, characteristics of the host have an effect on disease production in that a particular species, or even stock, may be more or less susceptible to being infected by a particular pathogen. Also, individuals of a particular stock, once infected, may not show clinical signs of disease. The literature is replete with examples of fish stock variability in resistance to diseases caused by pathogens such as infectious pancreatic necrosis virus (IPNV) in trout (Silim et al. 1982); infectious hematopoietic necrosis virus (IHNV) in salmon (Amend and Pietsch 1977); channel catfish virus in catfish (Plumb et al. 1975); or *Aeromonas salmonicida, Vibrio salmonicida,* and *Renibacterium salmoninarum* in Atlantic salmon *Salmo salar* (Gjedrem and Gjoeen 1995). In addition, certain diseases are only manifest during certain life stages of the host. In the case of viral diseases, for example, IPNV, IHNV, and viral hemorrhagic septicemia have historically been associated with disease only during the early life stages of salmonids (Wolf 1988).

The environment can have a significant influence on the transmission or development of disease. The population density, although not strictly an environmental parameter, is crucial to the dissemination of disease because a prime factor in epizootic disease is the frequency of contact between infectious and susceptible animals. Whether

TABLE 1.—Estimated duration of infectiousness of selected salmonid pathogens.

Pathogen	Duration of infectiousness	Reference
Vibrio anguillarum	2 weeks	Austin and Austin (1987)
Aeromonas salmonicida	2 weeks	Austin and Austin (1987)
Yersinia ruckeri	2 weeks	Austin and Austin (1987)
Infectious hematopoietic necrosis virus	2 months	Wolf (1988)
Infectious pancreatic necrosis virus	Lifelong (?)	Wolf (1988)
Viral hemorrhagic septicemia	1 year	Wolf (1988)
Renibacterium salmoninarum	Lifelong (?)	Austin and Austin (1987)
Myxobolus cerebralis	Lifelong (?)	Roberts (1986)
Ichthyophthirius multifiliis	About 6 months	Roberts (1986)

the contact is direct or indirect, from fish to fish or through an intermediate host, infection cannot occur unless the susceptible animal comes in contact with the pathogen. Because the total amount of a given pathogen in the water is determined by both the quantity released by an individual and the total number of fish in the area, population density can affect pathogen transmission. Other environmental factors may also influence the disease process by virtue of their impact on the survival of the pathogen in the environment or by affecting the host defense mechanisms. For example, temperature also plays a significant role in disease development. Although such diseases as vibriosis, enteric redmouth, and furunculosis tend to occur at temperatures exceeding 10°C, marine flexibacteriosis and freshwater cold-water disease occur at temperatures below 10°C (Roberts 1986). In addition, water flow and water chemistry can affect disease. Fast flow rates may either shorten the contact between a host and pathogen or disseminate pathogens more effectively than slow flow rates. Chemical components in the water can directly inactivate some sensitive agents.

A population of fish under invasion from a pathogen comprises three mutually exclusive cohorts that can change relative to each other during the course of disease. The susceptible group (*S*) is composed of those individuals that can become infected on contact with a pathogen. Their susceptibility is dependent on a general level of resistance that is inadequate to prevent the pathogen from invading the host. This level is predicated on species and innate stock resistance, as mentioned above, as well as prior exposure and the development of acquired immunity by humoral or cellular responses that confer protection.

The infected cohort (*I*) is made up of susceptible individuals that have contacted the pathogen and become infected. During the initial phase of the infectious process, the latent or prepatent phase, the host is infected but incapable of transmitting the pathogen to other susceptible fish. Subsequent to this period the infected host becomes infectious for a period characteristic of a particular host–pathogen system. This capacity for infecting others, the infectious state, may occur prior to the development of overt signs of disease or after signs appear. Another temporal factor associated with the infectious group is the duration of infectiousness. It is intuitively obvious that the longer an individual remains infectious, the greater the probability that it will transmit a pathogen to other susceptibles in the population. Likewise, the shorter the duration of infectiousness, the lower the probability that the pathogen will be disseminated to others in the population. The duration of infectiousness for fish pathogens has not been explicitly studied, but as shown in Table 1, an estimated length of infectiousness for selected pathogens of salmonids varies from weeks to years.

In most disease states, the host develops immunity after some period of infection. Those that become immune or refractory to reinfection are no longer a component of the susceptible population and become members of the removed cohort (*R*). As mentioned above, however, not all pathogens induce immunity, and therefore, even individuals that have been previously infected by these pathogens may become reinfected upon later exposure. Unfortunately, unlike several childhood viral diseases of humans that have been extensively studied, the immunity induced to fish pathogens is not lifelong; thus at some point, immune animals revert to their susceptible status. The only permanently nonsusceptible members of the removed cohort are those that have died. The proportion of these individuals is strictly associated with the specific disease mortality rate, which can vary markedly from episode to episode of disease.

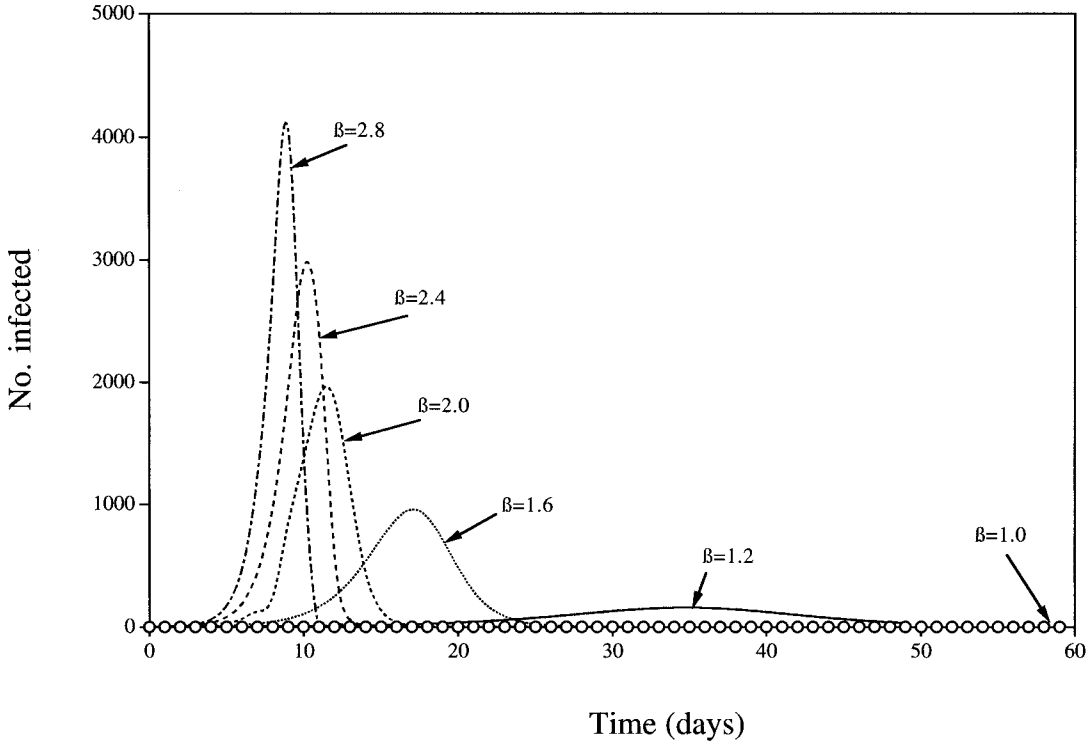

FIGURE 2.—The effect of changes in transmission coefficient, β, on the number of animals infected over time in a susceptible population of fish. An initial population of 10,000 susceptible individuals is assumed with the introduction of a single infectious individual at time 0. Beta varies from 1.0 to 2.8 contacts/d as listed. At β = 1.0, no infections occur (○); as β increase from 1.2 to 2.8 there is a decrease in the time to peak incidence and an increase in the incidence.

Transmission of Infection

The components of the *S–I–R* disease model discussed above are dynamic in time (and space). The relative movement of fish from one cohort to another is determined by the efficiency of pathogen transmission. The so-called ''force of infection,'' or rate of change of disease in a population, is determined by the following equation:

$$\text{force of infection} = \beta \times I \times S. \qquad (2)$$

In essence, the frequency of contact between an infectious individual (*I*) and a susceptible individual (*S*) multiplied by the transmission coefficient (β) will yield the disease incidence. Although other factors can alter the disease state, this is the prime interaction necessary for the development of epizootics.

The primary component of transmission is the transmission coefficient, β, which is defined as the efficiency of transfer of the pathogen from a single infectious individual to other susceptibles in the population. This transmission coefficient is independent of the density of individuals and relates to the probability of infection when one infectious individual transfers, directly or indirectly, a pathogen. A low β, or inefficient transfer, would probably not result in epizootic disease, whereas a large β will result in an epizootic. Even relatively small changes in β can markedly affect the development of disease (Figure 2). At β = 1.0, no infection occurs. Note that a change in β from 1.4 effective contacts per 10,000 fish/d to 2.8 contacts markedly affects not only the incidence of infection but also the time at which the peak infection occurs and the duration of the infection in the population. Beta, as might be expected, is affected by many factors, the most important of which are summarized in Table 2.

Basic Reproductive Rate R_0

When a pathogen is first introduced into a susceptible population of fish, the process of infectious disease is initiated. The components of an epizootic can be described as arrival, establish-

TABLE 2.—Factors affecting the transmission coefficient, β.

Host resistance factors
Species
Age
Natural immunity
Induced immunity
Pathogen factors
Ability to infect species
Dose
Vertical transmission
Environmental factors
Population density
Temperature
Water flow
Water chemistry

ment, spread, and persistence. The rates and intensities of these components can be calculated based on the basic reproductive rate of the pathogen, R_0. The R_0 calculation is based on β, the population density, and the duration of infectiousness. Simply expressed, R_0 is the number of successful infectious contacts per unit time made by an infective individual in a wholly susceptible population (Mollison 1995a). Consequently, if R_0 is less than 1, either no epizootic will be established (if R_0 is low enough) or the disease will die out and the pathogen will be eliminated from the population; if R_0 exceeds 1, an epizootic will occur with the severity dependent on the magnitude of R_0. If R_0 is slightly above 1, a persistent (enzootic) state of infection will occur with a low prevalence of infected animals in the population. If R_0 for a pathogen is large, it will infect most, if not all, susceptibles and eliminate itself from the population; for example, R_0 for measles in humans is approximately 15 (Anderson and May 1982), and it is known that this contagious viral infection is eradicated in a population after an epidemic and only reoccurs with the arrival of new susceptibles, as well as an infectious individual, into the population. If R_0 for a pathogen is low, it will be unable to infect an adequate number of hosts to establish and spread and, thus, will be eradicated; if R_0 is near 1, the pathogen will infect a proportion of the susceptibles but not enough to deplete the susceptible population to the point of elimination. Thus, pathogens that are of intermediate contagiousness tend to persist in populations for long time periods, perhaps indefinitely. Likewise, pathogens that have an intermediate mortality rate will not deplete the population of susceptibles so rapidly that the there will not be enough new hosts to infect.

Long-Term Effects of Disease: The Cycle of Disease

The discussion above described the process of disease in the short term, during the course of a single epizootic in which nondisease population fluctuations are discounted. During longer periods of time, however, there is considerable population fluctuation due to natural mortality from predation and other noninfectious agents, immigration and emigration, and influx from new progeny. The flux of any natural population is regulated by a carrying capacity characteristic of a given species and environment (Weatherly and Gill 1987). The presence of disease can alter this equilibrium under certain conditions. Figure 3 diagrams the interrelationships that occur in a deterministic *S–I–R*

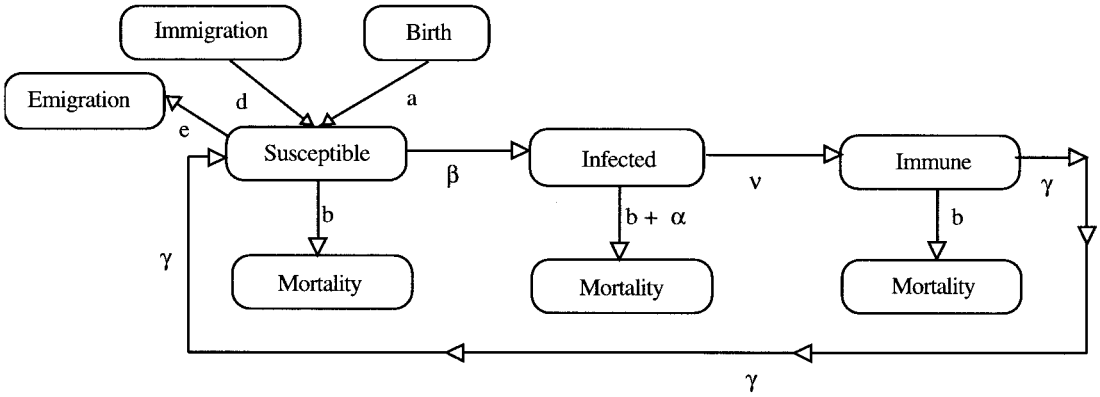

FIGURE 3.—The cycle of disease in a population over the long term: a = birth rate; b = natural mortality rate; d = recruitment excluding births; e loss by emigration; α = disease-specific mortality rate; ν = recovery (immune) rate; γ = rate of loss of immunity.

TABLE 3.—Relationship between β (the transmission coefficient) and the impact of disease on populations. Recruitment is live births (a) plus immigration (d, which excludes live births).

Relationship	Population effect	Pathogen persistence
$\beta <$ natural mortality (b)	None	Eliminated
$\beta >$ b, but $\beta <$ recruitment (a + d) + disease mortality (α)	None	Persistent, enzootic
$\beta >$ (a+ d) + α, but $\beta <$ (a + d) + recovery (ν) − b	Reduction	Persistent, enzootic
$\beta >$ (a + d) + ν − b	Reduction	Persistent, epizootic

model of disease. Natural increases in the population occur through recruitment of new progeny and immigration; losses occur due to ''natural'' mortality and emigration. Disease can markedly affect this intrinsic growth rate. If the disease is a ''benign'' one that does not directly kill fish or contribute to the loss of fecundity, there will be no effect on the population, even if the pathogen infects a high proportion of the population. A disease that has a direct mortality or reduces fecundity can alter the population to a greater or lesser extent. Because the growth rate of the disease is essentially dependent on β, the rate of conversion from susceptible to infected, the relative magnitudes of β and the intrinsic growth rate of the population will determine the outcome of disease in the long term, as shown in Table 3. Where β is small, disease will not regulate the final population size nor will the pathogen be retained. As β increases, however, the pathogen can be retained in the population and, if β is high enough, the pathogen can regulate the population size significantly.

Thus, depending on the contagiousness of the pathogen, the level of infection may be transient, minimal, enzootic, or epizootic. Again, it should be noted that if a disease causes no specific mortality and does not affect reproduction, it will not affect the population size or growth rate in the long term. In wild fish, disease may affect population size indirectly, for example, by weakening the host and making it more susceptible to predation. In cultured fish there are also other adverse effects that can be economically important despite a lack of direct deaths. For example, decreased growth rates at production facilities can cause economic loss, and if market-sized fish have visible lesions or skeletal deformations the market price of the product can be reduced.

Other Factors in the Dispersal of Disease

Although the basic reproductive rate of the pathogen is the primary component of the dynamics of disease, many other factors influence that component. Some of the main factors are discussed below.

Population density.—Because the potential for development of disease in a population depends on the contact rate between infectious and susceptible animals, the frequency of that contact is dictated by the population density. In any population, successful introduction of a pathogen depends on the host density being greater than a characteristic threshold density (N_t); if the host population density is below this level, no disease will occur (Grenfell and Dobson 1995). This spatial factor is inversely dependent on β: the greater the value of β, the smaller the critical population size for disease establishment, since transmission is more efficient. If *S* were plotted against *I* (Figure 4), the threshold density would be the point below which no new infection occurred (incidence = 0; for the hypothetical example presented, $N_t = 625$). The number of infectious animals would begin to decrease until either a steady state occurred (enzootic infection) or the pathogen was eliminated from the population. Another parameter that relates to the density threshold is the duration of infectiousness. With a longer period of infectiousness, more potentially effective contacts will occur and the threshold density will decrease. Therefore, quickly resolved acute diseases, such as the gram-negative septicemias of fish (Roberts 1986), may not remain in the population and may require a host population increase beyond the threshold density to become established again. Conversely, diseases with protracted infectious periods have a longer opportunity to effect transmission to susceptibles and would not require as high a host density as acute infections. For fish pathogens such as *R. salmoninarum* and IPNV, which are known to be harbored for long periods of time, this would imply that the N_t for these pathogens is small. However, long-term infections may not be transmitted over long periods of time, as for example in tuberculosis of humans (Brook and Madigan 1988).

Vertical transmission.—Another survival mech-

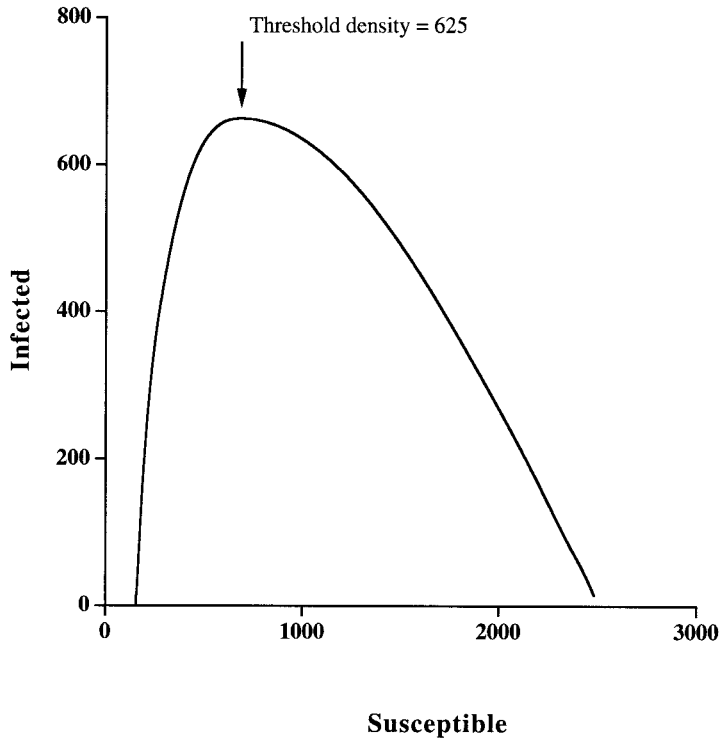

FIGURE 4.—Number of susceptible fish in a population versus number of infected fish. Original population = 2,500 fish; number of infectious fish at time 0 = 15. Threshold density (N_t) is inflection point (number of newly infected fish or incidence = 0) or maximum number of infected fish.

anism that pathogens have evolved is their ability to be passed directly from parent to progeny, that is, vertical transmission. There are several important diseases of fish in which this mechanism is operative, such as IPNV (Wolf 1988), IHNV (Mulcahy and Pascho 1985), channel catfish virus (Wolf 1988), and *R. salmoninarum* (Brown et al. 1990); and there are several others in which it is suspected, such as pike fry rhabdovirus (Roberts 1986) and *Flavobacterium psychrophilium* (W. Cox, California Department of Fish and Game, and R. P. Hedrick, University of California-Davis, personal communication). Because of the increased ability to transmit the pathogen under these circumstances, a low threshold population density is often sufficient to initiate an epizootic or maintain an enzootic state. In essence, the vertically infected fish serve as an initiating point for infection and, if conditions are favorable for the development of disease, epizootics can ensue. Another factor that comes into play with the success of vertical transmission is the likelihood that animals acquiring a pathogen from parents tend to harbor them for long periods, as in the examples cited above, and can extend the duration of infectiousness.

Multiple hosts.—Microparasites that infect a single host with no intervening secondary host may behave according to simple mass action principles in terms of disease development. Those microparasites and macroparasites that require more than one species of host to complete their life cycles must be described by more complex models. Some examples of fish pathogens that have multiple-host life cycles are listed in Table 4. Since there is more than one host involved, the models for dynamics involve essentially a multiplicative interaction of *S–I–R* among hosts. For example, in *Myxobolus cerebralis* infections, R_0 is dependent on fish density (the ratio of the vector to the fish host), contact rate, β, immunity, natural survival rate, etc., as well as on survival of the pathogen and its rate of development while in the worm host or in the environment, the latent period in the worm, and the survival rate of the worm. Models of important human diseases, such as malaria, with complex life cycles have been developed (May 1977), and if the appropriate information on the

TABLE 4.—Examples of salmonid pathogens that involve multiple hosts in their life cycles.

Pathogen	Group	Additional hosts
Myxobolus cerebralis	Myxosporean	Tubificid worms
Ceratomyxa shasta	Myxosporean	Polychaetes
Cryptobia sp.	Flagellate	Leeches
Sanguinicola sp.	Digenean	Snails
Nanophyetus salmincola	Digenean	Snails, mammal
Eubothrium sp.	Cestode	Copepods
Diphyllobothrium sp.	Cestode	Copepods, mammal
Philonema sp.	Nematode	Copepod
Philometra sp.	Nematode	Copepod

various components is available, there is no reason why models of infection cannot eventually be constructed for fish diseases such as whirling disease and others that have complex life cycles.

Spatial considerations.—The dynamic models described above assume homogeneity of the population with respect to both time and space, a simplistic assumption. This assumption, however, is probably valid for diseases in aquaculture, in which the densities are high and individuals tend to mix within the constraints of troughs, raceways, ponds, or seacages. This movement of potentially infectious individuals within a confined space over a long period will lead to spatial homogeneity. Also in aquaculture, the densities do not change markedly with time. Once a year-class has been placed into a container, they are graded at intervals and split to maintain appropriate, relatively constant densities.

On the other hand, in wild fish ecosystems, neither of these constraints is operable. For most of their life cycles, the salmonids are not particularly social and tend to occupy spatial niches separate from others of their own species and adhere assiduously to cover (Weatherly and Gill 1987). Thus, for a given stretch of river, stream, or lake, there are pockets where the local densities are high and others where few, if any, fish reside. This patchy distribution can promote the retention of disease, which may not otherwise occur if the population were distributed homogeneously; it would also protect a proportion of the population from infection. Likewise, during the annual—and longer—spawning cycles of the salmonids, a large fluctuation in density is promulgated by the spawning process.

During spawning season, higher concentrations of fish are migrating upstream to spawn and occupying redds in close proximity to each other, thereby increasing the probability of pathogen transfer. If spawning fish are infectious, they may consequently transfer the infectious agent directly to progeny or to susceptible fish residing nearby or downstream. As long as the parent fish is infectious, this could occur whether or not the disease is manifest at the time of spawning. This characteristic density increase is also manifest for the embryonation period and the fry stage when young-of-the-year fish are in the gravel on the redds and during outmigration. These types of density perturbations are also found for other wild and domesticated animals that mate only at relatively circumscribed periods, as compared with animals such as humans, which produce young at a rate unrelated to season. Consequently, for fish in the wild, adjustments must be made in models to deal with the relatively episodic but predictable changes in densities, as compared with a constant change over time.

Attempts at Disease Control in Ecosystems: Management Implications

The reduction of disease in wild mammalian and avian populations by human intervention has been effective in some instances (e.g., rabies in foxes, brucellosis in bison, botulism in ducks), for which active management practices have been employed (Peterson et al. 1991; Grenfell and Dobson 1995; Wobeser 1997). The ability to control diseases in wild fishes should be possible in concept, if there is an interest in doing so and if the economic and environmental price is acceptable. Control of disease in wild populations takes several forms, each directed at reducing R_0 to less than 1.0, which results in the elimination of the pathogen from the population. There are four main types of intervention:

Culling.—This is a form of ''active host control'' (Grenfell and Dobson 1995). By reducing the density of a stock in a given area, the population can, and must be, reduced to a level less than N_t, which will result in the loss of the pathogen from the population. In aquaculture, splitting populations to achieve lower densities is often carried out to reduce disease. In severe cases, culling infected stocks is done to remove pathogens from populations. However, although this management technique is effective in reducing or eliminating disease, populations of many stocks—especially endangered stocks—in the wild are usually low, and reducing their numbers further by this method would generally not be a viable management choice.

Vaccination.—''Active disease constraint'' by the use of vaccines to control diseases of wildlife is prominent, especially with reference to rabies and brucellosis in elk and bison and to phocine distemper (Campbell and Charleton 1988; Peterson et al. 1991; Grenfell 1992; Grenfell et al. 1992). There are explicit levels of immunization that must be achieved to reduce the susceptible population below the level permissive for disease development. In effect, the proportion of successfully vaccinated hosts must be greater than $1 - R_0^{-1}$ to prevent disease. Therefore, the smaller R_0 is, the fewer animals must be vaccinated to prevent disease. For example, 16.7% of the population should be immunized if $R_0 = 1.2$ (just above the threshold of 1.0), 50% if $R_0 = 2.0$, and 80% if $R_0 = 5.0$. Vaccination of fish in the wild would be technically challenging, but possible, perhaps by using vaccine-impregnated caddis flies.

Many of the difficulties associated with immunization of fish in the wild are not operative in aquaculture facilities, and vaccination has been efficacious for a number of fish diseases (see, for example, Ellis 1988). If R_0 can be calculated for a particular disease in an aquaculture facility, it should be simpler to ascertain the levels of vaccination necessary to prevent disease with some precision. This could be of considerable use when designing a vaccine regime. Obviously, the effectiveness of a vaccine program is contingent on an efficacious vaccine that is protective for the duration of fish residence at the facility (to release or market size) and on the cost–benefit ratio for administration of the vaccine.

Chemotherapy.—''Active disease constraint'' via chemotherapy operates by decreasing the duration of infectiousness by lowering the period during which the pathogen can be transmitted. It is unlikely that this would ever be a feasible method of reducing disease in wild fish, due to technical and environmental constraints.

Reducing spread to cherished populations.—''Passive acceptance'' indicates there is no active effort to reduce disease in a population that is not a focus of interest. Rather, exposure of a population of concern to an infected population is prevented. Physical isolation of captive populations is practiced routinely in aquaculture and is frequently effective in decreasing the dissemination of disease to stocks that are of particular value. The judicious movement of fish within and external to watersheds that have certain pathogens is even now a common management strategy for reducing the probability of disease in valued populations.

Summary and Conclusions

This review was designed to outline the principles of epizootiology relating to the dissemination, dynamics, distribution, and control of infectious diseases in populations, with an orientation toward those that may come into play in fish populations. There are few inherent differences between fish and mammals with respect to the factors that affect disease transmission. Consequently, the principles that apply to ungulates should also apply to finned denizens of the aquatic world.

While the modeling of diseases in mammalian wildlife is becoming more frequent, as yet very little information about the topic is available for fish. Bebak (1996) has reported some basic studies delineating β for IPNV in brook trout *Salvelinus fontinalis* in laboratory experiments. Scott and Anderson (1984) were able to determine many of the parameters needed to construct models for the dynamics of *Gyrodactylus* in guppies. The groundwork of determining β and R_0 is a laboratory task that must be carried out for each of the infectious diseases of interest. Because many wild populations of fishes are, and have been, actively monitored for many years by fisheries agencies, there are considerable data that can be applied to population densities, water flow rates, etc. These data can be used in the construction of disease models. For example, Patterson (1996) estimated the impact of *Ichthyophonus hoferi* infection on populations of Atlantic herring in the North sea by using catch data coupled with the infection rate of samples taken for estimation of the prevalence of the fungus. From data in the literature on *Aeromonas salmonicida* (Hjeltnes et al. 1995), infectious pancreatic necrosis virus (Bebak 1996), and infectious hematopoietic necrosis virus (H. Ögüt and P. W. Reno, Oregon State University, unpublished results), it appears that cohabitation of susceptible salmonids with these pathogens is an extremely efficient method of transfer; thus, the β-values for fish pathogens may ultimately be higher than those seen for mammals. It remains to be seen whether there are unique components to the mechanisms of disease dissemination in fishes.

This report has not explored how pathogens initially arrive in a population. More often than not, this is a consequence of movement of infected fish into a susceptible population by humans (knowingly or unknowingly), rather than by natural dispersal. That is not to say, however, that this type

of anthropogenic effect is ultimately responsible for diseases in wild stocks. After all, these diseases were originally found in wild populations, and the advent of aquaculture exposed fish to conditions more conducive to disease development than would have occurred in the wild. Also not addressed is the double-edged sword of pathogen transmission from captive to wild fish and vice versa. Data exist to support both avenues, but wild fish defenders and aquaculturists tend to envision the transmission going primarily unidirectionally. If enough information is accrued to construct models of disease dissemination in these instances, it may be possible to mathematically assess the probability of these transfers. This would certainly be advantageous to all parties.

Acknowledgments

I thank Robert Olson for critical review of the manuscript. I also acknowledge and thank the members of the Pacific Northwest Fish Health Protection Committee (PNFHPC) for the opportunity to present this information at the meeting on Pathogens and Diseases of Fish in Aquatic Ecosystems Symposium. Funded by grant AGS663 of the Oregon Agricultural Experiment Station; this is publication 11339 of the O.A.E.S.

References

Amend, D. F., and J. P. Pietsch. 1977. Variation in the susceptibility of sockeye salmon *Oncorhynchus nerka* to infectious hematopoietic necrosis virus. Journal of Fish Biology 11:567–573.

Anderson, R. M., and R. M. May. 1979. Population biology of infectious diseases: part I. Nature (London) 280:361–367.

Anderson, R. M., and R. M. May. 1982. Directly transmitted infectious diseases: control by vaccination. Nature (London) 297:1053–1060.

Austin, B., and D. A. Austin. 1987. Bacterial fish pathogens: disease in wild and farmed fish. Ellis Horwood, Chichester, UK.

Bebak, J. 1996. Infectious diseases of salmonid fish: risk factors and disease dynamics. Doctoral thesis. University of Pennsylvania, College Park.

Brock, T. D., and M. T. Madigan. 1988. Biology of microorganisms. Prentice-Hall, Englewood Cliffs, New Jersey.

Brown, L. L., R. Ricks, T. P. T. Evelyn, and L. J. Albright. 1990. Experimental intra-ovum infection of coho salmon (*Oncorhynchus kisutch*) eggs with *Renibacterium salmoninarum* using a microinjection technique. Diseases of Aquatic Organisms 8:7–11.

Campbell, J. B., and K. M. Charleton. 1988. Rabies. Kluwer, Boston.

Ellis, A, editor. 1988. Fish vaccination. Academic Press, London.

Gjedrem, T., and H. M. Gjoeen. 1995. Genetic variation in susceptibility of Atlantic salmon, *Salmo salar,* L, to furunculosis, BKD and coldwater vibriosis. Aquaculture Research 26:129–134.

Grenfell, B. T. 1992. Parasitism and the dynamics of ungulate grazing systems. American Naturalist 139: 907–929.

Grenfell, B. T., and A. P. Dobson, editors. 1995. Ecology of infectious diseases in natural populations. The Newton Institute, Cambridge, UK.

Grenfell, B. T., M. E. Lonergan, and J. Harwood. 1992. Quantitative investigations of the epidemiology of phocine distemper virus (PDV) in European common seal populations. Science of the Total Environment 115:15–29.

Hjeltnes, B., Ø. Bergh, H. Wergeland, and J. C. Holm. 1995. Susceptibility of Atlantic cod *Gadus morhua,* halibut *Hippoglossus hippoglossus,* and wrasse (Labridae) to *Aeromonas salmonicida* subsp. *salmonicida* and the possibility of transmission of furunculosis from farmed salmon *Salmo salar* to marine fish. Diseases of Aquatic Organisms 23:25–31.

Lorenzen, K., S. A. Des Clers, and K. Anders. 1991. Population dynamics of lymphocystis disease in estuarine flounder, *Platyichthys flesus.* Journal of Fish Biology 39:577–587.

May, R. M. 1977. Togetherness among schistosomes: its effects on the dynamics of the infection. Mathematical Biosciences 35:301–343.

May, R. M., and R. M. Anderson. 1979. Population biology of infectious diseases: part 2. Nature (London) 280:455–461.

Mollison, D., editor. 1995a. Epidemic models: their structure and relation to data. The Newton Institute, Cambridge, UK.

Mollison, D. 1995b. The structure of epidemic models. Pages 17–33 *in* D. Mollison, editor. Epidemic models: their structure and relation to data. The Newton Institute, Cambridge, UK.

Mulcahy, D., and R. Pascho. 1985. Vertical transmission of infectious hematopoietic necrosis virus in sockeye salmon, *Oncorhynchus nerka* (Walbaum): isolation of virus from dead eggs and fry. Journal of Fish Diseases 8:393–396.

Patterson, K. R. 1996. Modelling the impact of disease-induced mortality in an exploited population: the outbreak of the fungal parasite *Ichthyophonus hoferi* in the North Sea herring (*Clupea harengus*). Canadian Journal of Fisheries and Aquatic Sciences 53:2870–2887.

Peterson, M. J., W. E. Grant, and D. S. Davis. 1991. Simulation of host—parasite interactions within a resource management framework: impact of brucellosis on bison population dynamics. Ecological Modelling 54:299–320.

Plumb, J. A., O. L. Green, R. O. Smitherman, and G. B. Pardue. 1975. Channel catfish virus experiments with different strains of channel catfish. Transactions of the American Fisheries Society 104:140–143.

Roberts, R. J. 1986. Fish pathology, 2nd edition. Bailliére Tindall, London.

Scott, M.E., and R. M. Anderson. 1984. The population dynamics of *Gyrodactylus bullatarudis* (Monogenea) within laboratory populations of the fish host *Poecilia reticulata.* Parasitology 89:159–194.

Silim, A., M. A. S. Y. Elazhary, and A. Lagace. 1982. Susceptibility of trouts of different species and origins to various isolates of infectious pancreatic necrosis virus. Canadian Journal of Fisheries and Aquatic Sciences 39:1580–1584.

Snieszko, S. F. 1978. Control of fish diseases. U.S. National Fisheries Service Marine Fisheries Review 40(3):65–68.

Weatherly, A. H., and H. S. Gill. 1987. The biology of fish growth. Academic Press, London.

Wobeser, G. 1997. Avian botulism—another perspective. Journal of Wildlife Diseases 33:181–186.

Wolf, K. 1988. Fish viruses and fish viral diseases. Cornell University Press, Ithaca, New York.