

## Fish Pathogen Screening and Its Influence on the Likelihood of Accidental Pathogen Introduction during Fish Translocations

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**Abstract.**—Fish translocations are an important tool in fisheries management, yet translocating fish carries the risk of introducing unwanted pathogens. Although pathogen screening can be a useful tool for managing the risk associated with fish translocations, screening cannot eliminate this risk. This paper addresses these problems by demonstrating that two elements must be considered when designing efficient and effective aquatic pathogen screening programs: (1) how many fish to screen and (2) how long to continue screening programs when repeated testing detects zero infected individuals. The chance that infected fish are translocated despite screening is the joint probability of (1) the failure of the screening to detect infected fish in the sample and (2) the actual presence of infected fish in the translocation batch. Our analysis demonstrates that transfer of an infected fish is most likely to occur at moderately low levels of pathogen prevalence because the probability of detecting at least one infected fish through screening increases as pathogen prevalence increases. Small screening samples (i.e., with a low number of individuals) are most likely to detect infected fish when pathogen prevalence is relatively high (i.e., >5%). Screening programs should terminate after some number of successive screening events in which no infected individuals have been detected. The number of screening events is a function of the cost of the screening program, the cost of a pathogen translocation, and the probability that an infected fish will be transferred. Furthermore, our analysis indicates that the cost of a disease outbreak has relatively little effect on the length of time the screening program should continue. A more pronounced result is that screening programs that are inexpensive or allow a higher probability of pathogen translocation should be continued longer.

Fisheries managers traditionally use fish translocations to help achieve a variety of objectives, including the improvement or rehabilitation of existing stocks, the establishment of populations in new areas, the reintroduction of extirpated stocks, and the provision of biological pest control agents.<sup>1</sup> Fish translocations, however, have been implicated in undesirable and costly pathogen translocations (Stewart 1991; Reno 1998; Murray et al. 2002). Consequently, interest in conducting risk analyses to evaluate the tradeoffs

between stock improvement and disease risk is increasing (Stephen 2001; Bartley et al. 2006). The risk of transferring pathogens is influenced by human decisions and management actions in addition to biological and environmental factors (Shogren and Crocker 1999; Caley et al. 2006); therefore, key components to managing and evaluating risk are programs that influence managers' decisions, such as pretranslocation screening of fish.

Pathogen screening does not eliminate risk and imposes additional costs on fish translocation programs. First, there is the marginal cost of screening each additional individual fish (e.g., diagnostic tests and opportunity cost of the agency personnel). Moreover, many aquatic animal screening programs require the sacrifice of the screened individuals, thereby reducing the number of individuals left for

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<sup>1</sup> This paper focuses on fish translocation; however, the techniques and conclusions also apply to hatchery management programs.

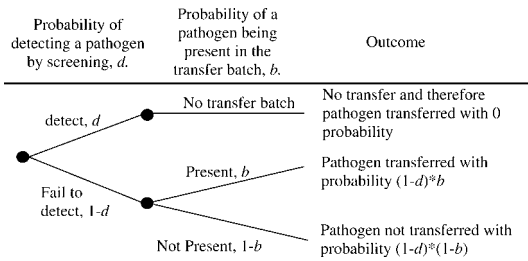


FIGURE 1.—Decision tree giving the probabilities of various outcomes when fish are screened for pathogens. The probability that a pathogen will be transferred is the joint probability that the pathogen is present ( $\text{Pr}[b]$ ) and that screening fails to detect it ( $\text{Pr}[1 - d]$ ).

transfer. Finally, the extra time that fish are held awaiting screening results before they can be transferred can reduce their survival. Given the benefits and costs of a screening program, an important question is how it should be designed. Mathews et al. (2006) advocate full veterinary screening of all mammals that are to be translocated, but they acknowledge that such screening is unlikely to be feasible, especially in the case where screened individuals must be sacrificed, and is likely to be extremely costly. A common approach in fisheries is to screen subsamples of the groups of organisms slated for transfer (USFWS and AFS-FHS 2005). This, too, often involves sacrificing the screened individuals.

Managers interested in designing screening programs to help evaluate and manage risk need to consider two questions: (1) how does the number of fish screened affect the likelihood that a pathogen is translocated and (2) how long should a screening program continue if no pathogens are found? The literature has focused mostly on statistical approaches for estimating prevalence from increasingly complex sampling designs (Williams and Moffitt 2001; Munoz-Zanzi et al. 2006), and less on how such estimates can be used to manage risk.

In this paper, we review screening design and explain the implications of pathogen screening for use in analyzing risks to fish health (not to be confused with surveillance). We emphasize the relationship between screening assumptions and objectives while addressing the two questions raised above. To illustrate key concepts, we present a case study of translocations of sea lampreys *Petromyzon marinus* in the Great Lakes undertaken as part of the sterile-male-release method for biological control in the St. Marys River integrated program for management of sea lampreys (Schleen et al. 2003; Twohey et al. 2003). We also critique the implementation of this screening program.

Ultimately, aquatic pathogen screening programs

need to be designed to achieve “acceptably low” probabilities of pathogen translocation. An interdisciplinary approach (e.g., a structured decision analysis; Peterman and Anderson 1999) is needed to determine the acceptable probability of pathogen translocation and overall risk. Such an analysis is beyond the scope of this paper. We present a narrower analysis that clarifies the linkages among screening program design, assumptions, likelihood of pathogen transfer, and risk analysis.

### How Many Fish to Screen for Unwanted Pathogens

Verifying the absence of a pathogen is all but impossible; given a probability greater than 0 that the organism is present, the harder one looks, the more likely one is to find it (Regan et al. 2006). Consider the situation in which a batch of fish is collected for the purpose of transfer. A subsample of fish drawn from the batch is first screened for pathogens. Assume that if an infected fish is detected in the subsample, then the remainder of the batch will not be transferred.<sup>2</sup> The transfer proceeds if no infected fish are detected in the subsample. Assume that screened fish are sacrificed and not transferred. Further, assume that the subsample of fish represents (i.e., is a random sample of) the transfer batch. That is, the probability that any given fish hosts a pathogen is independent of whether any other fish hosts a pathogen, and the probability that any given fish hosts a pathogen is the same (i.e., identical), regardless of whether the fish comes from the subsample or from the batch that is transferred.

A simple decision tree (Figure 1) illustrates that the relevant statistic is the probability that a pathogen is present among the fish released, given that the pathogen was not detected in the subsample. Therefore, the probability of transferring a pathogen, given subsample screening, is

$$\text{Pr}(t) = [1 - \text{Pr}(d)] \times \text{Pr}(b), \quad (1)$$

where  $\text{Pr}(d)$  is the probability of detecting the pathogen during screening, and  $\text{Pr}(b)$  is the probability that the transfer batch contains at least one infected fish.

To calculate the probability of failing to detect a

<sup>2</sup> This is a fundamental assumption in our analysis. It is, however, necessary to assume that some probability of pathogen transfer is acceptable. Therefore, it is conceivable that the prevalence in the source population would still be acceptably low so that the transfer would proceed when a small number of fish in a large sample tested positive. Williams and Moffitt (2001) and Munoz-Zanzi et al. (2006) provide techniques for estimating prevalence and confidence bounds when a proportion of fish in a sample test positive. We believe, however, that our assumption is typical of the way most screening programs operate.

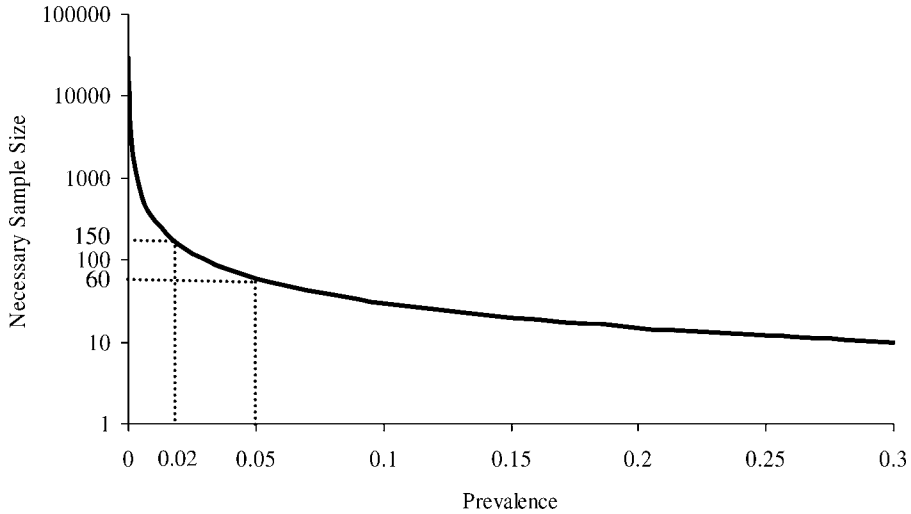


FIGURE 2.—Numbers of fish that need to be screened to achieve 95% confidence that a pathogen is absent at given prevalence levels (assuming that sensitivity = specificity = 1). The numbers of fish required at 2% and 5% prevalence are indicated by dotted lines. Note that the y-axis is on a log scale. Equation (2) was used to generate this graph.

pathogen (i.e.,  $[1 - \text{Pr}(d)]$ ) in a given sample, the Poisson or binomial distribution can be used (Green and Young 1993; Dell’Omodarme and Prati 2005). The Poisson distribution approximates the binomial distribution when the population (batch) is large; for small batches, however, representative sampling assumptions for both approaches may be violated (Dell’Omodarme and Prati 2005). We base our analysis on the Poisson distribution (but see the footnotes for the analogous equations for the binomial distribution). The necessary sample size,  $n$ , for detecting at least one infected fish from a population with a prevalence of infection  $m$  at a specified confidence level (probability)  $x$  is<sup>3</sup>

$$n = -\log_e(1 - x)/m. \quad (2)$$

The true prevalence of pathogens in a wild population is often unknown and must be assumed. This assumption can greatly affect the likelihood of translocating at least one infected fish. As the assumed prevalence level decreases, the number of fish that need to be tested to achieve a given confidence of detection increases at a rapidly increasing rate, going to infinity as the assumed prevalence declines to zero (Figure 2). Similarly, as the desired confidence level increases, the number of fish that need to be tested also increases rapidly.

Equation (2) can be rearranged to provide the probability of detecting at least one infected individual

in a sample of size  $n$  from a population with a known (or assumed) prevalence  $m$ :<sup>4</sup>

$$x = 1 - \exp(-mn). \quad (3)$$

Thus, the probability of failing to detect a pathogen is  $\text{Pr}(d) = 1 - x$ .

Equations (2) and (3) implicitly assume that the screening instrument’s diagnostic specificity and sensitivity are perfect and equal to 1 (i.e., that infected animals always test positive and uninfected animals always test negative). Equations (2) and (3) can be generalized to account for the probability of obtaining a false negative,  $p$ , and a false positive,  $q$ . Equation (2) provides the necessary sample size if one requires confidence  $x$  when the observable prevalence is  $m$ . If there is a known bias in the observed prevalence resulting from an imperfect test specificity or sensitivity, then  $m$  in equations (2) and (3) is replaced with the observable prevalence

$$m' = m(1 - p) + (1 - m)q. \quad (4)$$

If only false negatives are considered ( $q = 0$ ), then the observable prevalence decreases, resulting in the need for a larger  $n$ . When only false positives are considered ( $p = 0$ ), the observable prevalence increases, reducing  $n$ . Issues regarding sensitivity and specificity of tests are addressed in more depth by

<sup>3</sup> The formula using the binomial distribution is  $n = \log_e(1 - x)/\log_e(1 - m)$ .

<sup>4</sup> The formula using the binomial distribution is  $x = 1 - (1 - m)^n$ .

TABLE 1.—Probability that a pathogen will be present in a sample of given size (or detected in a subsample with specificity = sensitivity = 1) at different prevalence levels among source fish.

Prevalence	Number of fish in sample						
	30	60	150	200	300	500	1000
0.001	0.030	0.058	0.139	0.181	0.259	0.393	0.632
0.01	0.259	0.451	0.777	0.865	0.950	0.993	1.000
0.02	0.451	0.699	0.950	0.982	0.998	1.000	1.000
0.05	0.777	0.950	0.999	1.000	1.000	1.000	1.000
0.1	0.950	0.998	1.000	1.000	1.000	1.000	1.000

Dell’Omodarme and Prati (2005) and Munoz-Zanzi et al. (2006).

Equation (3) also allows us to calculate the probability that a pathogen will be present in the translocation batch by replacing the subsample size with the number of (untested) fish in the batch to be transferred (note that  $m$ , and not  $m'$ , should be used for this calculation). Table 1 provides calculated probabilities for a range of prevalence levels and sample sizes. For all prevalence levels, as the number of individuals screened or in the batch increases, so does the probability that at least one infected fish will be detected in the screening subsample or will be present in the transfer batch. For example, if prevalence is 5%, then the probability of detecting at least 1 infected fish

in the subsample increases from 0.78 to nearly 1.0 as the sample size increases from 30 to 200 fish.

When the prevalence of a pathogen is high, the situation is straightforward: infected fish will be detected during screening and the translocation will be halted (Figure 1, top branch; Figure 3). Similarly, when the actual prevalence is near zero, the situation is again straightforward: the pathogen is unlikely to be detected in the screened sample and is unlikely to be present in the translocation batch. In such a case, the fish transfer proceeds with a low likelihood of pathogen transfer (Figure 1, bottom branch; Figure 3). Moderately low prevalence rates (less than approximately 0.05) present a more challenging situation, because the pathogen may go undetected in the subsample but is likely to be present in the larger transfer batch (e.g., when prevalence = 0.01 and sample size = 60, there is a 45% chance that an infected fish is in the transfer batch; see the middle branch of Figure 1 and Figure 3).

All else being equal, screening smaller subsamples results in higher probabilities of translocating at least one infected individual over a wider range of prevalence. The ability to decrease the likelihood of a translocation event by increasing subsample size, however, decreases as prevalence increases. If prevalence is sufficiently high, then smaller subsamples are nearly as likely to detect a pathogen as are larger subsamples (Figure 3). Increasing subsample size

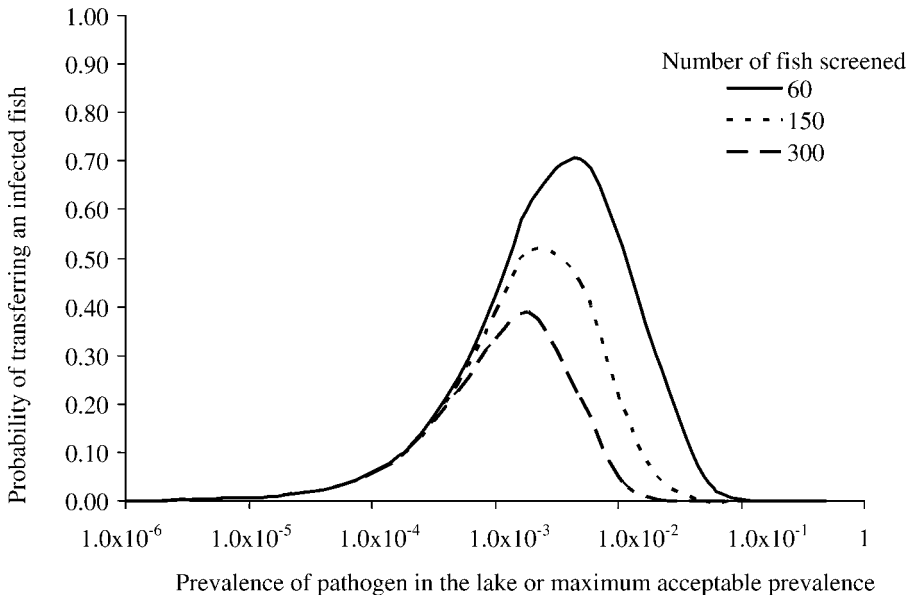


FIGURE 3.—Probability that an infected fish would be transferred given different levels of prevalence and screening effort, and assuming the translocation of 600 fish. Note that the  $x$ -axis is on a log scale. Equations (1) and (3) were used to generate this graph.

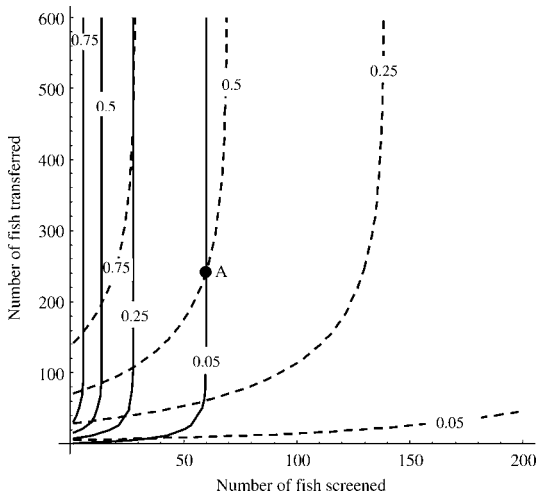


FIGURE 4.—Probabilities (indicated on the contour lines) of translocating at least one infected fish given the numbers screened and transferred. The solid lines represent cases in which the true prevalence in the transfer batch is 5%, the dashed lines cases in which the true prevalence is 1%. Point A indicates how the probability of transferring at least one infected fish increases 10-fold when the true prevalence is 1% rather than 5%. Equations (1) and (3) were used to generate this graph.

generates the greatest effect at moderately low prevalence levels (Figure 3).

Figure 4 illustrates the interaction between number of fish screened and number of fish transferred, assuming a given true source prevalence (solid lines: true prevalence = 0.05; dashed lines: true prevalence = 0.01). This figure shows that the probability of transferring an infected fish decreases as the number of fish screened increases, for a given number of fish in the transfer batch. The probability of transferring an infected fish increases, however, as the number of fish transferred increases, for a given number of fish screened. Decreases in true prevalence increase the probability of transferring an infected fish for a given number of fish screened and a given number of fish transferred. This is illustrated by considering the situation where 60 fish are screened and 240 fish are transferred (point A on Figure 4). If the true prevalence were 5%, there is a 5% chance of transferring an infected fish, whereas if the true prevalence were 1% then the likelihood of transferring an infected fish climbs to 50% (Figure 4).

The utility of a screening program for preventing the transfer of an infected fish depends on pathogen prevalence. In the absence of a screening program, high prevalence is more likely to result in a transfer because at low prevalence the probability that there are

infected individuals in the batch is lower. However, as the number of fish screened increases, the isolines in Figure 4 cross, because at high prevalence, screening is likely to detect infected fish and thus stop the translocation.

### How Long to Continue Screening for Pathogens

At some point the aquatic pathogen screening program should be terminated if pathogens are not found in multiple successive screening events and there is no evidence that a new (existing) pathogen has been introduced (reintroduced). Regan et al. (2006) develop a framework for evaluating programs to search for invasive plants that is applicable to this pathogen screening question. The length of time a screening program should persist, given that no infected individuals are found, should be based on three factors: (1) the cost of the screening program, CS; (2) the expected cost of a pathogen translocation, CT; and (3) the probability of facilitating a pathogen translocation ( $\text{Pr}[t] < 1$ ). Regan et al. (2006) offer a “rule of thumb” calculation that balances these factors, namely,

$$y = \log_e \left( \frac{-CS}{CT \times \log_e[\text{Pr}(t)]} \right) \bigg/ \log_e[\text{Pr}(t)] \quad (5)$$

where  $y$  is the number of screening events (given a constant interval) that should be undertaken when no pathogen is being detected. This criterion can be applied to screening programs and “disease-free” certification programs. This approach assumes that no other data conflict with the results of the screening program, such as new accounts of pathogen introductions. This rule implies that when the expected damages from translocation are small,  $CT < -CS/\log_e[\text{Pr}(t)]$ , then no screening should take place.

### A Case Study

We now present the case of sea lamprey transfers to illustrate the design considerations for risk management in a screening program and demonstrate the application of the methods discussed above. Sea lampreys are parasitic fish that invaded the North American Great Lakes during the early 20th century and have been the object of a pest control program since 1955 (Smith and Tibbles 1980). The sterile male release technique (SMRT) is a component of the sea lamprey control strategy for the St. Marys River, which is a major sea lamprey spawning area and therefore an important source of parasitic sea lampreys for Lake Huron (Schleen et al. 2003). The SMRT provides social and economic benefits through increased production of lake trout *Salvelinus namaycush* (Lupi et al. 2003). Sterilized male sea lampreys are released

to compete with wild fertile males to attract female mates and thereby reduce female reproductive output. A high ratio of sterile to fertile males is desirable for cost-effective control of sea lampreys (Haeseker et al. 2007). Managers go to considerable effort to obtain adult male sea lampreys for sterilization. More than 85% of the collection comes from upper Great Lakes sources close to the St. Marys River (Twohey et al. 2003), but some sea lampreys used in the SMRT program are collected in Lake Ontario, which is isolated from the upper Great Lakes by Niagara Falls.

Interest in screening sea lampreys for pathogens before translocation to prevent unwanted introductions has intensified as a result of the discovery of "pathogens of concern" in Lake Ontario. Specifically, a screening program has been initiated to screen for *Heterosporis* sp., a microsporidian parasite associated with percids (Bergstedt and Twohey 2005), that has not been detected in Lake Huron. *Heterosporis* sp. is known in Lake Ontario, and sea lampreys there potentially feed on infected fish. Therefore, there is concern that the movement of sea lampreys from Lake Ontario to the St. Marys River could facilitate the spread of *Heterosporis* sp. to valuable fish species in the upper Great Lakes (Bergstedt and Twohey 2005). The actual disease status and role of sea lampreys in pathogen transmission are unknown. Sea lampreys from the Great Lakes have been found to host two other pathogens of concern that are already present in Lake Huron fish: *Aeromonas salmonicida* (which causes furunculosis) and *Renibacterium salmoninarum* (which causes bacterial kidney disease; Eissa et al. 2006). Because these pathogens are already present in Lake Huron fish, they are not seen as a reason to prevent transfers of sea lampreys.

#### *Screening Effort for Lake Ontario Sea Lampreys and the Likelihood of Pathogen Translocation*

The Great Lakes Fishery Commission (GLFC) has adopted a policy of screening 60 fish before transfer (G. Christie, GLFC, personal communication).<sup>5</sup> In 2004, sea lampreys were collected from Lake Ontario tributaries for sterilization and transfer. The Aquatic Animal Health Laboratory at Michigan State University examined a subsample for the presence of emerging and restricted pathogens identified by the Office International des Epizooties (OIE) and the American Fisheries Society (AFS), using the AFS

aquatic animal health survey procedures (G. Christie, GLFC, personal communication). All fish tested negative for *Heterosporis* sp., resulting in the sterilization and transfer of 600 fish to the St. Marys River (Klar and Young 2004).

Neither the maximum acceptable probability of *Heterosporis* sp. translocation nor the expected true prevalence of *Heterosporis* sp. in Lake Ontario is documented for the sea lamprey transfer program. Therefore, we assume an initial value of 5% prevalence of *Heterosporis* sp. in Lake Ontario sea lampreys to illustrate the calculations described above. Assuming perfect specificity and sensitivity, screening 60 fish from the batch affords a probability of 0.95 of detecting at least 1 infected fish (equation 3). If the prevalence of *Heterosporis* sp. in the batch of sea lampreys were exactly 5%, then testing 60 sea lampreys would result in a 5% chance of failing to detect the pathogen in the screened subsample despite its presence in the batch (equation 3). For a prevalence of 5% and a batch size of 600 fish, the probability of the presence of at least 1 infected fish in the batch is essentially 1.0 (see Table 1). We then use equation (1) to calculate the probability of a pathogen translocation as  $(1 - 0.95) \times 1.00 = 0.05$ .

These calculations are sensitive to the assumption made about the assumed prevalence  $m$ . Had the actual prevalence of *Heterosporis* sp. in Lake Ontario sea lampreys been 1%, we could be 45.1% confident that at least 1 infected fish would be detected in a subsample of 60 sea lampreys (equation 3; Table 1). There would have been a 99.8% chance that at least one infected fish was present in the batch, implying that there would have been a  $(1 - 0.451) \times 0.998 = .548$  (54.8%) chance that at least one infected individual was moved from Lake Ontario to the St. Mary's River. These calculations illustrate the importance of explicitly determining the maximum acceptable likelihood that a pathogen is transferred as well as assumptions about the prevalence in the source population. Managers need to be aware of all the factors affecting the risk of a translocation and carefully consider their implications before making decisions.

The likelihood of pathogen translocation given a screening program is also sensitive to assumptions about diagnostic sensitivity and specificity (Figure 5), an issue that has not received much attention (for exceptions see Dell'Omodarme and Prati 2005; and Munoz-Zanzi et al. 2006). The sensitivity and specificity of screening results for sea lampreys were not reported to Great Lakes managers (G. Christie, GLFC, personal communication). Therefore, to illustrate the implications of sensitivity assumptions for the sea lamprey example, let us assume, hypothetically, that the sensitivity of the test were 0.7 and specificity

<sup>5</sup> In 2004, 119 fish were screened (approximately 60 from two different rivers). Since 2004, however, only 60 fish total have been screened annually. We therefore use the number 60 in our analyses because it is current policy and represents a common level of screening effort.

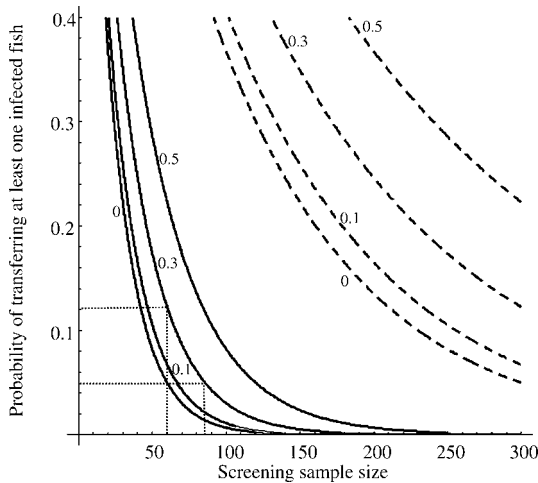


FIGURE 5.—Probabilities of translocating at least one infected fish given the number screened and the probability of a false-negative screening result (labeled contour lines). The solid lines represent cases in which the true prevalence in the transfer batch is 5%, the dashed lines cases in which the true prevalence is 1%. The dotted lines illustrate the adjustment needed in sample size and the increase in the likelihood of a pathogen transfer when the probability of a false negative increases from 0 to 0.3 (representing a sensitivity of 0.7). Equations (3) and (4) were used to generate this graph.

were 1, implying a probability of a false negative = 0.3. Thus, if the true prevalence were 5%, the observable prevalence would be 3.5% (equation 4). This would increase the chance of failing to detect an infected individual in the subsample from 5% to 12.2%. The corresponding probability of pathogen translocation for a 600-fish batch would be 12.2%. Alternatively, it would be necessary to screen 86 fish, as opposed to 60, to provide a 5% chance of transferring at least 1 infected fish (dotted lines in Figure 5). Lower levels of assumed prevalence accentuate the effect of false negatives (in Figure 5, notice the increase in distance between the solid lines associated with 5% prevalence and the dashed lines associated with 1% prevalence).

Assumptions about specificity also affect decisions. Specificity of less than 1 can reduce the probability that pathogen will be transferred because such tests inflate the likelihood of a transfer-blocking positive result. This, too, needs to be accounted for when designing screening programs, given the cost that results when otherwise beneficial transfers are forgone.

#### *Determining the Duration of a Program for Screening Lake Ontario Sea Lampreys for Pathogens*

We now demonstrate how to determine how long a screening program should continue, given successive

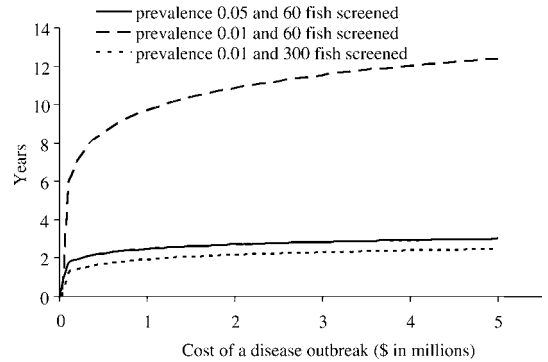


FIGURE 6.—Effects of screening costs, the cost of a disease outbreak, and the probability of pathogen introduction on the number of years that a screening program should continue when no infected individuals are detected. The cost of the screening program was calculated as \$30 per fish screened. The probability of transferring at least 1 infected fish, assuming that 600 or more fish are translocated, was determined from Table 1. We assume that the translocation of a single infected fish is sufficient to cause damage. Equations (3) and (5) were used to generate this figure.

failures to detect a pathogen in screened samples and assuming that there is no independent evidence for new pathogen introductions. The GLFC pays a direct cost of about US\$30 per sea lamprey screened (G. Christie, GLFC, personal communication), which does not include indirect costs such as transportation. The cost of transferring a pathogen has not been estimated, so for this example we compute the duration of the screening program over a range of costs. The probability of pathogen transfer has already been addressed.

Figure 6 illustrates how the likelihood of translocation, the cost of screening, and the cost of translocation of at least one infected fish interact to determine the number of years to continue screening, assuming no new pathogen introduction (see equation 5), and leads to four observations. First, the economic impact of a disease event has little effect on the length of time the screening program should continue when zero infected individuals are detected, except in situations when such costs are minor. Second, if the expected damages from a pathogen translocation are small (<\$601 if the true prevalence were 5% and the screening sample size were 60), then no screening should take place. Third, using Table 1 and Figure 6, we see that the cases where  $n=60$  and  $m=5\%$  (solid line) and  $n=300$  and  $m=1\%$  (dotted line) have the same probability of pathogen translocation. In the latter case, more fish must be screened to achieve this low probability, the screening program is more costly, and thus screening should terminate slightly sooner because of higher costs.

Finally, in comparing the cases where  $n = 60$  and  $m = 5\%$  (solid line) versus  $m = 1\%$  (dashed line), the lower source prevalence in the latter case increases the probability of transferring a pathogen (with a transfer of 600 sea lampreys) to 54.8%. Thus, screening programs that result in lower confidence of pathogen detection and higher likelihood of pathogen translocation should persist longer.

These calculations are based on the assumption that the pathogen prevalence in the source population is stable or declining rather than increasing. If there is evidence, independent of the screening program, that pathogen prevalence is increasing in the source population (e.g., through its invasion of a new host or detection of the pathogen through other means), then screening efforts should persist. In such cases—where the prevalence is increasing or a pathogen has been introduced—it would be expected that infected individuals would begin to appear in the screening subsample.

### Discussion and Conclusion

Fish translocations create a likelihood of pathogen translocation, which may have adverse consequences for society. This risk can be managed, in part, through pretranslocation screening programs, and the effective and efficient design of these programs is important for two reasons. First, the design will affect the likelihood of pathogen detection and thus translocation decisions. Second, screening programs are not cost-free, and allocating resources to screening diverts them from other beneficial uses including other methods of managing fish pathogen transfer risk (e.g., disinfection or treatment). This is not to say resources should not be used for pathogen screening, but that tradeoffs and the value of information gained must be considered.

Our analysis demonstrates that the translocation of an infected fish is most likely to occur at moderately low prevalence levels (see Figure 3). This is because the probability of failing to detect infected fish through screening declines as pathogen prevalence increases, whereas the probability that an infected individual would be in a batch for translocation declines as prevalence decreases. The probability that the screening program prevents a translocation event is the intersection of these two probabilities. Fish screening is most likely to provide benefits when pathogen prevalence is relatively high (e.g.,  $>5\%$ ), in which case, relatively small subsamples may be adequate (see Figure 3). Increasing subsample size, however, may be beneficial because the probability of a pathogen translocation event decreases as subsample size becomes a substantial fraction of the translocation batch (Figure 4). Increasing subsample size may,

however, be infeasible when screening is lethal. As expected, decreases in diagnostic sensitivity increase the likelihood of transferring at least one infected fish, but sample size and assumed prevalence interact with sensitivity to determine the size of the effect (Figure 5). Information about the sensitivity and specificity is vital to decision makers for interpreting results and designing screening programs.

Our analysis also examined the length of time a screening program should continue, given no detection of new pathogens and no evidence of new pathogen invasions. The probability of transferring a pathogen, which is determined by assumptions about the observable pathogen prevalence ( $m$ ) and management decisions, followed by the cost of screening, have the greatest impacts on the length of the time a program continues.<sup>6</sup> Pathogen translocation costs are also important to consider but have a lower impact on how long to continue the program, particularly when they are large relative to screening costs, which is typically the case. We provided a formula for determining the minimum expected costs of a pathogen transfer that justifies screening. These costs are usually modest ( $< \$601$  in the case study).

Aquatic disease and fish health activities must be evaluated within the context of fisheries or ecosystem management objectives (Stephen 2001). Historically, fish health policy has presumed that the consequences of any pathogen translocation are unacceptable (Stephen 2001). Simplistic goals such as estimating and “minimizing disease prevalence” are not appropriate. Such goals do not account for the opportunity cost of using resources to manage disease that could have been used elsewhere in the fisheries management program, nor do they adequately address real management tradeoffs.

We have presented a case study where transfers of sea lampreys create the potential for pathogen transfer with negative consequences; yet, the overall consequences of these translocations may be positive for the fishery because of the benefits that the sterile sea lampreys provide to the overall health of Lake Huron fisheries. *Heterosporis* sp. has not been detected in the St. Marys River or Lake Huron, and SMRT-related

<sup>6</sup> Formally, the marginal impacts are the partial derivatives of  $y$  with respect to each variable in equation (5). These are  $\partial y / \partial CS = 1 / \{CS \cdot \log_e [Pr(t)]\}$ ,  $\partial y / \partial CT = -1 / \{CT \cdot \log_e [Pr(t)]\}$ , and  $\partial y / \partial Pr(t) = -1 + \log_e (-CS / \{CS \cdot \log_e [Pr(t)]\}) \cdot \log_e [Pr(t)]^{-2} \cdot Pr(t)^{-1}$ . The marginal effect of a change in either cost is the same in absolute value but depends on the cost, larger costs resulting in effects that are smaller in absolute value. Given that screening should begin and under realistic conditions,  $CT > CS$  (this will always hold if  $Pr[t] \geq 1/e$  and will hold for a range of  $Pr[t] < 1/e$ ). Also,  $|\partial y / \partial Pr(t)| > |\partial y / \partial CT|$  for given values of  $Pr(t)$ ,  $CT$ , and  $CS$ .

suppression of sea lampreys has improved Lake Huron fisheries (Lupi et al. 2003; Klar and Young 2004; G. Christie, GLFC, personal communication). This result prompts one of two possible interpretations: either the screening program is adequate or the managers have been lucky. Because good outcomes do not always imply good past decisions, a full review of the screening program for sea lampreys in the context of overall fishery objectives is merited. We found no evidence that managers had documented a probable prevalence for *Heterosporis* sp. in Lake Ontario or specified a maximum acceptable likelihood of pathogen transfer. We encourage managers to address these issues explicitly as a part of screening program design. In general, fish health diagnostic professionals should provide, and decision makers should request, information on the performance of the diagnostic tests, namely, diagnostic sensitivity and specificity, so that decision makers have a clear context for interpreting screening program results and modifying screening programs.

The concerns raised in the case study are not unique. Managers and researchers seek to understand the issues associated with controlling the spread of aquatic pathogens. For example, Great Lakes fishery managers are currently grappling with disease issues associated with the potential reintroduction of extirpated spoonhead sculpins *Cottus ricei*, deepwater sculpins *Myoxocephalus thompsonii*, and ciscoes *Coregonus* spp. (Eshenroder and Krueger 2002). Recent positive screening results for *R. salmoninarum*, however, may prevent the reintroduction of these fish (G. Wright, Chippewa–Ottawa Resource Authority, personal communication). In this case, the likelihood of pathogen translocation and the potential damage must be considered in terms of broader fishery objectives, such as the impact of the translocations on the overall community or ecosystem. Thrush and Peeler's (2006) "contingency planning" model for the spread of the monogenean parasite *Gyrodactylus salaricus* in Britain may best illustrate the potential for screening programs to prevent damage from pathogen translocations. Although these authors do not explicitly include screening, they identify the ability to detect and prevent the movement of infected fish as the main component in preventing a "major outbreak." Including simulated screening programs based on the principles presented here in such models could help identify efficient screening policies.

In this paper, we outline the design characteristics of screening programs that affect the likelihood of detecting a pathogen and explain how they can affect the risk of pathogen transfer. Both over- and under-allocation of resources to screening can have adverse

consequences—striking a balance requires a sophisticated consideration of risk.

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