3.0 Risk Analysis of Biota Transfers–Biological Invasions and Shifting Metapopulation Dynamics

Abstract. Section 3 summarizes the outcomes of the risk analysis completed for the biota transfer project. The analysis of risks associated with potential biota transfers yielded multiple, complementary outcomes stemming from the range of analytical tools applied to the evaluation of risks. Outcomes of the analysis of risks resulted from qualitative evaluations, largely based on narrative analyses dependent upon existing information on past and current distributions and life-history attributes potentially associated with future species incursions that might result in successful invasions or shifts in metapopulations. Quantitative evaluations based on categorical analysis considered life-history attributes and assigned numerical scores to each biota of concern, yielding a priority list of species likely to be problematic if biota transfers occurred in the future. Outcomes of categorical analysis suggested that potential transfers of species already occurring in both Missouri River and Red River basins may occur in the future since existing multiple competing pathways may link these basins regardless of whether designed water diversions are realized. Whether transfers of species already occurring in both basins would be associated with a measurable shift in metapopulations is unclear, given the relatively sparse data available for the analysis. While georeferenced distribution data were not sufficient for characterizing potential species distributions for all biota of concern, when sufficient data were available, spatiotemporal analysis considered biota transfers and prediction of species distributions through an ecological-niche-based model algorithm. Illustrative projections of potential distributions for representative aquatic nuisance species such as Zebra mussel, New Zealand mudsnail, and riparian plants such as tamarisk, were incorporated into the quantitative analysis as available and suggested that some biota of concern may become invasive in the future, although these species invasions are not uniquely linked to interbasin water diversion, due to multiple pathways available for incursion.

3.0 Overview of Biological Invasions and Shifting Metapopulation Dynamics

As Sjödin et al. (2004) noted, "[S]implifying assumptions are necessary in order to turn complex biological systems into caricatures that are, on the one hand, simple enough to analyze, and on the other hand, realistic enough to capture key features of the process under investigation." A better characterization of the current investigation's context could not be written. In order to address the questions of Reclamation and Technical Team, we necessarily had to develop models that captured their concerns and helped focus the analysis. Data analysts, whether detailed to scientific or engineering problems, generally look at models as one of three types which are variously identified as conceptual or heuristic models, mathematical or statistical models, or physical models (see Burnham and Anderson 2002). Various authors have characterized models along these or similar lines (see Burnam and Anderson 2002, Jensen and Bard 2002), and all express similar views similar to Puccia and Levins (1985):

> “Every model distorts the system under study in order to simplify it. . . .There are two dangers in model building: one is that the model does not tell us about the world; the other is that is a faithful representation, and therefore we are overwhelmed. Simplification is both legitimate and necessary as long as we are cautious, are willing to change the original underlying assumptions as necessary and build new models, and carefully interpret the model’s predictions.”

Regardless of the various names and approaches to categorizing models, experienced analysts note that these general types of models are not necessarily independent in their application to complex environmental issues such as those related to water use and land use, as characterized in the various realizations of water diversions envisioned for the Upper Missouri and Red River basins.

Practically speaking, models fit into of one of three groups: (1) those that are accurate, precise, and field validated; (2) those that are useful as analytical tools for evaluating a range of “what-if” scenarios but have not been validated and present varying levels of precision and accuracy; and (3) those that are variously available as largely theoretical abstractions whose value to the risk assessment process is poorly characterized. Models of the first group are lacking in studies such as these of the current investigation (see Scott et al. 2002 for critical review), and tools of the third group have relatively limited value in adaptive management practices where bounds of certainty are critical to the assessment, management, and update process (see Walters 1986). Hence, we have applied a set of analytical tools of the second variety to the evaluation of risks and consequences potentially associated with biota transfers realized as a result of interbasin water diversions. These tools have a long history in applications similar to those of the current investigation (see Scott et al. 2002), and although lacking rigorous field validation, each analytical tool contributes outputs valuable to stakeholders in their decision-making process.

Our primary tools have been detailed in Section 2. As needed, brief presentations of lesser used tools are included in this section to set the stage for results that are limited to a few species of concern, due to sparsely available data (e.g., dispersal analysis following Fisher (1937), Kolmogorov et al. (1937), and Skellam (1951) and more recently extended others such as Clark et al. (2001a,b, 2003)). Depending on the empirical data available for biota of concern, the evaluation of risks followed a three-part analysis as detailed in Section 2: (1) a categorical analysis focused on species’ attributes that would influence the ability of a biota of concern to successfully traverse geographic boundaries between Missouri River source waters, (2) a simple probability analysis that characterized risk as outcomes of a multiple-step flow of events linking source system with receiving system (see Section 2, Annex Figure 1 through Annex Figure 5), and (3) a spatial analysis that characterized potential distribution of biota of concern through a preliminary ecological-niche analysis using GARP (see Section 2).

Not all biota of concern were amenable to analysis with each of these three tools, but a narrative analysis of risks was completed for each biota of concern regardless the level of effort devoted to the evaluation of risks associated with biota transfers consequent to water diversion. When data were sufficient for a spatial analysis and metadata included time record sufficient to the task, a spatiotemporal analysis was completed such that output from the investigation considered predicted distribution of biota of concern through time (e.g., zebra mussel and New Zealand mudsnail). While biota of concern identified by stakeholders were not limited to invasive species, the evaluation of effects associated with species invasions as well as potential shifts in metapopulations associated with water diversions were considered using the same categorical and spatial analysis tools.

For a quantitative evaluation of risks, available data must have been amenable to analysis with a wide range of tools (see Appendix 4). Data quantity and quality would not only influence predictions of a particular species invasion (e.g., Will invasion occur, and what expansion of a species' distribution will be realized?), but also strongly influenced the uncertainties associated with risks associated with each prediction of species invasion subsequent to biota transfer (e.g., How certain are these predictions?). Data may have been limited or incomplete, often times reflecting the difficulties in observing or studying the invasion process (see Elton (1958) for a classical perspective or Kolar and Lodge (2001, 2002) for recent updates). Each step of the invasion process varies with respect to its data quality and quantity, and the interrelationships between steps will necessarily reflect these differences in data sources. In the current investigation, effects data (e.g., adverse effects of invasive species on indigenous species) were abundant for nearly all biota of concern, yet each reflected a different level of effort in mining available data for categorical, quantitative (i.e., spatial or spatiotemporal), or narrative analysis. For example, in identifying transfer coefficients to characterize transport from source system to receiving system, data availability varied from species having data sufficient to estimate numerical values (e.g., zebra mussel and New Zealand mudsnail) to those having data sufficient for a categorical evaluation (e.g., tamarisk) to those having little empirical data in the existing literature (e.g., *Polypodium hydriforme* and its hosts). Ranges in data quantity and quality varied for each representative included in the list of biota of concerned identified during problem formulation (Section 1).

As noted in Section 2 and in Appendix 4, in the current investigation the discrimination between species invasions linked to interbasin water transfers and those linked with other pathways was considered within the context of competing risks related to system failure (i.e., biota transfer and successful invasion). From the perspective of competing risks, if a species invasion is considered a failure, then each of *k* different failure modes or ways a failure can occur (i.e., for species invasions, different pathways may be interpreted as different failure modes) are competing, and underlying each failure mode is a failure mechanism (i.e., for a given pathway, each mode will have one to many different failure mechanisms; see Annex Figure 1 through Annex Figure 5). When data were not sufficient for quantitative estimates of competing risks, a narrative evaluation of competing risks was completed within the context of the competing risks conceptual model summarized in Annex Figure 1 through Annex Figure 5 of Section 2.

3.1 Categorical Analysis of Species Attributes for Ranking Biota of Concern

Given the early efforts of researchers and especially since Elton's classical publication focused on invasive species (Elton 1958), work has been pursued to establish principles of invasion biology and develop tools for predicting successful invasions (see Carlton 1996 for marine and estuarine habitats; Rejmánek 1996 for invasive plants; Kolar and Lodge 2002a,b for invasive aquatic species). As a consequence of these past efforts, a large body of literature exists that describes general characteristics of invasive species, with some attributes (e.g., related to reproduction) being of apparently greater significance than others when attempting to characterize the "ideal" invasive species (see Ehrlich 1989; Williamson and Fitter 1996; Ricciardi and Rasmussen 1998; McKinney and Lockwood 1999, 2001). For example, successful invaders generally reproduce rapidly (see Elton 1958; Leung et al. 2004; Lodge 1993), are habitat or diet generalists (see Elton 1958; Moyle and Light 1996a, b), or have a broad native range (Lodge 1993; Ricciardi and Rasmussen 1998), these global characterizations fall short with respect to their contributing to a quantitative analysis amenable to developing an initial predictive capability needed for developing management strategies to prevent or limit successful invasions.

Recently, in an effort to develop predictive models of species invasions, many authors have offered observations on the processes involved in biological invasions (see Verimeij 1996; Williamson 1996; Kolar and Lodge 2001; D'Antonio et al. 1992, 1999, 2001). These observations are consistent with anecdotal accounts of species invasions in the older literature (see Elton 1958), and suggest that species invasions reflect a complex process involving five generalized steps: transport, release, establishment, spread, and integration (see Marchetti et al. 2004). Each of these steps, or stages, in the invasion process may be decomposed into constituent events and may be dependent on contingencies reflecting collateral processes required for invasion of specific species, e.g., host-parasite relationships will influence the successful invasion of disease organisms. In part, these steps in the invasion process, but especially those related to transfer and release, are captured in the nested conceptual models summarized in Annex Figure 1 through Annex Figure 5.

3.1.1 Categorical analysis of risks. Given the taxonomic range of the biota of concern identified by Reclamation and stakeholders—bacteria and viruses to aquatic and terrestrial plants to aquatic invertebrates and vertebrates—the current investigation captured a variety of life histories across multiple taxonomic groups that was responsive to suggestions that "predictive understanding of the invasion process can only emerge from taxonomically focused studies" (Lodge 1993). In the current investigation we relied on guidance of Kolar and Lodge (2001) and others (see Elton 1958; Moyle and Light 1996; Verimeij 1996; Williamson and Fitter 1996; Kolar and Lodge 2001; D'Antonio et al. 1992, 1999, 2001; Marchetti et al. 2004), and considered life-history attributes identical or similar to those Kolar and Lodge (2001; depending on species of concern) for our categorical analysis (see Section 2). For the categorical analysis completed as part of this investigation, biota of concern were scored within groups, based upon life history attributes shared by members of those groups, e.g., plants and microorganisms, and aquatic invertebrates and aquatic vertebrates (fishes).

Tables for the categorical analysis have been included as grouped outputs for biota of concern (Table 1 through Table 7), with a summary table (Table 8) included wherein all biota of concern are considered equally weighted using a simple ratio estimator, i.e., "species score relative to total possible" (Fleiss et al. 2003). Although beyond the scope of the current investigation, future applications of the categorical analysis may extend to Delphi methods of analysis (see Adler and Ziglio 1996; Bernard 1999). Figure 1 plots arcsin-transformed scores (Sokol and Rohlf 1981) and Table 9 lists selected summary statistics for these arcsin transformed scores.

As listed in Table 9, biota of concern presented simple rank scores ranging from 1.0 (e.g., cyanobacteria) to nearly 1.0 (e.g., Eurasian water-milfoil, purple loosestrife, and bacterial and protozoan infectious disease agents) to less than 0.6 (e.g., Utah chub, paddlefish, and pallid sturgeon), which suggests that biota transfers of these representative biota, if realized, would present a range of outcomes reflecting life-history attributes favoring transport and establishment in the receiving area. The majority of those species presenting high rank scores were not candidate invasive species identified by Reclamation and Technical Team as biota of concern. Rather, these high-ranking species were currently present in both the Missouri River and Red River basins and were included as biota of concern because proposed interbasin water transfers could potentially represent sources for shifts in metapopulations between the two basins. In this initial rank categorization, the nine highest-ranking biota of concern presented a widespread occurrence, not only in the Missouri River and Red River basins, but throughout North America. Invasive species potentially of greatest concern, if interbasin water diversions are realized, included numerous representative biota falling into the second and third quartiles, e.g., zebra mussel, New Zealand mudsnail, Asian carp, and others presenting similar scores (see Table 8, Table 9, and Figure 1). Species falling into the first quartile may be reconsidered by stakeholders, if species life-history attributes and current status, e.g., pallid sturgeon, are entered into the selection process in subsequent iterations in the reformulation of lists of biota of concern (see also Appendix 3A and Appendix 3B). Similarly, Reclamation and Technical Team may revisit the list of biota of concern, given the ongoing discussions related to control systems envisioned as part of water diversion infrastructure (see Section 4).

Table 1. Categorical analysis of fishes included as biota of concern.

Attribute	Fishes						
	Gizzard shad	**Rainbow smelt**	**Asian carp[†]**	**Paddlefish**	**Pallid sturgeon**	**Utah chub**	**Zander**
Trophic status (Score 1–5)	3	3	3	2	2	3	2
Parental investment in offspring (Score 1–4)	3	3	3	2	2	3	3
Maximum adult size (Score 1–3)*	2	2	3	3	3	1	3
Size of native range (Score 1–4)	3	3	4	2	2	2	2
Physiological tolerance (Score 1–4)	3	3	4	3	3	3	3
Distance of native source (Score 1–4)	3	3	4	2	2	3	4
Prior invasion success (Score 1–5)	3	3	3	2	2	3	2
Fecundity and propagule pressure (Score 1–4)	3	3	4	3	3	3	3
Total score (possible 36)	**23**	**23**	**28**	**19**	**19**	**21**	**22**

*relative size within broad categories of "Fishes" with 1 "small-bodied" to 3 "large-bodied"

[†] composite grouping of bighead carp, silver carp, and black carp (see Appendix 3A)

Table 2. Categorical analysis of aquatic invertebrates included as biota of concern.

Attribute	**Aquatic invertebrates**			
	Dreissena polymorpha	***Corbicula fluminea***	***Potamopyrgus antipodium***	***Bythotrephes cederstroemi***
Trophic status (Score 1–5)	4	4	4	4
Parental investment in offspring (Score 1–4)	4	4	4	4
Maximum adult size (Score 1–3)*	1	1	1	1
Size of native range (Score 1–4)	4	4	4	3
Physiological tolerance (Score 1–4)	3	3	3	3
Distance of native source (Score 1–4)	3	3	3	1
Prior invasion success (Score 1–5)	4	4	4	3
Fecundity and propagule pressure (Score 1–4)	3	3	4	4
Total score (possible 36)	**26**	**26**	**27**	**23**

*relative size within broad categories of "Aquatic Invertebrates" with 1 "small-bodied" to 3 "large-bodied"

Table 3. Categorical analysis of aquatic vascular plants included as biota of concern.			
Attribute	**Aquatic vascular plants**		
	Hydrilla verticillata	***Myriophyllum spicatum***	***Eichhornia crassipes***
Trophic status (Score 1–5)	5	5	5
Parental investment in offspring (Score 1–4)	4	4	4
Size of native range (Score 1–4)	2	4	2
Physiological tolerance (Score 1–4)	1	4	2
Distance of native source (Score 1–4)	1	4	1
Prior invasion success (Score 1–5)	3	4	3
Fecundity and propagule pressure (Score 1–4)	4	4	4
Total score (possible 30)	**20**	**29**	**21**

Table 4. Categorical analysis of riparian and wetland vascular plants included as biota of concern.

Attribute	**Riparian and wetland vascular plants**	
	Lythrum salicaria	***Tamarix spp.***
Trophic status (Score 1–5)	5	5
Parental investment in offspring (Score 1–4)	4	4
Size of native range (Score 1–4)	4	4
Physiological tolerance (Score 1–4)	4	4
Distance of native source (Score 1–4)	4	4
Prior invasion success (Score 1–5)	4	5
Fecundity and propagule pressure (Score 1–4)	4	4
Total score (possible 30)	**29**	**30**

Table 5. Categorical analysis of cyanobacteria included as biota of concern.

Attribute	Cyanobacteria		
	Anabaena flos-aquae	***Microcystis aeruginosa***	***Aphanizomenon flos-aquae***
Trophic status (score 1–5)	5	5	5
Size of native range (Score 1–4)	4	4	4
Physiological tolerance (Score 1–4)	4	4	4
Distance of native source (Score 1–4)	4	4	4
Prior invasion success (Score 1–5)	5	5	5
Fecundity and propagule pressure (Score 1–4)	4	4	4
Total score (possible 26)	**26**	**26**	**26**

Table 6. Categorical analysis of bacteria and viruses included as biota of concern.

Attribute	**Microorganisms and Disease Agents**				
	IHNV	**ERM**	***E. coli***	***Salmonella spp.***	***Legionella spp.***
Trophic status (score 1–5)	1	1	1	1	1
Size of native range (Score 1–4)	4	4	4	4	4
Physiological tolerance (Score 1–4)	3	3	3	3	3
Distance of native source (Score 1–4)	4	4	4	4	3
Prior invasion success (Score 1–5)	4	4	5	5	5
Fecundity and propagule pressure (Score 1–4)	4	4	4	4	3
Total score (possible 26)	**20**	**20**	**21**	**21**	**19**

Table 7. Categorical analysis of protozoa and myxozoa included as biota of concern.

Attribute	**Protozoa and Myxozoa**			
	Myxosoma cerebralis	***Polypodium hydriforme***	***Cryptosporidium parvum***	***Giardia lamblia***
Trophic status (score 1–5)	1	1	1	1
Size of native range (Score 1–4)	4	4	4	4
Physiological tolerance (Score 1–4)	3	3	3	3
Distance of native source (Score 1–4)	3	3	4	4
Prior invasion success (Score 1–5)	5	4	5	5
Fecundity and propagule pressure (Score 1–4)	3	4	4	4
Total score (possible 26)	**19**	**19**	**21**	**21**

Table 8. Summary scores of biota of concern and their relative rankings from high score to low score.

Biota of concern	Score	Possible score	Simple Rank Score (Score/Possible Score)
Microcystis aeruginosa	26	26	1.000
Anabaena flos-aquae	26	26	1.000
Aphanizomenon flos-aquae	26	26	1.000
Myriophyllum spicatum (Eurasian watermilfoil)	29	30	0.967
Lythrum salicaria (Purple loosestrife)	29	30	0.967
Escerichia coli (primarily O157:H7)	21	26	0.808
Salmonella spp. (various serotypes)	21	26	0.808
Cryptospordium parvum	21	26	0.808
Giardia lamblia	21	26	0.808
“Asian carp”	28	36	0.778
Infectious Hematopoietic Necrosis Virus	20	26	0.769
Yersinia ruckeri (Enteric Redmouth)	20	26	0.769
Potamopyrgus antipodarum (New Zealand mudsnail)	27	36	0.750
Legionella spp.	19	26	0.731
Myxosoma cerebralis	19	26	0.731
Polypodium hydriforme	19	26	0.731
Dreissena polymorpha (zebra mussel)	26	36	0.722
Corbicula flumenia (Asian clam)	26	36	0.722
Eichhornia crassipes (water hyacinth)	21	30	0.700
Hydrilla verticillata	20	30	0.667
Tamarix spp. (tamarisk)	20	30	0.667
Dorosoma cepedianum (gizzard shad)	23	36	0.639
Osmerus mordax (rainbow smelt)	23	36	0.639
Bythotrephes cederstroemi (spiny water flea)	23	36	0.639
Sander [Stizostedion] lucioperca (zander)	22	36	0.611
Gila atraria (Utah chub)	21	36	0.583
Polyodon spathula (paddlefish)	19	36	0.528
Scaphirhynchus albus (pallid sturgeon)	19	36	0.528

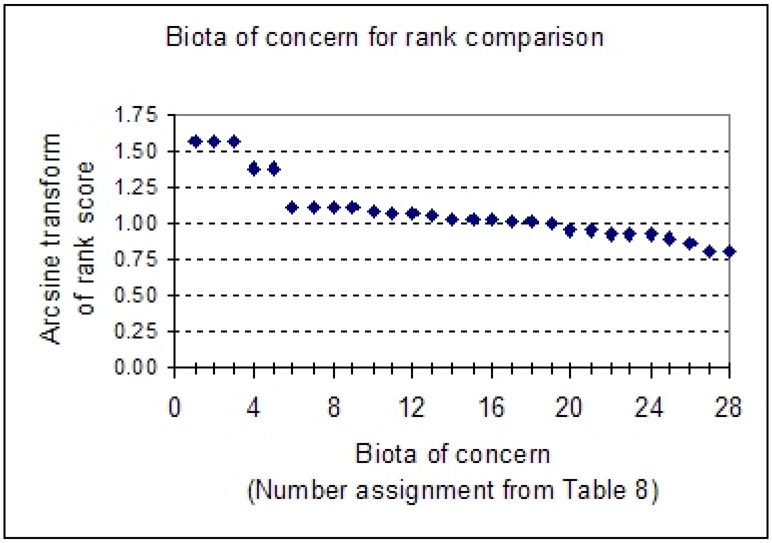


Figure 1. Transformed rank scores plotted from high to low with summary statistics on transformed rank scores listed in Table 9.

Table 9. Selected summary statistics for rank scores listed in Table 8 and plotted "high to low by transformed rank score" in Figure 1.

Sample size (N)	28	Percentiles:	10	0.8635
Minimum	0.8132		25	0.9334
Maximum	1.5708		50	1.0253
Mean	1.0857		75	1.1168
Median	1.0253		90	1.5708
Kurtosis	0.8487			
Coeff kurtosis	3.8487	First quartile:		0.9334
Skewness	1.2632	Second quartile:		1.0253
Coeff skewness	0.6316	Third quartile:		1.1168

3.2 Simple Probability Models and Quantitative Analysis of Risks

In evaluating competing risks, a system's reliability is considered as a "build-up" model based on evaluations of the reliability of each failure mode. As in any analysis of competing risks, three assumptions were specified in the current analysis: (1) each failure mechanism leading to a particular type of failure (i.e., failure mode) proceeds independently of every other mode at least until a failure occurs; (2) a failure event occurs when the first of all the competing failure mechanisms reaches a failed state; and (3) each of the *k* failure modes has a known life distribution model $F_i(t)$ (see Appendix 4 and Blischke and Parbhakar Murthy, 2000). In the initial analysis summarized here, the third of these assumptions defaulted to a distribution of failure events that approached normality upon iteration in simulation study (see Appendix 13).

Quantitatively, a focus on competing risks is best applied when all three assumptions hold. If $R_c(t)$, $F_c(t)$, and $h_c(t)$ denote the reliability, cumulative distribution function (CDF), and failure rate for the constituent event, respectively, and $R_i(t)$, $F_i(t)$ and $h_i(t)$ are the reliability, CDF and failure rate for the *i*-th failure mode, respectively, then the competing risk model formulas are

$$R_c(t) = \prod_{i=1}^{k} R_i(t)$$

$$F_c(t) = 1 - \prod_{i=1}^{k} \{1 - F_i(t)\}$$

$$h_c(t) = \sum_{i=1}^{k} h_i(t) \quad .$$

For evaluating competing risks, we assume that all failure mechanisms are “racing to see which can reach failure first” (NIST/SEMATECH 2004, see Appendix 4), e.g., which competing risk is most likely to yield a species invasion? If the failure mechanisms are assumed independent, then the component reliability is the product of the failure mode reliabilities, and the component failure rate is the sum of the failure rates. Within an engineering context (e.g., analysis of failure in a control system made of multiple components), this algorithm holds for any arbitrary life distribution model, as long as “independence” and “first mechanism failure causes the component to fail” assumptions are not violated. In the field, each of these assumptions may be violated, but the model provided a common tool with a long history in its application to an initial analysis of risks of invasion (see Williamson 1989, 1996).

In our simple probability calculations we relied on an elementary stochastic simulation (see Bartlett 1955, 1960; Thompson 2000; Huzurbazar 2005) to directly evaluate invasion scenarios captured by pathways summarized in the conceptual models in Annex Figure 1 through Annex Figure 5 (see Section 2). Given the range in data quality and quantity across menu of biota of concern, as well as the range in their life-history attributes, the simple probability analysis focused on groups of biological agents potentially involved in interbasin transfers with the representative biota of concern handled as indicated in Table 10 for interpretation.

Table 10. Groups of representative biota of concern targeted in the simple probability analysis.

Grouping of representative biota of concern	Focus of simple probability estimation
Microorganisms and Disease Agents Enteric redmouth (ERM) Infectious hemtopoietic necrosis virus (IHNV) *Legionella* spp. *Escherichia coli* (various serotypes but data focused on O157:H7) *Salmonella* spp. (various species and serotypes including, but not limited to *S. typhi*, *S. typhmurium*) *Anabaena flos-aquae* *Microcystis aeruginosa* *Aphanizomenon flos-aquae* Protozoa and Myxozoa *Cryptosporidium parvum* *Giardia lamblia* *Myxosoma cerebralis* (*Myxobolus cerebralis*) *Polypodium hydriforme*	Interpreted as a single-event type
Aquatic Vascular Plants and Riparian & Wetland plants Hydrilla (*Hydrilla verticillata*) Eurasian water-milfoil (*Myriophyllum spicatum*) Water hyacinth (*Eichhornia crassipes*) Purple loosestrife (*Lythrum salicaria*) Salt cedar (*Tamarix* spp., including *T. rammossima*, *T. chinensis*, *T. aphylla* and others)	Interpreted as a single-event type
Aquatic Invertebrates: Mollusks *Dreissena polymorpha* (zebra mussel) *Corbicula flum*inea (Asian clam) *Potamopyrgus antipodarum* (New Zealand mudsnail) Aquatic Invertebrates: Crustacean *Bythotrephes cederstroemi* (spiny water flea)	Interpreted as a single-event type
Aquatic Vertebrates: Fishes *Dorosoma cepedianum* (gizzard shad) *Osmerus mordax* (rainbow smelt) “Asian carp” *Polyodon spathula* (paddlefish) *Scaphirhynchus albus* (pallid sturgeon) *Gila atraria* (Utah chub) *Sander [Stizostedion] lucioperca* (zander)	Interpreted as a single-event type

Quantitative analysis focused on a simple probability estimate for potential biota transfers associated with water diversions and relied upon available data related to failures in distribution infrastructure (see Deb et al. 1995; Schippers et al. 2004) and dispersal of species of concern recorded in the literature (see Appendix 3A and Appendix 3B) for an interpretative context in Section 4. Empirical data were limited or not available in most cases, and general distribution properties, e.g., assumptions of normality as limiting distribution for Poisson processes (see Appendix 4) or comparative data for related taxonomic groups, were considered within an interpretive context to characterize outcomes of the multiple-step invasion process. Distribution assumptions and reliance on comparative data, however, influenced uncertainties associated with interpretation of these simple probability estimates risk. These uncertainties are subsequently considered in Section 4 focused on risk characterization.

Figure 2 illustrates all outcomes from the simulations completed as part of the stochastic process envisioned as occurring during any of the flows of events depicted in Annex Figure 1 through Annex Figure 5 (Section 2). As such, those simple probability estimates graphically summarized in Figure 1 range from "practically 1.0" to values "practically 0." Appendix 13 lists all outcomes from experiments generated in the iterative process that focused on the train of events required to realize a species invasion (or shift in metapopulation) from biota transfers from the Missouri River to Red River basins.

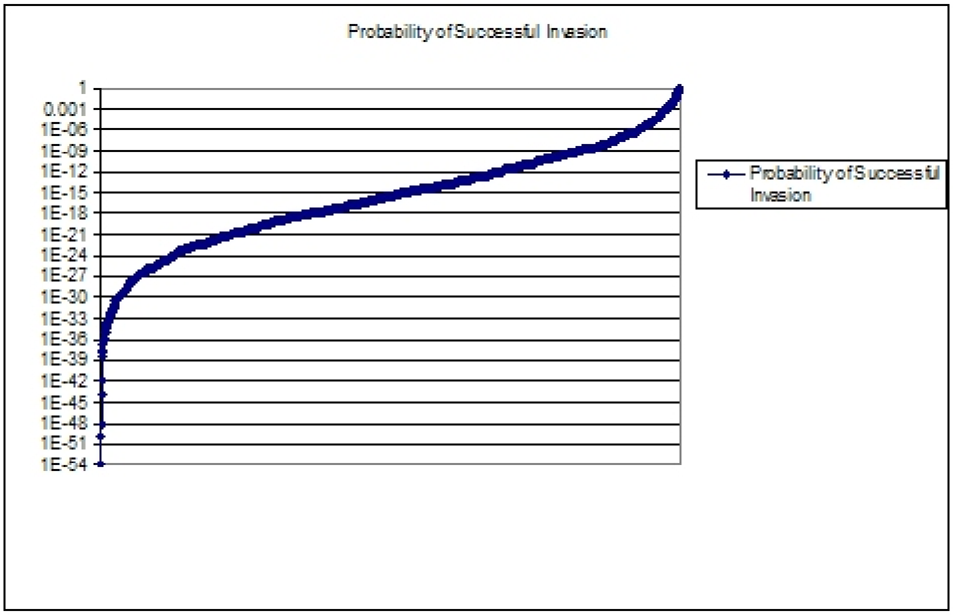


Figure 2. Plot of outcomes from iterative calculation (n=1728) of probability of successful invasion. Outcomes plotted from low risk (left side of panel) to high risk (right side of panel).

In Figure 2, the outcomes of "successful invasion" (or for species currently present in both source and receiving basins, "increased metapopulation in receiving area") are simply plotted from lowest probability outcome to highest probability outcome derived from iterative experiments completed in this investigation. These outcomes of "successful invasion" incorporate various inputs (e.g., probability of biota of concern occurring in source waters transferred to receiving system, probability of control system failure) following a stochastic process, which is amenable to greater resolution as risks are characterized (see Section 4). At this level of simulation, however, no distinction is made regarding biota of concern or whether control systems of any specific type are located at nodes along the flow of events depicted in each of the FPTs in Annex Figure 1 through Annex Figure 3. Instead, the simulation focuses on serial flows of events characterized by nodes other than those presenting sources of interaction between nodes, as illustrated, e.g., in FPTs 3, 4, and 5. Even in these relatively coarse-grained conceptual models, the recognition of interactions between nodes within serial events precludes simple probability analysis as a tool applicable to the current investigation, given these interactions obviate assumptions of independence.

As a prelude to risk characterization in Section 4, an preliminary analysis focused on control systems and their relationships to species invasions (or shifts in metapopulations), which is graphically summarized in Figure 3a,b. Here, an arbitrary probability of control system failure set at 10^{-3} was applied as a filter to the range of "successful invasion" outcomes.[1] When control system performance was associated with probabilities of failure less than 10^{-3}, probabilities of successful invasions ranged between 10^{-4} and 10^{-54} (Figure 3a). In contrast, if a control system was absent and biota transfer occurred as simply a stochastic event, or if the control system failed at probabilities bounded by 10^{0} and 10^{-3} (Figure 3b), then probabilities of successful invasions ranged from near unity to 10^{-34}. Although an exhaustive sensitivity analysis focused on specific control systems (e.g., slow sand filtration, pressure-driven membrane filters) must be deferred until greater specification is identified in infrastructure design, these preliminary results suggested that interbasin water transfers would be amenable to a characterization of risks reflecting different levels of control in the diversion, e.g., "open conveyance," "closed conveyance without treatment," and "closed conveyance with treatment" (see Section 4)

In addition to the varying influences of control systems potentially incorporated into interbasin water diversion infrastructure (e.g., aboveground and buried distribution piping, and water treatment systems as designed), biota of concern are also key elements of the analysis of risks and their subsequent characterization in Section 4, especially within the context of a species'

---

[1] For these analyses, preliminary values for control system failures were developed after review of Deb et al. 1995; Hughes 2002; Moser 2001; Nayyer 2000; and Schippers et al. 2004, with a particular focus on failures observed in piping and water distribution networks, and a range of chemical treatment and membrane filtration technologies.

potential distribution within the area of concern (see §3.3) and the time course of dispersal and spread of the founding group.

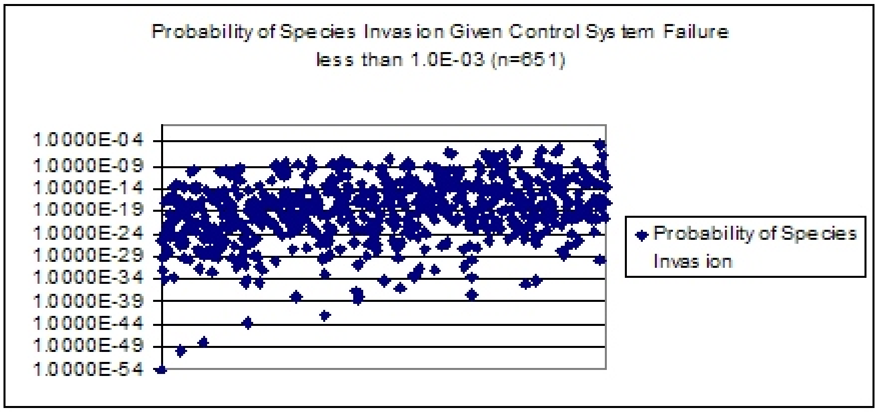


Figure 3a. Probability of species invasions given control system failure less than 10^{-3}.

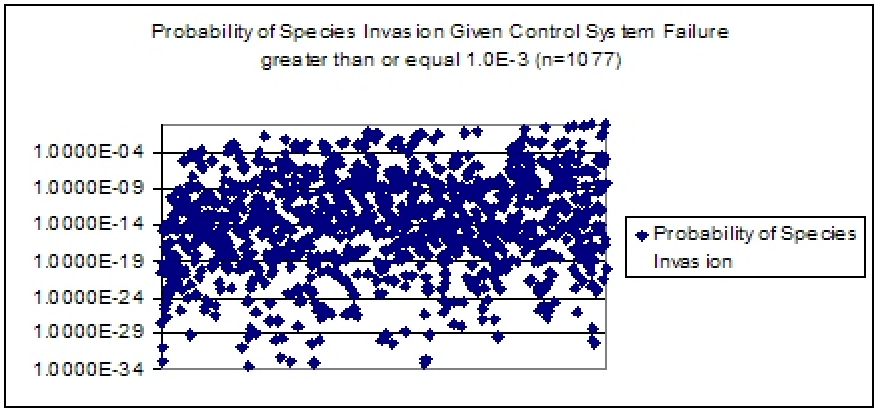


Figure 3b. Probability of species invasion given control system failure greater than or equal to 10^{-3}.

3.2.1 Spatiotemporal analysis. Few biota of concern presented data sufficient for a spatiotemporal analysis. Yet, for zebra mussel and New Zealand mudsnail an initial characterization of the dispersal and growth provided data sufficient to complete an illustrative analysis of the spatiotemporal features of the invasion process. To complete these analyses, methods relied on those originally formulated by Skellam (1951) and subsequently elaborated by Shigesada and Kawasaki (1997), Okubo and Levin (2001), and Cantrell and Cosner (2003).

Once a founding population has emigrated to previously unoccupied, yet suitable habitat, its density typically will increase and individuals will disperse into adjoining areas of suitable habitat. The spread of a species is driven by two processes, population growth and dispersal, and most models of population spread have focused on these processes. For the current investigation, the simplest and probably the most widely applied model of population spread was used in the analysis. Reaction-diffusion type models combine random diffusion with exponential growth (Skellam 1951):

$$N_{x,t} = \frac{N_{0,0}\ e^{rt-x^2/4Dt}}{4\pi Dt}$$

where $N_{x,t}$ = density of organisms at distance, x, from the point of release and at time, t, from the time of release of $N_{0,0}$ organisms at time 0, D is the “diffusivity” or “diffusion coefficient” that measures dispersal, and r is the “intrinsic rate of natural increase” (“birth rate minus death rate” under optimal conditions; e.g., without crowding or resource limitation).

While our focus lies with zebra mussel and New Zealand mudsnail, the dispersal and growth process that characterizes biological invasions is similar, if not identical, to a generalized process reflected in bacterial growth on defined laboratory media (Figure 4) or expansion of vertebrate populations in new habitat (see Okubo and Levin 2001 for examples).

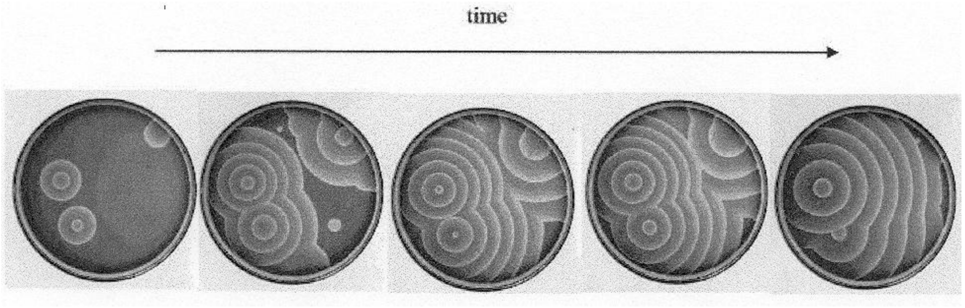


Figure 4. Bacterial growth on laboratory agar plates.

The assumption of random movement in a simple reaction-diffusion model implies that the population will spread radially at an equal rate in all directions (Figure 5). Skellam (1951) originally showed that for any detection threshold, T, such that the infested area at any time t is restricted to points where $N_{x,i} > T$, the expansion velocity of the infested front (radial rate of spread), V, is constant and can be described as

$$V = 2\sqrt{rD}$$

in a simple Skellam equation. There has generally been close congruence between predictions of this model and observed rates of spread of exotic organisms (see Andow et al. 1990), including zebra mussel where data are relatively well characterized (see Appendix 3A).

The simple Skellam model assumes a single, continuous form of dispersal, and it predicts that range expansion should be a smooth, continuous process (Figure 5a). However some species may be able to disperse in at least two ways. If the invasion process reflects both diffusive and jump dispersal, it has been referred to as "stratified dispersal" (see Shigesada and Kawasaki 1997; Kot et al. 1996), and range expansion will proceed through the formation of multiple discrete, isolated colonies established ahead of the infested front. These colonies in turn will expand their ranges and ultimately coalesce (Figure 5b). One consequence of this phenomenon is that range expansion may occur much faster than under a simple diffusion model.

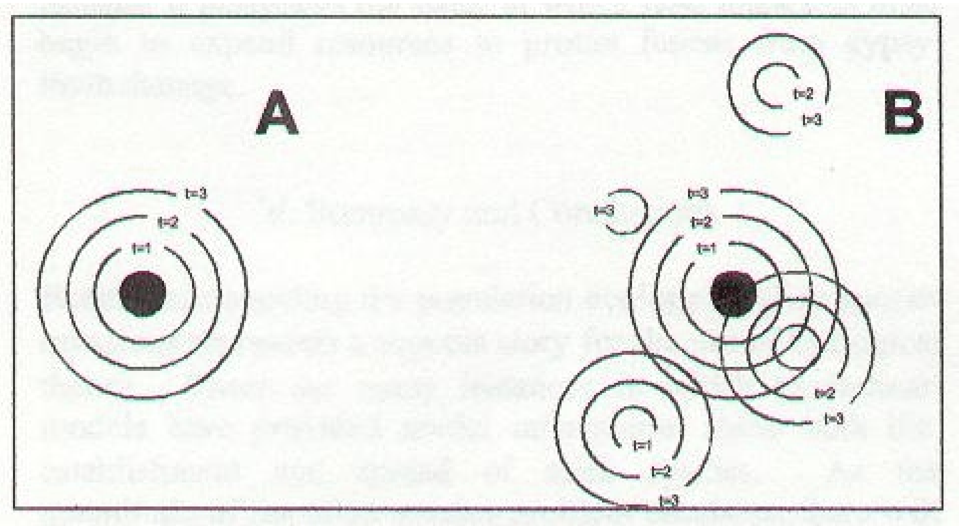


Figure 5. Frame A resolves about a single focus of diffusion, and Frame B illustrates diffusion from multiple foci.

Predicated on published accounts of life history (see Speirs and Gurney 2001; Appendix 3A), values for ***r*** and **D** were applied to the original Skellam equation, and the predicted wavefront for both invasive mollusks (zebra mussel and New Zealand mudsnail) would be nearly 100 kilometers (km) per year. The range about this estimate, however, reflects the variability in the available empirical data (50–250 km/year). More importantly, either species would likely exceed these values given the stratified diffusion that best characterizes the dispersal process currently exhibited by each species. In the absence alteration of preferred habitats and intervention measures, both these mollusks may arrive in the Red River basin within the next 20–25 years, and sooner (e.g., within the next 5 years), if jump events contribute to the stratified dispersal that currently characterizes the invasion process of each species (see Appendix 3A).

3.3 Spatial Analysis: Predicted Distributions for Biota of Concern

While all biota of concern did not present data sufficient for an evaluation of their predicted "potential distributions," georeferenced data were available for some of the fishes

(“Asian carp” as a compilation of bighead carp, black carp, and silver carp), gizzard shad and rainbow smelt), zebra mussel, New Zealand mudsnail, and tamarisk (compiled as *Tamarix chinensis*, *T. aphylla*, *T. parviflora*, *T. ramosissima*, and hybrids). Nearly all biota of concern presented occurrence data on a county or state basis (see Appendix 3A and Appendix 3B), but such data collections do not present sufficient resolution for evaluating historic, current, or future distributions using GARP. Preparation of this report precluded incorporation of data sets that are currently being compiled and may become available during 2005 (see also, Section 4).

3.3.1 Asian carp. Current distributions for “Asian carp” are noted in Appendix 3A, and given the similarity in life-history attributes of these species as those relate to their invasiveness, current distribution data were collapsed across species lines to capture the potential distribution of these selected carp species in North America for this preliminary analysis of dispersal and spread. Figure 6 and Figure 7 project the spatial sum of best subsets yielding a predicted “species distribution” for Asian carp world wide and within the area of concern, respectively. Given the current distribution record of those species included in the composite Asian carp, potential distribution of members of the composite group includes the Missouri River, Upper Mississippi River and Great Lakes, with 25% to 50% of the best subsets projections suggesting that Asian carp could potentially expand into the Red River basin, if pathways for founding groups were realized. These projections are not dependent on interbasin water diversion to be realized, but represent experimental outcomes dependent on any pathways potentially serving as conduits for passage between Missouri River and Red River basins. Current North American distributions of carp included in this species compilation are consistent with these projections (see Appendix 3A).

3.3.2 Gizzard shad. Figure 8 and Figure 9 present the potential distribution of gizzard shad throughout North America and within the area of concern, respectively. In contrast to Asian carp, the spatial sum of best subsets suggests that gizzard shad would be successful in the Missouri River, Upper Mississippi, and Great Lakes basins, but with the available georeferenced data characterizing the species’ current distribution, the species does not appear to be as great a threat to establishing long-term populations in the Red River basin regardless the pathways that potentially link source areas with receiving waters. Less than 25% of best subsets reflected potential distribution in the Red River basin, as well as other basins within HUC09. As with Asian carp, these projections for gizzard shad are not dependent on interbasin water diversion to be realized but represent experimental outcomes dependent on any pathways potentially serving as conduits for passage between Missouir River and Red River basins. Current distributions of gizzard shad in North America are consistent with these projections (see Appendix 3A).

3.3.3 Rainbow smelt. Figure 10 and Figure 11 present the potential distribution of rainbow smelt in North America and the area of concern, respectively. Since the early 1980s, rainbow smelt have successfully expanded their distribution to HUC09 (see Appendix 3A), which is consistent with spatially summed best subset projections in Figure 11. Based on predicted distribution of rainbow smelt, continued expansion of rainbow smelt in HUC09 is anticipated, including waters within Red River basin, if pathways are realized that link source areas within HUC09 with receiving waters in the basin of concern. Continued expansion in the surface waters of the Great Lakes and Upper Mississippi basin should continue if management practices do not limit diffusion or stratified diffusion processes from promoting dispersal and spread of the species. On the basis of the spatial sums of best subset projections, rainbow smelt dispersal and spread within the Missouri River basin would appear limited, which is consistent with the species current distribution (see Appendix 3A). As evident from the current distribution, these projections are not dependent on interbasin water diversion to be realized, but represent experimental outcomes dependent on any pathways potentially serving as conduits for passage between Missouri River and Red River basins.

Figure 6. Asian carp predicted distribution projected world wide.

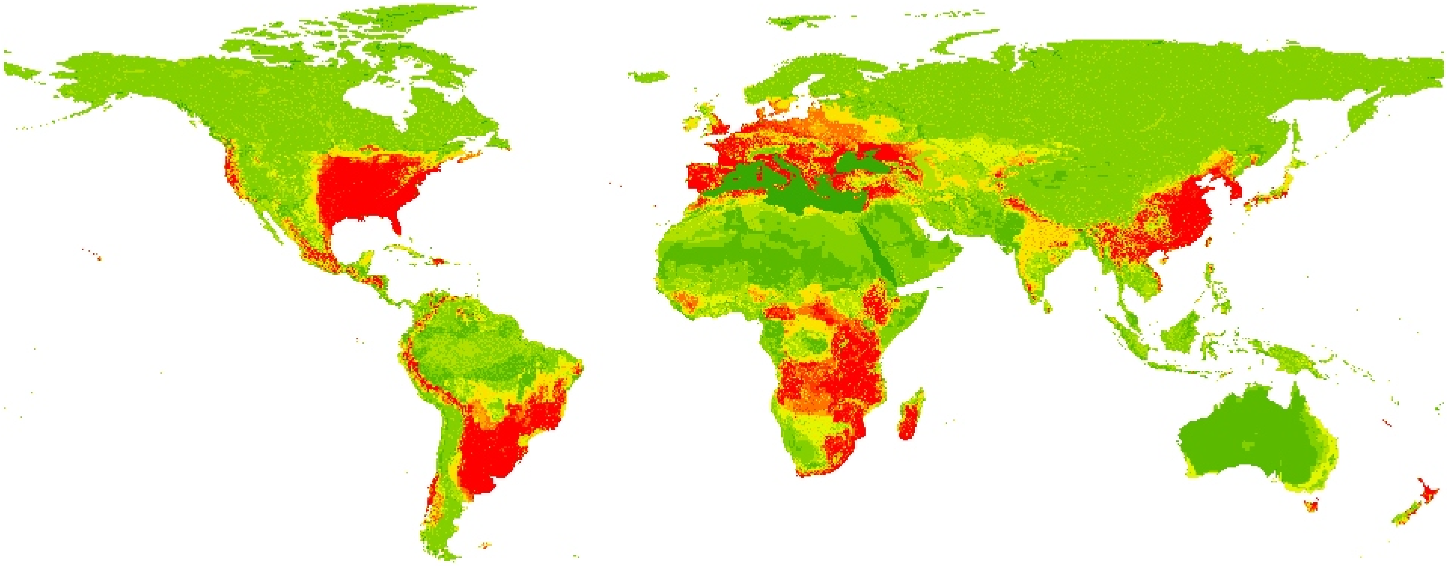


Figure 7. Zoom-scale projection of Asian carp predicted distribution in area of concern.

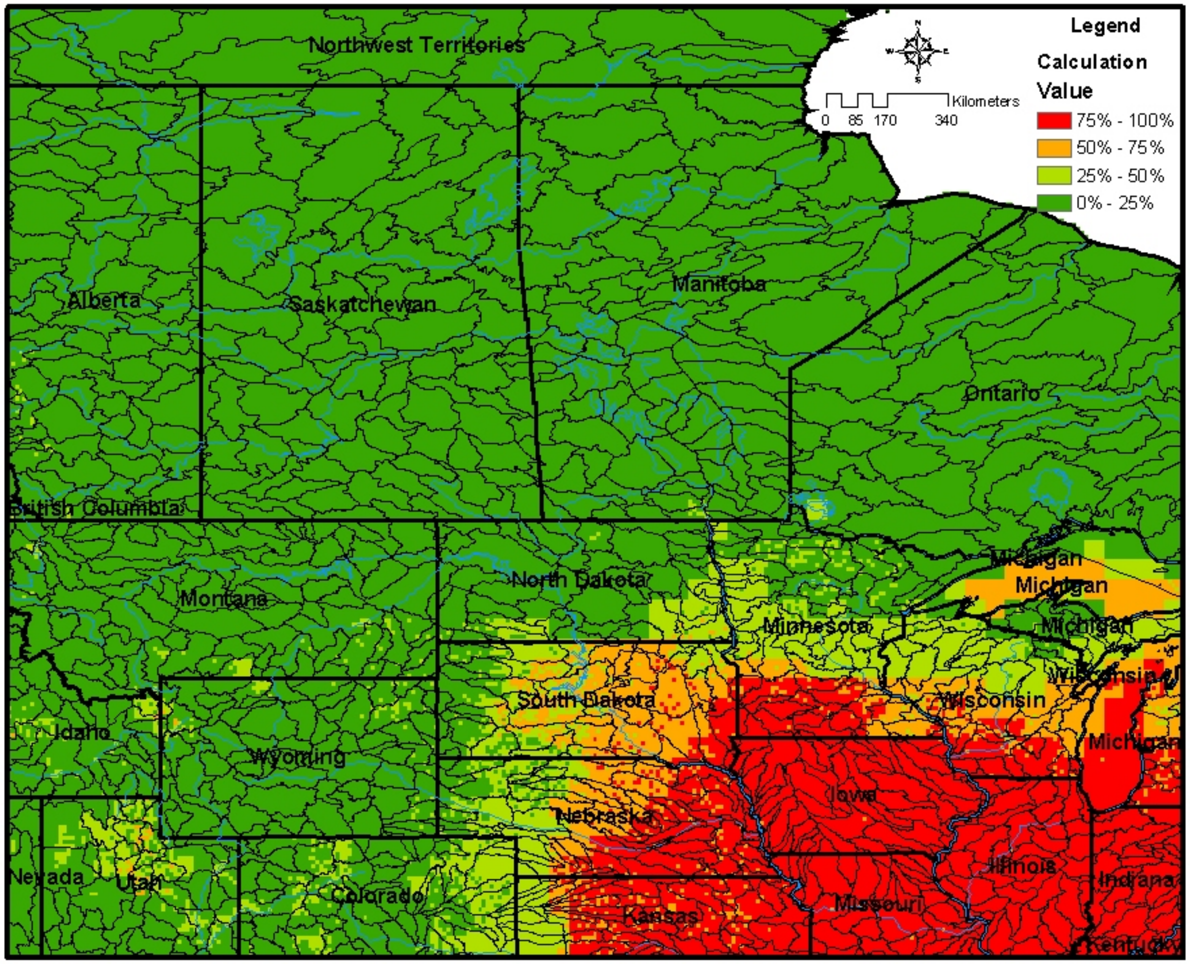


Figure 8. Gizzard shad potential distribution predicted to North America.

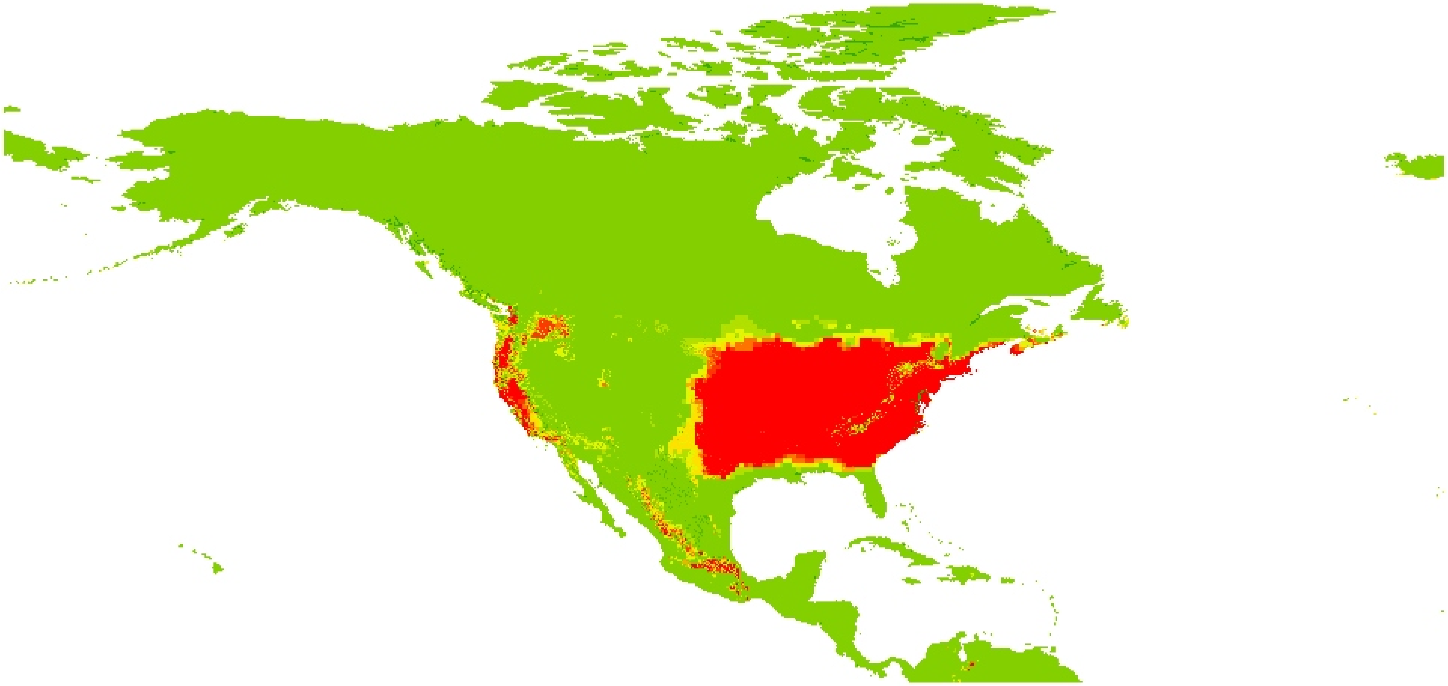


Figure 9. Zoom-scale projection of gizzard shad potential distribution in area of concern.

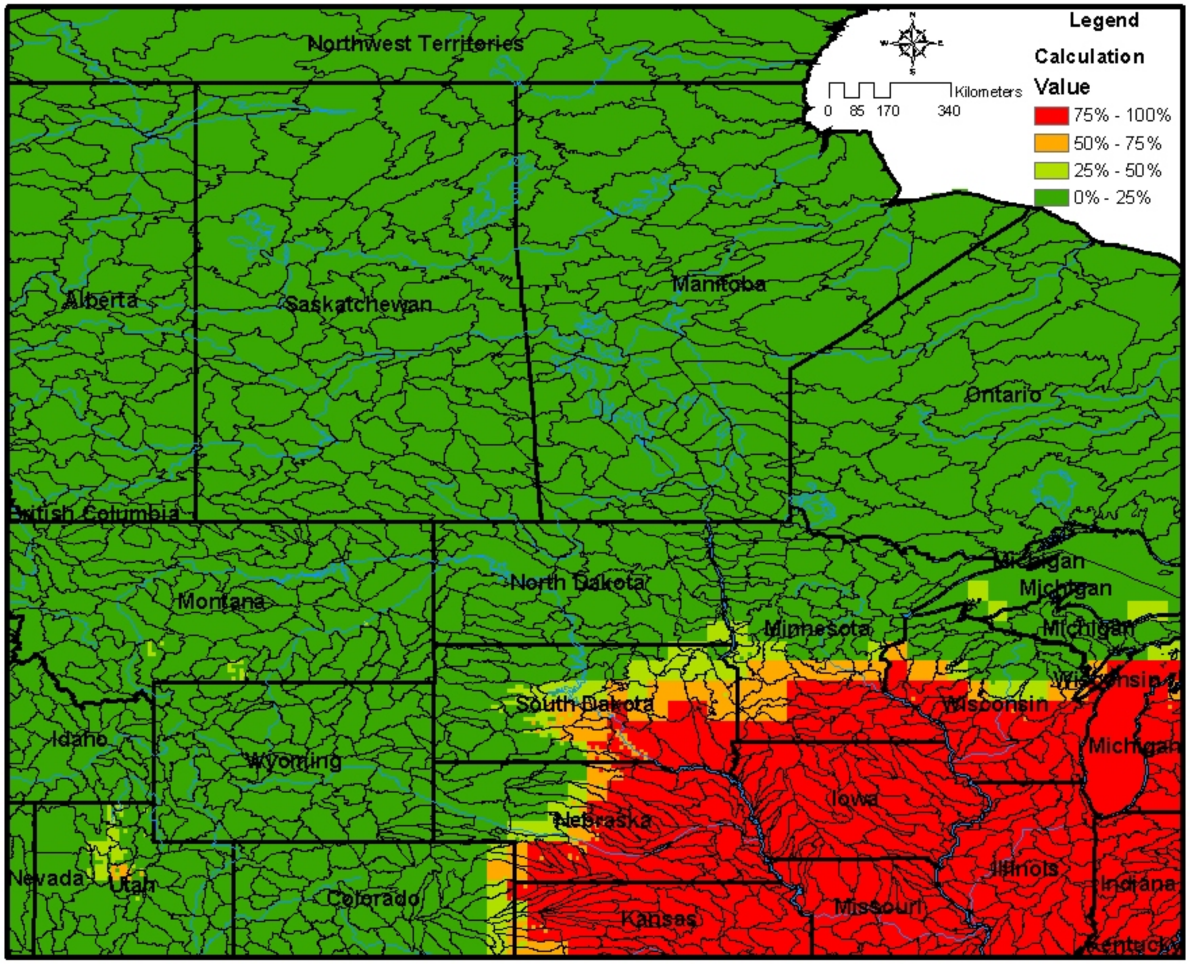


Figure 10. Rainbow smelt predicted distribution projected to North America.

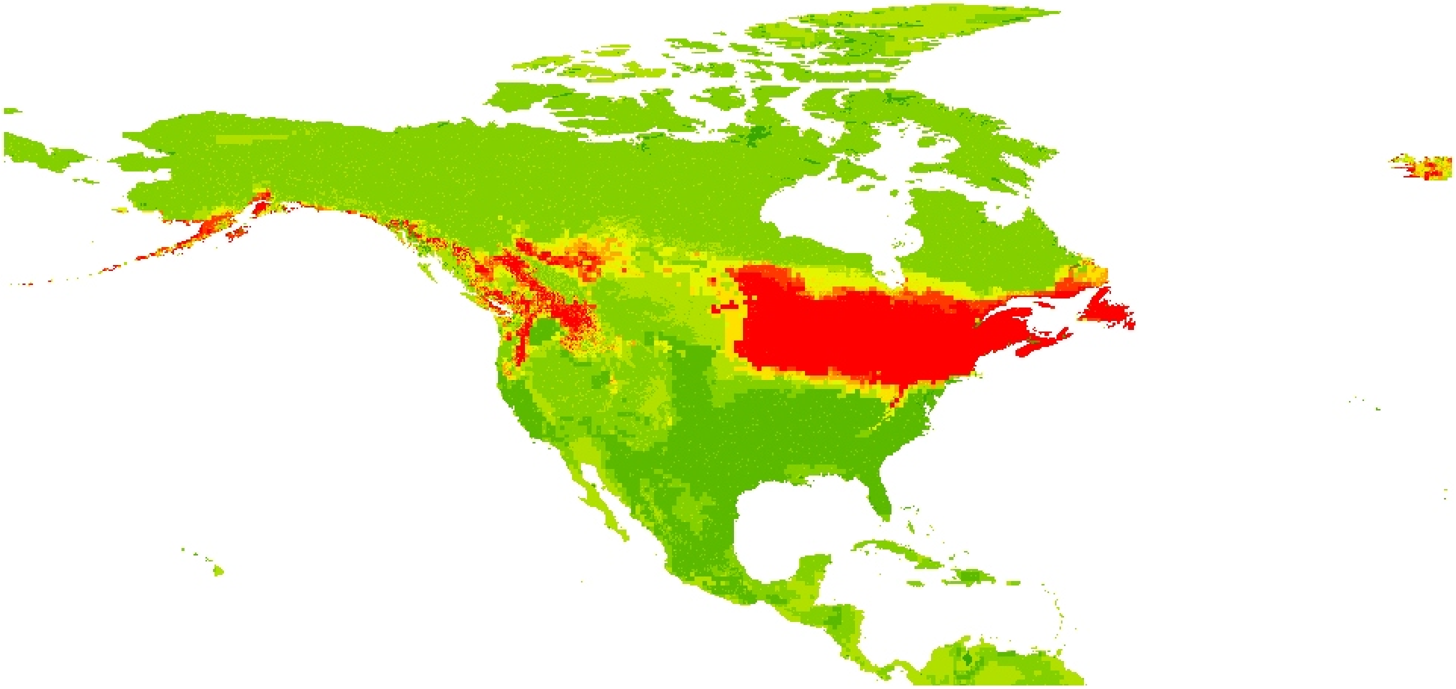
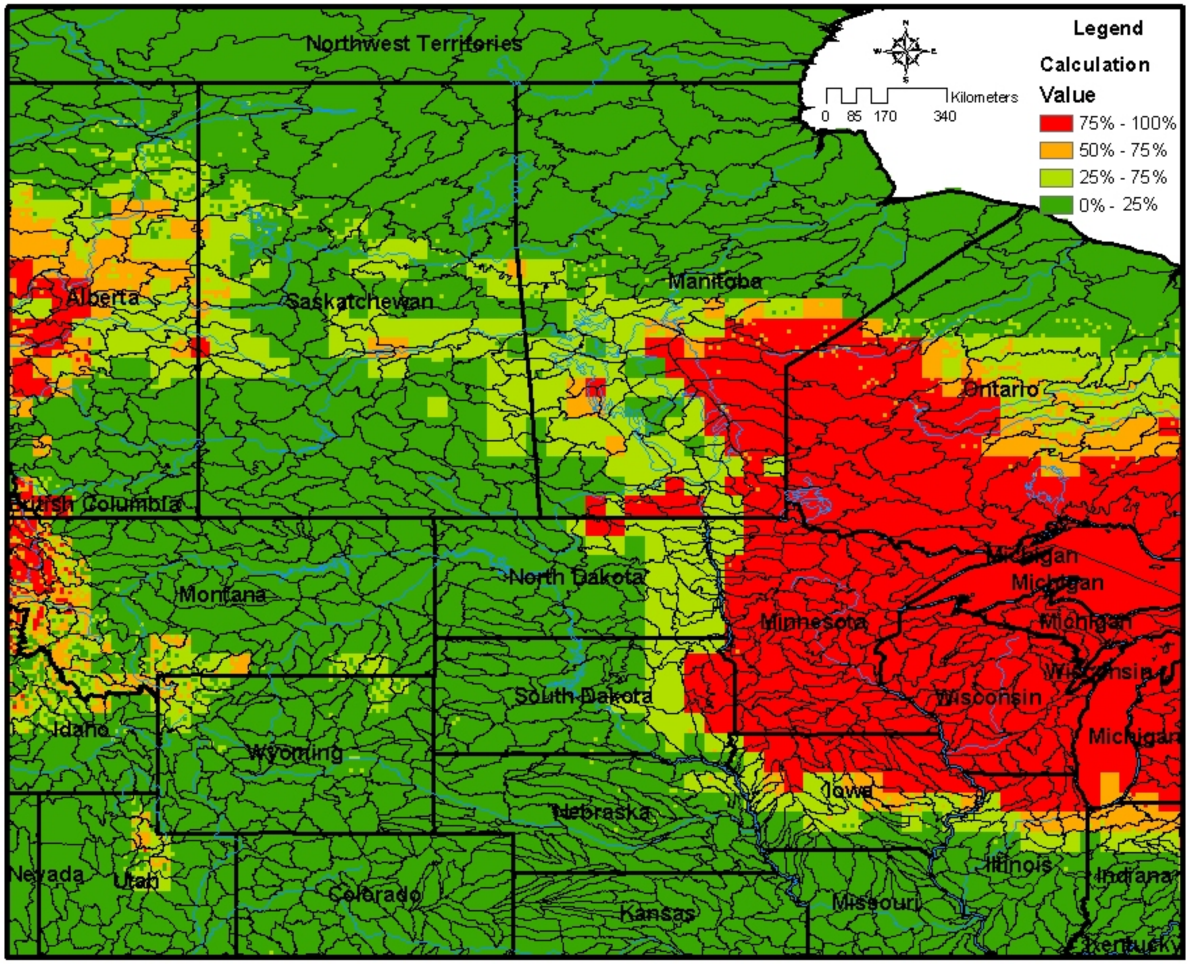


Figure 11. Zoom-scale projection of rainbow smelt predicted distribution in area of concern.



3.3.4 Aquatic invertebrates. Georeferenced data were available for zebra mussel and New Zealand mudsnail and enabled analysis of predicted species distribution using GARP. Appendix 3A summarizes current species distributions state wide and county wide for other aquatic invertebrates whose invasive status should also be considered from an ecological perspective similar to that guiding the analysis focused on zebra mussel and New Zealand mudsnail as representative aquatic invertebrates.

3.3.4.1 Zebra mussel. Zebra mussel presented georeferenced data that afforded an opportunity for a time-series analysis of the species dispersal and spread in surface waters of North America (see Appendix 3A and Section 4, especially related to uncertainty analysis). With the currently available georeferenced data for zebra mussel, predicted distribution of the species in North American is illustrated in Figure 12 and Figure 13 which present spatial sum of best subsets for North America and the area of concern, respectively. In contrast to other spatial analysis using GARP, the potential distribution of zebra mussel clearly fits with the species current distribution (see Appendix 3A), but the species distributions projected as sum of best subsets indicates that dispersal and spread of the species may go beyond the 100th meridian, if pathways linking sources and receiving systems are realized. This observation is drawn in light of the relatively high number of projected distributions (25%–50%, 50%–75%) occurring as outputs from GARP, which is contrasted with other species projections in this spatial analysis of potential distributions where relatively clear limits to species distributions are indicated. Spatial sum of best subsets, however, are influenced by time-related observations, which should be considered in the course of adaptive management focused on prevention and control of zebra mussel in North America (see uncertainty analysis, Section 4).

Current distribution records for zebra mussel are consistent with spatial sum of best subsets, and summed projections indicate that Red River basin affords suitable physical habitat for the dispersal and spread of the species in surface waters of the area of concern. The predicted species distribution in Red River basin is a consistent projection across all possible distributions projected by GARP with 75% to 100% of best subset projections including Red River basin in output projections, suggesting that completed pathways linking source with receiving waters would yield sustainable populations, if completed pathways were realized. These projections are not dependent on interbasin water diversion to be realized but represent experimental outcomes dependent on any pathways potentially serving as conduits for passage between Missouri River and Red River basins. Additionally, given the available time-series data for the dispersal and spread of zebra mussel in the Great Lakes and Upper and Lower Mississippi River basins, these projections could be realized within 20–25 years, and sooner if stratified dispersal occurred between basins of interest.

3.3.4.2 New Zealand mudsnail. Although later in its arrival to North America than Zebra mussel, New Zealand mudsnail presents ample georeferenced data for an analysis of spatial distribution using GARP. Figure 14 and Figure 15 present spatial sum of best subsets from GARP for New Zealand mudsnail for North America and area of concern, respectively. These projections are consistent with the species' current distribution and suggest that Red River basin presents physical habitat features amenable to species dispersal and spread in the future. Summed best subsets projected from GARP also indicate that surface waters throughout the Missouri River, Mississippi River, and Great Lakes basins provide potential areas for species distribution expansion. Following a pattern similar to zebra mussel, best subset projections derived from spatial analysis completed using GARP suggested that habitats open to invasion and establishment of sustainable populations were potentially widespread throughout North America, given the species' distribution conservatively predicted by 50%–75% of best subset projections.

As noted for zebra mussel, projections of potential distribution for New Zealand mudsnail are not dependent on interbasin water diversion to be realized but represent experimental outcomes dependent on any pathways potentially serving as conduits for passage between Missouri River and Red River basins. And, given the available time-series data for the dispersal and spread of New Zealand mudsnail in the western US, these projections could be realized within 20–25 years and sooner if stratified dispersal occurred between basins of interest (as occurred from the initial observation of New Zealand mudsnails along the Snake River in Idaho, and subsequent sightings at various locations in the Colorado River system; see Appendix 3A).

Figure 12. Zebra mussels' predicted distribution projected to North America.

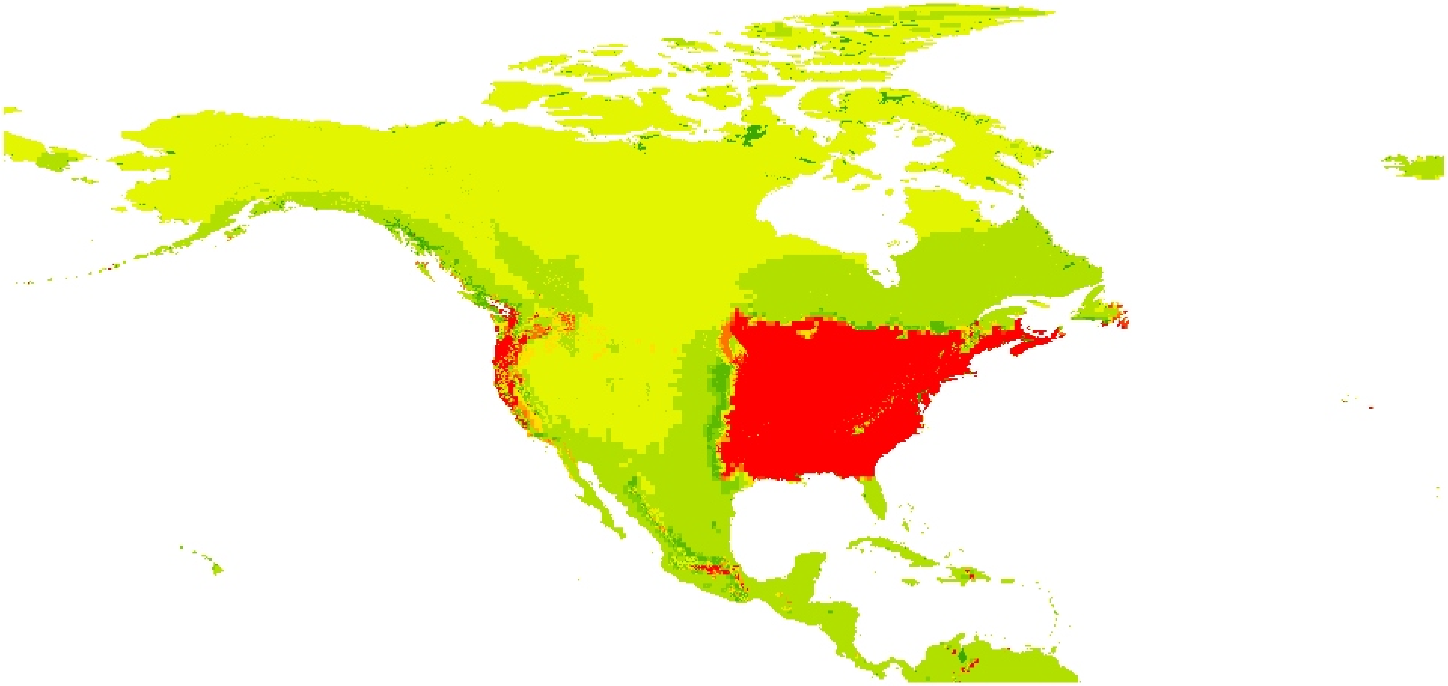


Figure 13. Zoom-scale projection of predicted distribution of zebra mussel in area of concern.

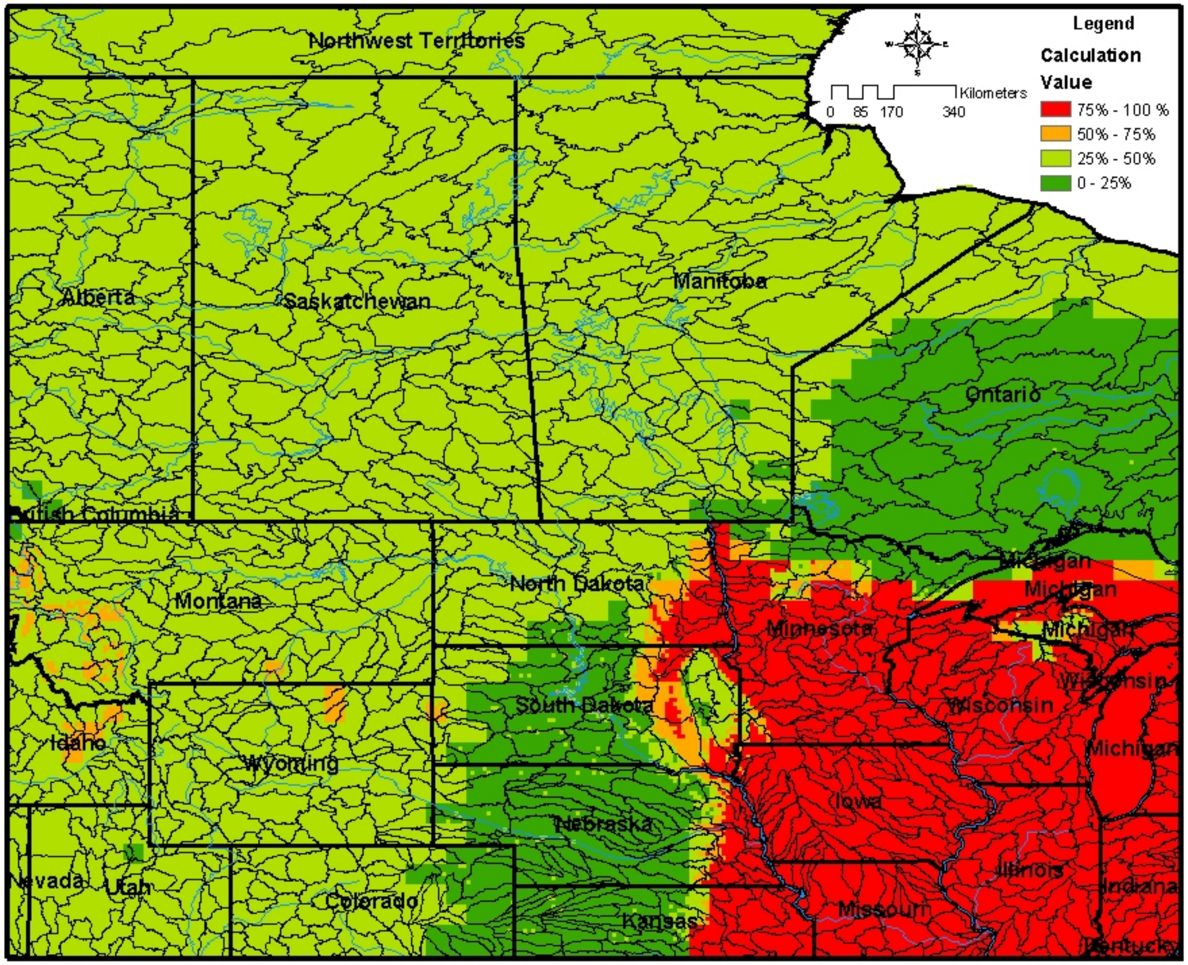


Figure 14. New Zealand mudsnails' predicted distribution projected to North America.

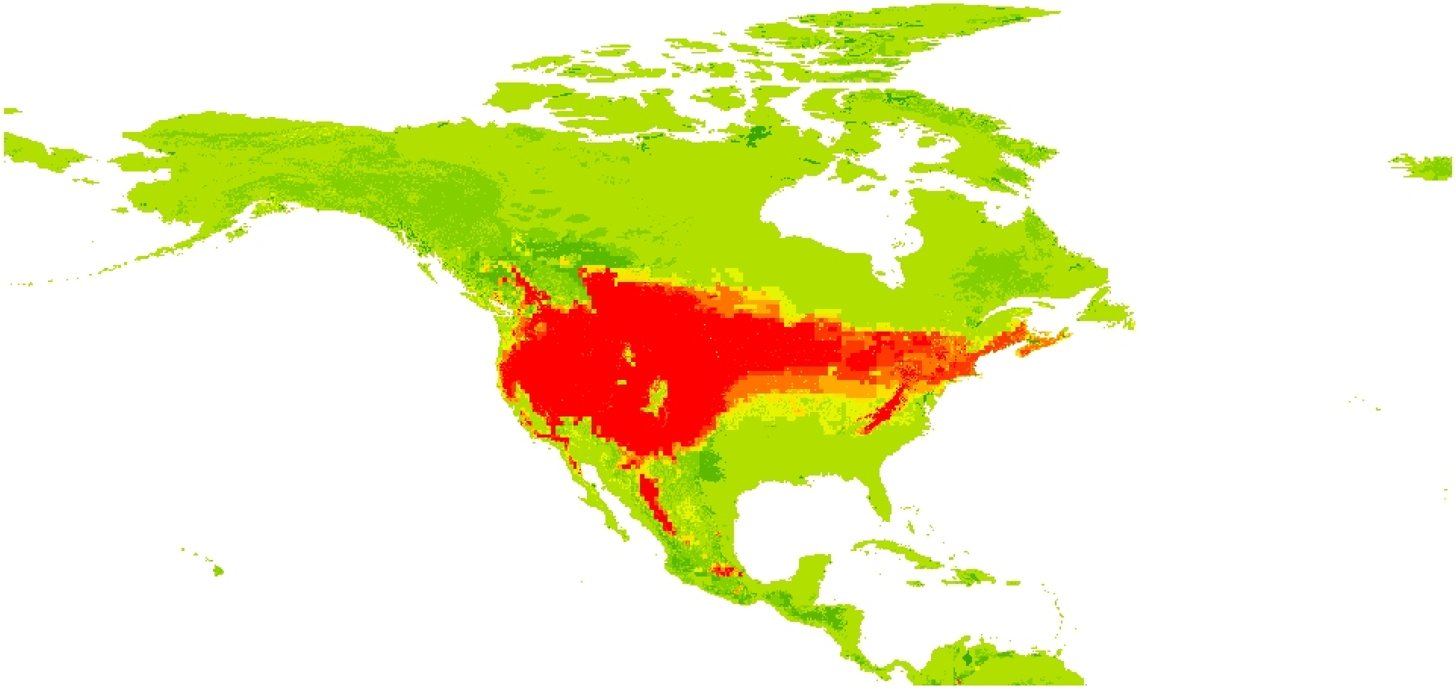
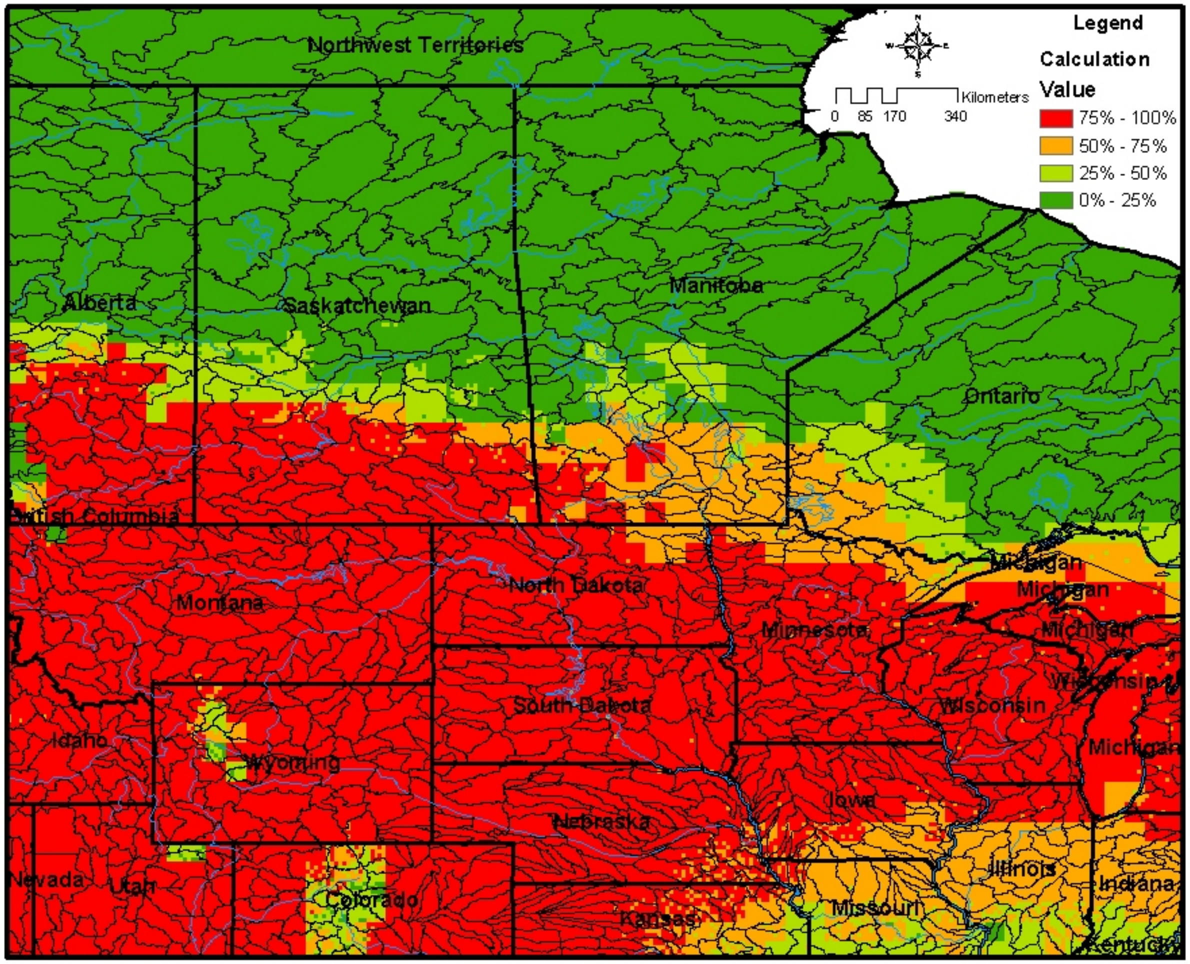


Figure 15. Zoom-scale projection of predicted distribution of New Zealand mudsnail in area of concern.



3.3.5 Aquatic vascular plants–*Tamarix* spp. While various state wide and county wide records are available for aquatic vascular plants, and wetland and riparian vascular plants (see Appendix 3A), only tamarisk presented georeferenced data sufficient to developing predicted species distribution. Here, tamarisk projections are generated based on a compilation of species presence data for *Tamarix chinensis*, *T. aphylla*, *T. parviflora*, *T. ramosissima*, and hybrids, which is represented by the dot map in Figure 16.

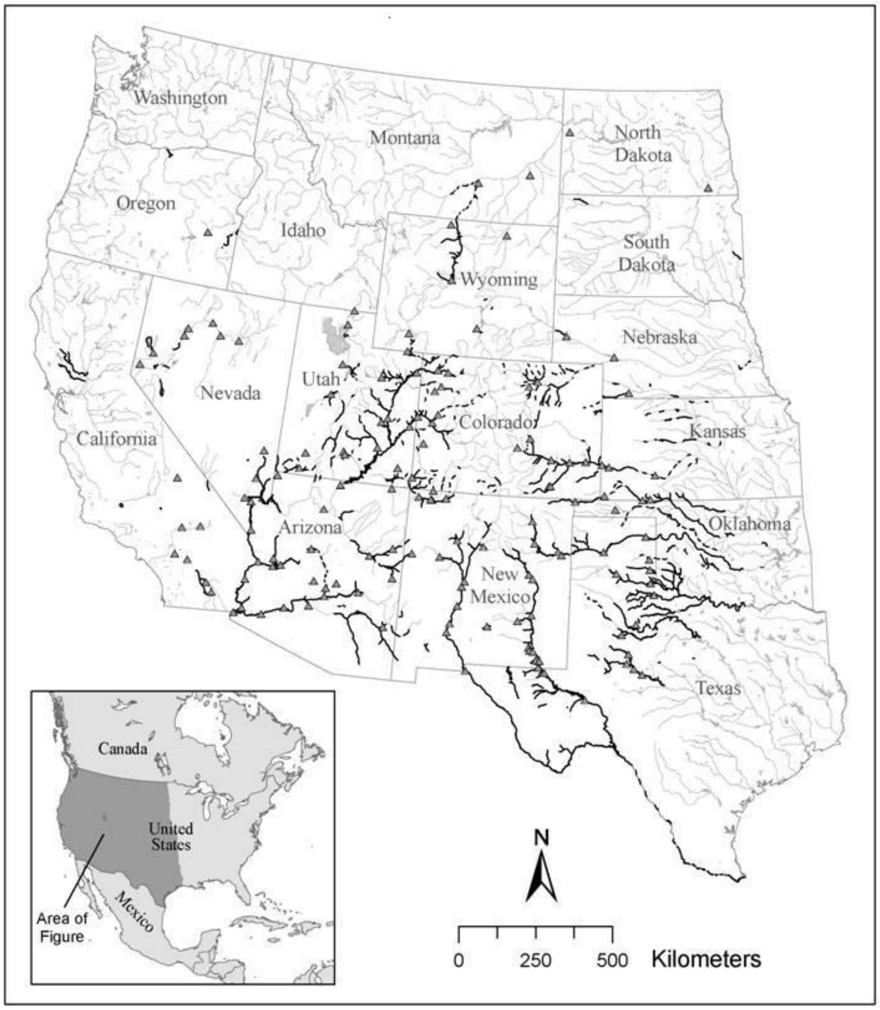


Figure 16. Dot map of tamarisks' (as various species within the genus) current distribution in North America.

Figure 17 and Figure 18 present predicted distributions for tamarisk species in North America and area of concern, respectively. As noted for other species amenable to spatial analysis with GARP, the current distribution of tamarisk in North America is consistent with the spatial sum of best subsets generated in the analysis. On the basis of these projected distributions for *Tamarix* spp., ongoing distribution expansions in the Upper Missouri River drainage, including recent entry into North Dakota along riparian habitats of tributaries to the Missouri River, should continue. Expansion of distribution will continue regardless of status of water diversions. The eastern and northern limits of expanded distribution, however, may be limited (e.g., due to physiological constraints associated with latitudinal advance) and riparian habitats in Red River basin are currently not included in these spatial sum best subsets. Projected best subsets currently present a relatively well-delineated limit to northern and eastern expansion, and future updates in species occurrence data may warrant additional spatial analysis (see uncertainty analysis in Section 4). Indeed, updated forecasts for *T. ramosissima, T. chinesis*, and their hybrids may be encouraged given observations of Pearce and Smith (2002, 2003) that suggest historic dispersal rates of 2.5 and 25 km/year may be realized in the northern expansion of species distribution (depending on extent of stratified disperal). Additionally, these authors noted that the northern limits of the species' native distributions in cold, dry deserts of northeastern Asia do not contraindicate invasion of the northern Great Plains of North America.

Ongoing compilation of georeferenced data, as available, continues for vascular plants as well as other biota of concern, although subsequent additions to this facet of analysis for inclusion to the revised report will necessarily be limited to species for which such data are available or can be assembled from existing museum records (e.g., hydrilla, Eurasian water milfoil).

Figure 17. Tamarisks' (as multiple species) predicted distribution projected to North America.

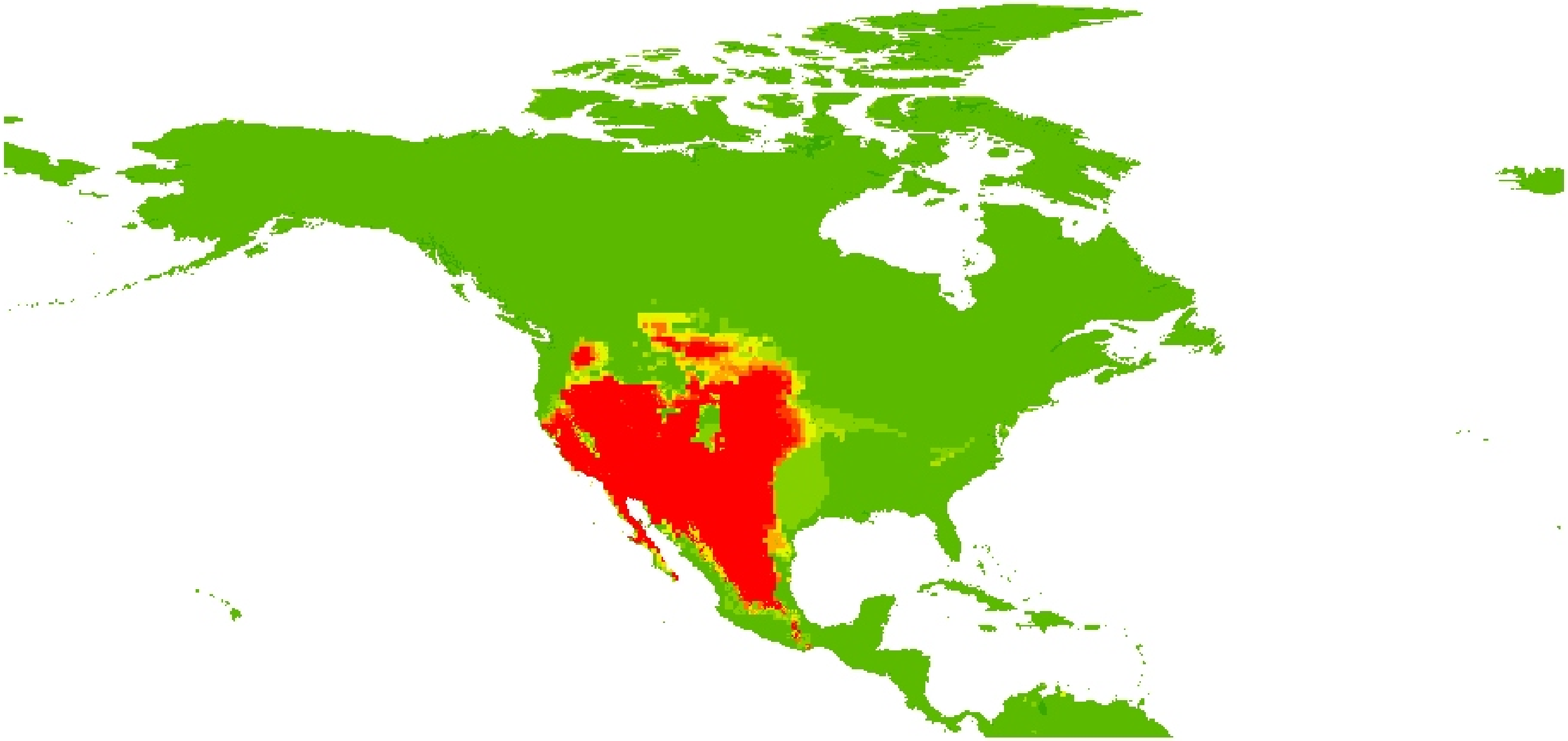
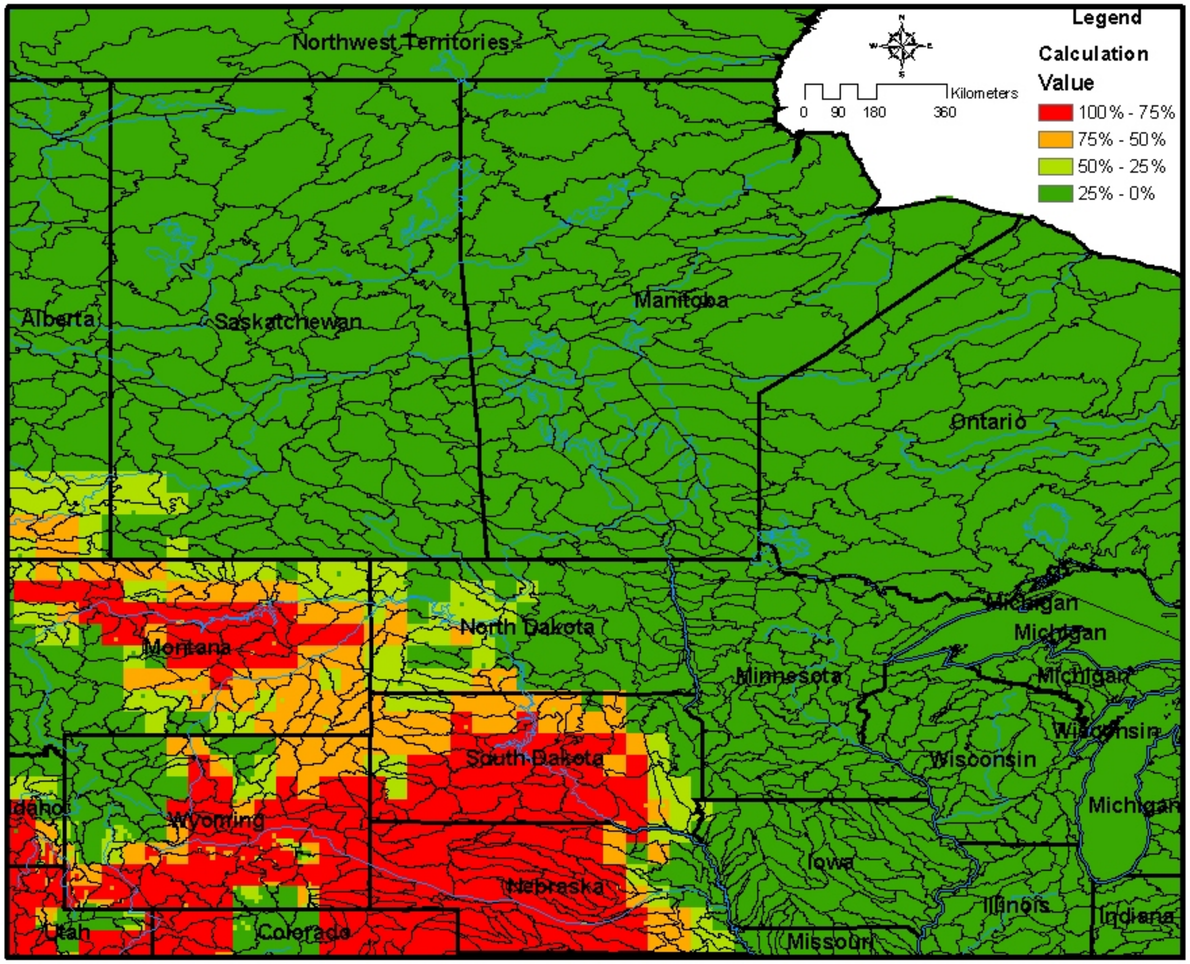


Figure 18. Zoom-scale projection of tamarisks' predicted distribution in area of concern.



3.3.6 Diseases of fish and waterborne disease. Georeferenced occurrence data for disease agents is relatively limited, although state wide and county wide records (especially for zoonoses and diseases of humans) are available for most of the biota of concern and have been included in Appendix 3B. For spatial analysis of disease agents included as biota of concern to stakeholders, the current investigation employed analytical approaches similar to those applied by other authors in developing predictive models of disease dispersal and spread in an illustrative analysis focused on whirling disease (see Peterson et al. 2002; Peterson et al. 2003).

While georeferenced data for the causative agent of whirling disease is limited or highly disperse and unavailable in compiled form, distribution data as “presence only” data for the disease host is readily available; hence, we viewed the potential introduction of *M. cerebralis* as the causative agent for whirling disease as a function of occurrence of its host, rainbow trout (*O. mykiss*). Figure 19 and Figure 20 illustrate the spatial sum of best subsets of predicted species distribution for rainbow trout as projected by GARP. Current distribution of rainbow trout is consistent with GARP’s projection based on spatial sum of best subsets. The occurrence of whirling disease compiled on a state wide basis (see Appendix 3B) suggests that the potential for occurrence of the disease is clearly widespread in North America, with the limiting factors being vectors serving to transport diease agent from source areas to previously unoccupied habitats occupied by sensitive host species. Simply stated, if potential for expanded species distributions are realized through unaided or aided (e.g., active stocking programs) transport of rainbow trout, then the potential for whirling disease exists. And given the natural history of the disease (see Appendix 3B), the occurrence of whirling disease in these expanded rainbow trout distributions will be realized through time.

Although analytically speculative, based on current and presumptively potential species distributions realized by host species, similar outcomes for occurrence of diseases among other fishes may be realized for other disease agents such as ERM and IHNV. Similar outcomes might also be anticipated for terrestrial vertebrates, e.g., wildlife diseases, if hosts (primary and intermediary, if necessary) occur in the receiving system and pathways linking sources and receptors are realized. As noted in previous summaries focused on categorical and quantitative outcomes, these conclusions are not solely dependent on interbasin water transfers, but unrestricted diversions (e.g., water transfer via open conveyance) could potentially afford routes for emigration from Missouri River basin that were otherwise absent.

Figure 19. Predicted distribution of rainbow trout, the primary host for whirling disease, projected to North America.

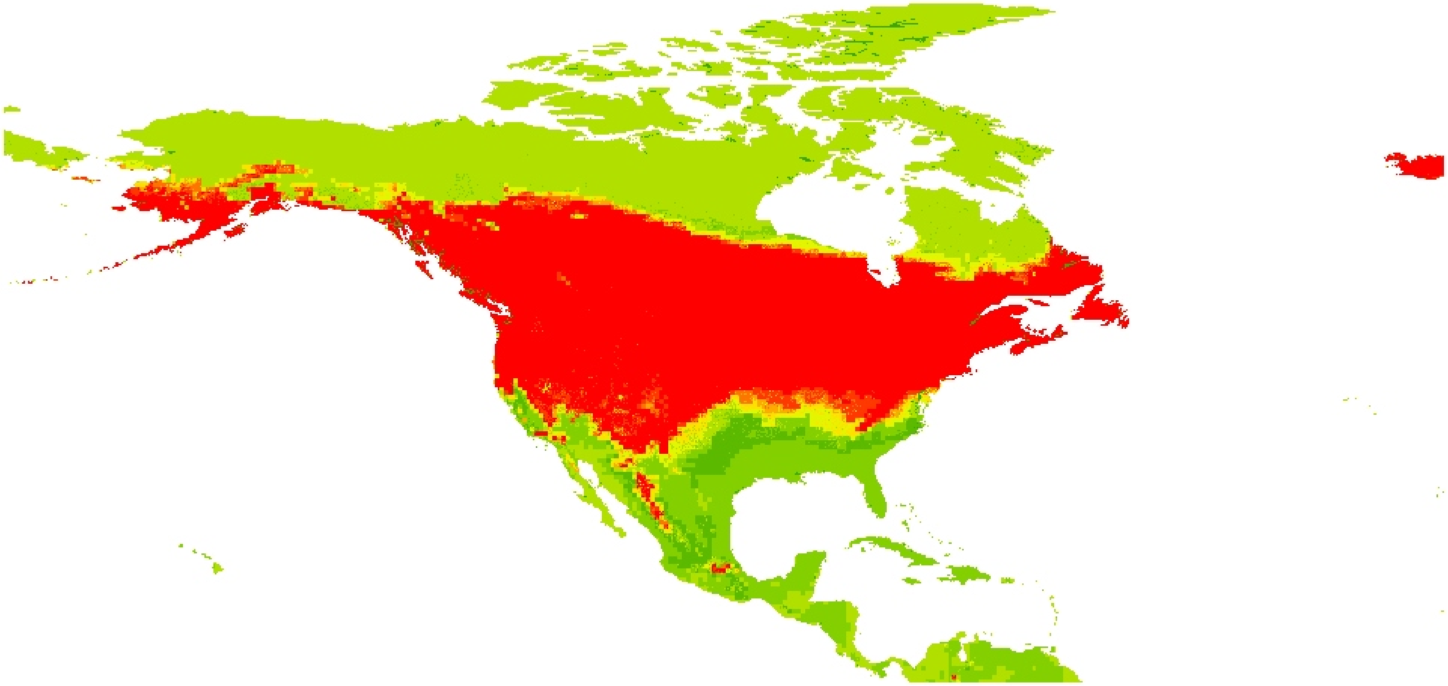
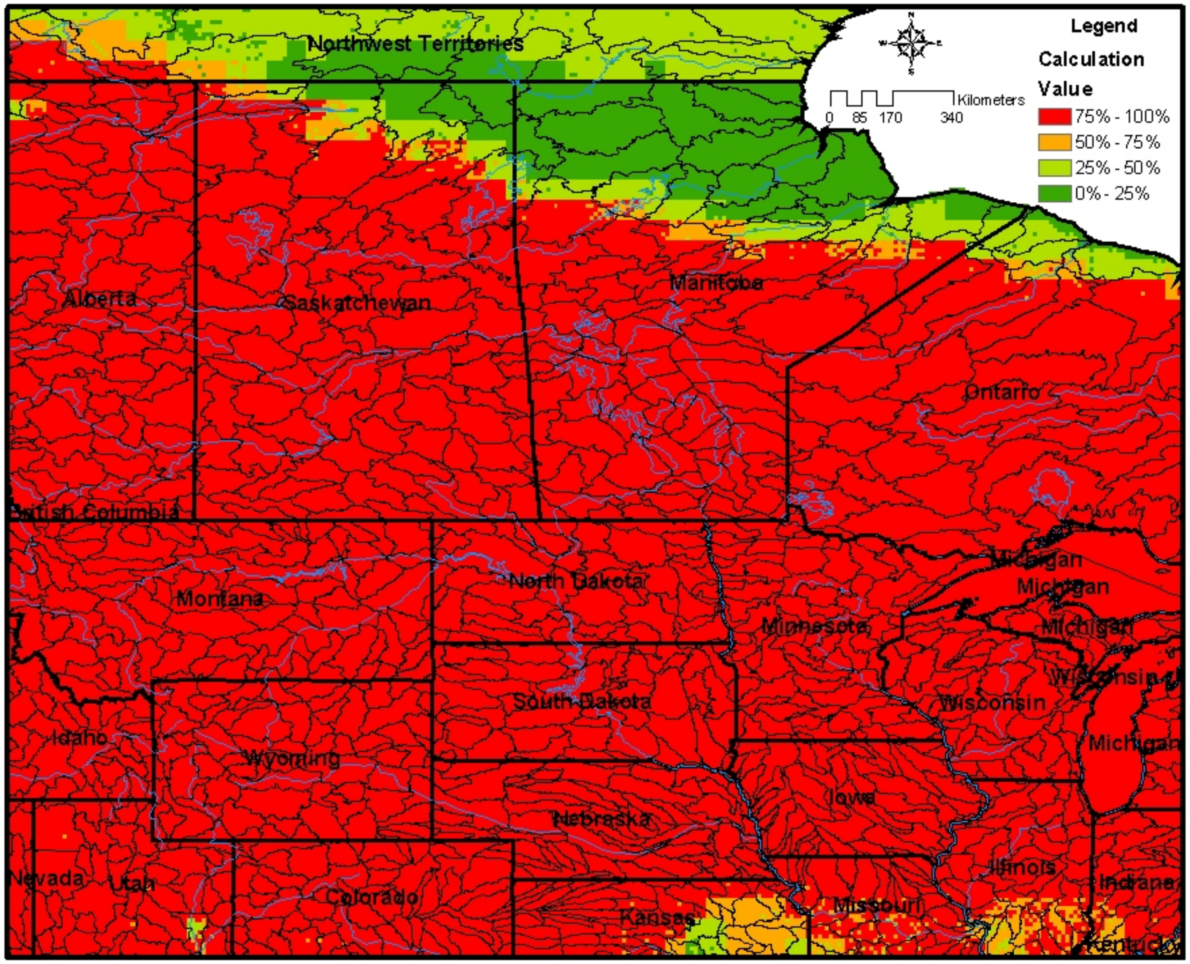


Figure 20. Zoom-scale projection of rainbow trout predicted distribution in area of concern.



3.4 Narrative Risk Analysis for Biota of Concern

Each of the groups of biota of concern identified in Table 10 will be considered in a narrative integration of outcomes derived from categorical analysis, simple probabilistic analysis captured in FPTs, spatiotemporal analysis for representative mollusks and riparian plants, and predictive species distributions generated for selected biota of concern. Regardless of biota of concern, from the perspective of invasion biology, the process of emigration reflects greater stochasticity than does the establishment of sustainable populations, which is highly dependent on life-history attributes related to, e.g., intrinsic rates of increase and other traits characteristic of the species.

3.4.1 Narrative analysis: Fishes.[2] Limited georeferenced data needed to evaluate predicted distributions for paddlefish and pallid sturgeon are available, and preliminary efforts to develop comparable numerical and map outputs of predicted distributions suggested that the existing records were not sufficient for analysis. This judgment largely reflected an initial review of preliminary outputs from GARP that clearly indicated that projected distributions based on available georeferenced occurrence data did not correspond to current museum records for distribution of sturgeon (i.e., either pallid or shortnose; see Section 4). The fishes, however, have been subject to much biogeographical study over the past 100 years (see historic accounts Jordan and Everman 1896-1900; Woolman 1896 and more recent accounts Eddy et al 1972; Scott and Crossman 1973; Eddy and Underhill 1974; Crossman and McAllister 1986; Underhill 1989; Loomis et al. 1999), with much of the regional focus on the ichthyofauna stemming in part from recent concerns associated with water diversions such as those currently under consideration (see Petreka 1978, 1992; Swain et al. 1980; North Dakota Game and Fish Department 1986, 1994; Ryckman 1981; Stewart et al. 1985; Petreka and Koel 1996; Koel 1997).

For example, Peterka and Koel (1996) and Koel (1997) completed a distributional survey of the fishes of the Red River then analyzed their survey finds relative to historic records in characterizing the ichthyofauna of the basin. Koel (1997) had observed that historic fish distribution lists for the Red River basin cited different species occurrence records, e.g., Crossman and McAllister (1986) had listed 75 fish species for the Red River basin in the United States, while Underhill (1989) had listed 80 species. Koel (1997) subsequently compiled historic records for fish distributions in the region, including field survey records of fish occurrence, and documented records for 77 native and 7 introduced fish species in the Red River basin during the recording period, 1892–1994. Diversity of fishes in the Red River basin was considered relatively high, particularly in contrast to other rivers in the basin. Observations similar to those of other workers publishing during the period were noted for fish species common to the Red River and

---

[2] Updated and edited from material originally developed by John J. Peterka and Todd M. Koel, Zoology Department, North Dakota State University, Fargo, ND 58105 (October 1996); Todd Marvin Koel, Zoology Department, North Dakota State University, Fargo, ND (May 1997) for USGS/BRD/NPWRC, Jamestown, ND.

immediately adjacent basins. For example, Koel (1997) observed that 69 fish species were listed as occurring in the Upper Mississippi River (above St. Anthony Falls, Minneapolis), and 72% of those species (62 out of 69) also occurred in the Red River basin. Similar observations were noted for the Minnesota River where 72 of 88 species (84%) were shared with the Red River and for the Missouri River (in North Dakota) where 46 of 65 species (54%) were common to Red River and Missouri River waters (Ryckman 1981). Koel speculated that the ichthyofauna of the Red River basin appeared more closely related to that of the Minnesota River to the south and the upper Mississippi River to the east, a hypothesis reflecting a previously posited suggestion that current day fishes of the Hudsonian region reflect postglacial dispersal patterns of fishes (see Underhill 1989). Koel (1997) suggested that "the low faunal similarity between the Red and Missouri Rivers may indicate a lack of any significant postglacial dispersal route between the two basins, or it may simply be due to differences in habitat that are available to fishes."

Petreka and Koel (1996) and Koel (1997) continued a line of published documentation that reinforces observations related to survey sample designs (e.g., difficulty in characterizing presence-absence of "rare targets;" see Thompson and Seber 1996; Manly et al. 2002; Helsel 2005) and the dynamic character of biogeographic distributions of plants and animals throughout North America (see Scott et al. 2002). A focus on fishes clearly illustrates how a characterization of a faunal distribution through a sample collected during a "snippet of time" can lead to seemingly confounding observations, particularly when these snippets are compiled in a haphazard time-series analysis reliant on sample designs of different specifications. For example, a focus on interfaces between major drainage basins (e.g., HUC10, Missouri River and HUC09, Red River-Souris River-Rainy River) clearly cannot avoid considering source areas for "immigrants" from areas other than those of principal concern. Koel (1997) and others (see Crossman and McAllister 1986) clearly indicate the importance of geographic interfaces with other drainage basins, especially the Upper Mississippi (HUC07) and the Great Lakes (HUC06). For example, Table 11 and Table 12 list occurrences of grass carp (*Ctenopharyngodon idella*) and silver carp (*Hypophthalmichthys molitrix*), respectively, in the Red River and Missouri River basins, as well as basins immediately adjacent to these basins of concern. Not surprisingly, fish species lists for the Red River basin do not include either of these exotics, yet these species have emigrated or have been released, then subsequently collected from locations in Missouri River basin, Red River basin, and adjacent basins, apparently before sustainable populations were established. As with Asian carp, these fishes considered biota of concern in the current investigation have previously been collected from waters in the Red River basin, so opportunity for invasion has occurred in the past. Those documented occurrences, although transient, suggest that future emigrations from any of the adjacent HUCs or releases by human agency (e.g., intentional or accidental releases mediated by human intervention) may establish "beachheads" that subsequently serve as a pioneering collection of individuals that potentially lead to sustainable populations. Distinguishing sources of these pioneering individuals may be frustrated by inadequate characterization of baseline or given our current range of diagnostic tools may not be technically plausible (see Scott et al. 2002).

Interpretation of risks associated with fishes potentially transferred collaterally with interbasin water diversion. As suggested by the preceding narrative regarding the current status of fishes in the Missouri River and Red River basins and the observations of Scott et al. (2002), the only certainty is we may never realize a complete list of ichthyofauna for these or any other river basins in North America. And the status of the fishes of the Missouri River and Red River basins represents an effort to catalog species of a region that equals or exceeds those efforts for other biota identified for characterization in the current investigation. While the literature variously documents the effects of one species on another, e.g., the effects associated with introduced fishes in the Great Lakes, and general observations regarding the effects of invasive species on native fishes (see Fuller et al. 1999), we can only interpret risks associated with biota transfers that may occur collaterally with interbasin water diversions within the context of probability—largely, qualitative—shaped by integrating outcomes derived from analysis using tools such as those applied in the current investigation.

While Section 4 will focus on risk characterization and an analysis of uncertainties, from the perspective of our categorical analysis, interbasin water diversions mediating transfers of fishes such as those representatives included as biota of concern from the Missouri River to the Red River basin would be less likely to be a problem than transfers yielding other biota, e.g., propagules of invasive plants or microbiological agents already established in the Red River basin (see Table 8). Some of those species, e.g., pallid sturgeon, although identified as species of concern by other investigators 20 to 25 years ago (Swain et al. 1980), present little risk to receiving waters in the Red River basin in view of the species' current plight in maintaining populations in waters of the Missouri River.

While fishes consistently presented relatively low categorical scores relative to other biota of concern (Table 8), risks associated with fishes vary across species in line with each species' life history attributes favoring their being successful invaders. For example, of those fishes identified as biota of concern in the current investigation, Asian carp (e.g., bighead carp) appears the mostly likely fish species to present other than low risk to the Red River basin. Top ranking scores of biota of concern summarized in Table 8 are dominated by species already present in both the Missouri River and Red River basins, but the highest ranking "nonresident" that presents risk of invasion is bighead carp (and by extension, other Asian carp; see Appendix 3A). Projected species distributions generated by GARP suggest that bighead carp and other exotic carps originating from Asia may be successful at establishing sustainable populations in the Red River basin, if pathways are completed, linking Missouri River sources with receiving waters. These completed pathways, however, are not limited to those realized in the event of an interbasin water diversion (see Section 4).

Based on outcomes of the categorical analysis, but recognizing our inability to project potential species distributions using GARP, other fish species identified as biota of concern—especially, Utah chub, paddlefish, zander and by extension, those fishes presenting life history attributes similar to these fishes—would appear to present relatively low risks for invasion of Red River basin via interbasin water diversions, given their current status and distribution (see Appendix 3A). In contrast, rainbow smelt and gizzard shad present marginally higher rank categorical scores (Table 8), suggesting their potential as species of concern to the Red River basin exceeds that of zander, Utah chub, paddlefish, and pallid sturgeon. Projections of potential species distributions suggest that gizzard shad may be less problematic than rainbow smelt, which is consistent with each species current status and distribution (see Appendix 3A).

Of biota of concern identified by Reclamation and Technical Team, the fishes appear to present the least risk of becoming problematic as collateral transfers realized consequent to an interbasin water diversion. Depending on implementation of the proposed water diversion (e.g., open conveyance *vs* closed conveyance of treated waters; see Section 4), risks associated with fishes would appear to become less an issue to resource managers when greater control is practiced in the implementation, especially in light of those biota of concern that would challenge a highly managed diversion with multiple-step control technologies in place (see Section 4).

Table 11. Grass carp (*Ctenopharyngodon idella*) records from HUCs immediate adjacent to Rainy River-Red River-Souris River basin (HUC09).

State	County	Locality	Year	HUC Number	Drainage Name	Status
IA	Delaware	Delaware County	1987	07000000	Upper Mississippi	collected
IA	Linn	Linn County	1987	07000000	Upper Mississippi	collected
IA	Washington	Washington County	1987	07000000	Upper Mississippi	collected
IA	Lee	Lee County	1987	07000000	Upper Mississippi	collected
IA	Van Buren	Van Buren County	1987	07000000	Upper Mississippi	collected
IA	Jefferson	Jefferson County	1987	07000000	Upper Mississippi	collected
IA	Davis	Davis County	1987	07000000	Upper Mississippi	collected
IA	Monroe	Monroe County	1987	07100009	Lower Des Moines	collected
IA	Koekuk	Koekuk County	1987	07080000	Upper Mississippi-Iowa	collected
IA	Mahaska	Mahaska County	1987	07000000	Upper Mississippi	collected
IA	Tama	Tama County	1987	07080200	Iowa	collected
IA	Lucas	Lucas County	1987	07000000	Upper Mississippi	collected
IA	Wayne	Wayne County	1987	10280000	Chariton-Grand	collected
IA	Jasper	Jasper County	1987	07080100	Upper Mississippi-Skun	collected
IA	Story	Story County	1987	07000000	Upper Mississippi	collected
IA	Black Hawk	Black Hawk County	1987	07080000	Upper Mississippi-Iowa	collected
IA	Hamilton	Hamilton County	1987	07000000	Upper Mississippi	collected
IA	Winnebego	Winnebego County	1987	07000000	Upper Mississippi	collected
IA	Worth	Worth County	1987	07080200	Iowa	collected
IA	Kossuth	Kossuth County	1987	07100000	Des Moines	collected

Table 11. Grass carp (*Ctenopharyngodon idella*) records from HUCs immediate adjacent to Rainy River-Red River-Souris River basin (HUC09).

State	County	Locality	Year	HUC Number	Drainage Name	Status
IA	Warren	Warren County	1987	07100008	Lake Red Rock	collected
IA	Decatur	Decatur County	1987	10280100	Grand	collected
IA	Clarke	Clarke County	1987	00000000	>1	collected
IA	Madison	Madison County	1987	07000000	Upper Mississippi	collected
IA	Union	Union County	1987	10000000	Missouri	collected
IA	Adair	Adair County	1987	10280102	Thompson	collected
IA	Cass	Cass County	1987	10240000	Missouri-Nishnabotna	collected
IA	Pottawattamie	Pottawattamie County	1987	10000000	Missouri	collected
IA	Mills	Mills County	1987	10240000	Missouri-Nishnabotna	collected
IA	Montgomery	Montgomery County	1987	10240000	Missouri-Nishnabotna	collected
IA	Page	Page County	1987	10240000	Missouri-Nishnabotna	collected
IA	Taylor	Taylor County	1987	10240000	Missouri-Nishnabotna	collected
IA	Guthrie	Guthrie Weld County	1987	07100007	South Raccoon	collected
IA	Audubon	Audubon County	1987	10240000	Missouri-Nishnabotna	collected
IA	Monona	Monona County	1987	10230000	Missouri-Little Sioux	collected
IA	Woodbury	Woodbury County	1987	10230000	Missouri-Little Sioux	collected
IA	Ida	Ida County	1987	10230000	Missouri-Little Sioux	collected
IA	Sac	Sac County	1987	00000000	>1	collected
IA	Buena Vista	Buena Vista County	1987	00000000	>1	collected
IA	Plymouth	Plymouth County	1987	10000000	Missouri	collected

Table 11. Grass carp (*Ctenopharyngodon idella*) records from HUCs immediate adjacent to Rainy River-Red River-Souris River basin (HUC09).

State	County	Locality	Year	HUC Number	Drainage Name	Status
IA	O'Brien	O'Brien County	1987	10230000	Missouri-Little Sioux	collected
IA	Osceola	Osceola County	1987	10000000	Missouri	collected
IA	Lyon	Lyon County	1987	10170200	Big Sioux	collected
IA		Mississippi River	1987	07000000	Upper Mississippi	collected
IA		Missouri River drainage in Iowa	2002	00070600		unknown
IL	Randolph	Mississippi River near Chester	1971	07140105	Upper Mississippi-Cape	collected
IL	Randolph	Mississippi River near Chester	1971	07140105	Upper Mississippi-Cape	collected
IL		Mississippi River	1971	07000000	Upper Mississippi	collected
IL	Randolph	Mississippi River near Chester	1971	07140105	Upper Mississippi-Cape	collected
IL		Mississippi River up to Pike County	1979	07000000	Upper Mississippi	collected
IL	Clinton	Kaskaskia River, Pelican Pouch, about 4 mi. SSW Carlyle	1991	07140202	Middle Kaskaskia	collected
IL	Jackson	Big Muddy River at Rattlesnake Ferry	1992	07140106	Big Muddy	collected
IL	Alexander	Horseshoe Lake spillway (west side ditch) (Cache R. dr) 1.0 mi. E of Miller City	1993	07140108	Cache	collected
IL	Alexander	Horseshoe Lake (Cache R. dr) west arm and near dam	1993	07140108	Cache	collected
IL	Calhoun	Mississippi River, Pool 25, Cockerill Hollow Access at Batchtown, RM 243.5	1993	07110004	The Sny	collected

Table 11. Grass carp (*Ctenopharyngodon idella*) records from HUCs immediate adjacent to Rainy River-Red River-Souris River basin (HUC09).

State	County	Locality	Year	HUC Number	Drainage Name	Status
IL	Alexander	Horseshoe Lake, Cache River drainage, at spillway, ditch, west side, flooded ditch	1993	07140108	Cache	established
IL		Illinois River, river mile 157.8	2000	07130003	Lower Illinois-Lake Chautauqua	collected
IL		Illinois River, river mile 157.8	2000	07130003	Lower Illinois-Lake Chautauqua	collected
IL		Illinois River, river mile 157.8	2000	07130003	Lower Illinois-Lake Chautauqua	collected
IL		Illinois River, river mile 157.8	2000	07130003	Lower Illinois-Lake Chautauqua	collected
IL		Illinois River, river mile 157.8	2001	07130003	Lower Illinois-Lake Chautauqua	collected
IL		Illinois River, river mile 157.8	2001	07130003	Lower Illinois-Lake Chautauqua	collected
IL		Illinois River, river mile 157.8	2001	07130003	Lower Illinois-Lake Chautauqua	collected
IL		Illinois River, river mile 157.8	2001	07130003	Lower Illinois-Lake Chautauqua	collected
IL		Illinois River, river mile 157.8	2001	07130003	Lower Illinois-Lake Chautauqua	collected
IL		Illinois River, river mile 157.8	2001	07130003	Lower Illinois-Lake Chautauqua	collected
MI	Newaygo	Little Muskegon River (?) [See Atlas]	1980	04060102	Muskegon	collected
MI		St. Clair-Detroit drainage	1980	04090001	St. Clair	collected
MI		southeastern Lake Michigan drainage	1980	04060200	Lake Michigan	collected
MN		Mississippi River, lower portion in MN	1971	00070400		unknown
MN	Winona	pond near the Mississippi River near Winona, pond overflows into	1977	07040003	Buffalo-Whitewater	extirpated

Table 11. Grass carp (*Ctenopharyngodon idella*) records from HUCs immediate adjacent to Rainy River-Red River-Souris River basin (HUC09).

State	County	Locality	Year	HUC Number	Drainage Name	Status
		Gilmore Creek, which in turn flows into Lake Winona				
MN		upper St. Croix River	1982	07030001	Upper St. Croix	collected
MN	Kanabeck/ Aitkin	Snake River	1982	07030004	Snake	collected
MN		lower Mississippi River drainage	1991	07040000	Upper Mississippi-Blac	collected
MO	Perry	Mississippi River near Chester	1971	07140105	Upper Mississippi-Cape	collected
MO	Cole	Missouri River near Jefferson City	1973	10300102	Lower Missouri-Moreau	collected
MO		Mississippi River	1974	00000000	>1	collected
MO		Missouri River	1974	10300000	Lower Missouri	collected
MO		St. Francis River	1974	08020200	St. Francis	collected
MO		Mississippi River whole length of border	1975	00000000	>1	collected
MO		Missouri River - whole distance through state	1975	10300000	Lower Missouri	collected
MO	Cole	Moreau River 2, 4, and 8 km from mouth	1987	10300102	Lower Missouri-Moreau	established
MO	Callaway	Auxvasse Creek, 2, 4, and 8 km from mouth	1987	10300102	Lower Missouri-Moreau	established
MO	Carroll	ditch off of river (tributary of Missouri River floodplain), Norbourne, MO	1989	10300101	Lower Missouri-Crooked	established
MO	Miller	Osage River at Osage Beach	1994	10290111	Lower Osage	collected

Table 11. Grass carp (*Ctenopharyngodon idella*) records from HUCs immediate adjacent to Rainy River-Red River-Souris River basin (HUC09).

State	County	Locality	Year	HUC Number	Drainage Name	Status
MO		Osage River	1998	10290100	Osage	established
MO		Mississippi River	1998	00000000	>1	established
MO		Mississippi River	1998	00000000	>1	established
MO		Missouri River	1998	10300200	Lower Missouri	established
MO		Missouri River	1998	10300100	Lower Missouri-Blackwa	established
ND	Barnes	Sheyenne River, Barnes County (probably Lake Ashtabula)	1980	09020200	Devils Lake-Sheyenne	collected
ND		non-specific	1994	00000000	>1	collected
ND	Stutsman	Spiritwood Lake, 20 miles N of Jamestown	1998	10160003	Upper James	stocked
NE		non-specific	1984	10000000	Missouri	collected
NE		Missouri River	1998	10240000	Missouri-Nishnabotna	collected
NE		Missouri River	1998	10230000	Missouri-Little Sioux	collected
NE		Platte River	1998	10200200	Lower Platte	collected
SD	Union	Missouri River, Lewis and Clark Lake	1980	10170101	Lewis and Clark Lake	collected
SD		non-specific	1994	00000000	>1	collected
WI		eastern Wisconsin	1975	04000000	Great Lakes	collected
WI		southern Wisconsin	1975	07000000	Upper Mississippi	collected
WI	La Crosse	La Crosse	1984	07040006	La Crosse-Pine	collected
WI	Waukesha	Oconomowoc Country Club near	1990	07090001	Upper Rock	extirpated

Table 11. Grass carp (*Ctenopharyngodon idella*) records from HUCs immediate adjacent to Rainy River-Red River-Souris River basin (HUC09).

State	County	Locality	Year	HUC Number	Drainage Name	Status
		Oconomowoc				
WI	Waukesha	Edgewood Country Club near Edgewood on Pewaukee Lake	1990	07120006	Upper Fox	extirpated
WI	?	Abbey Springs Country Club, WI	1990		?	extirpated
WI	Waukesha	Westmoor Country Club	1990	07120006	Upper Fox	extirpated
WI	Dane	Blue Mound Country Club	1990	07090004	Sugar	extirpated
WI	Milwaukee	Tuckaway Country Club	1990	04040003	Milwaukee	extirpated
WI	Washington	West Bend Country Club	1990	04040003	Milwaukee	extirpated
WI		non-specific	1992	00000000	>1	collected
WY		lakes and ponds east of the Continental Divide (Missouri drainage)	1994	10000000	Missouri	collected
WY		found in lower elevation lakes, resevoirs, and ponds east of the Continental Divide	1994	10000000	Missouri	collected

Table 12. Silver carp (*Hypophthalmichthys molitrix*) recorded in the HUCs immediately adjacent to Rainy River-Red River-Souris River basin (HUC09).

State	County	Locality	Year	HUC Number	Drainage Name	Status
IL		Illinois River, river mile 157.8	2000	7130003	Lower Illinois-Lake Chautauqua	collected
IL		Illinois River, river mile 157.8	2000	7130003	Lower Illinois-Lake Chautauqua	collected
IL		Illinois River, river mile 157.8	2000	7130003	Lower Illinois-Lake Chautauqua	collected
IL		Illinois River, river mile 157.8	2000	7130003	Lower Illinois-Lake Chautauqua	collected
IL		Illinois River, river mile 157.8	2001	7130003	Lower Illinois-Lake Chautauqua	collected
IL		Illinois River, river mile 157.8	2001	7130003	Lower Illinois-Lake Chautauqua	collected
IL	Monroe	Mississippi River, RM 160 at Merrimac	1990	7140101	Cahokia-Joachim	collected
MO	Scott	Mississippi River, 16 river miles south of Cape Girardeau	2001	7140105	Upper Mississippi-Cape Girardeau	established
IL	Jackson	Big Muddy River at Rattlesnake Ferry	1994	7140106	Big Muddy	collected
MO		Headwater Diversion Channel (Castor River, Cape Girardeau County)	1998	7140107	Whitewater	established
IL	Alexander	Horseshoe Lake (Cache R. dr)	1994	7140108	Cache	established
IL	Alexander	ditch at Horseshoe Lake, 0.25 mi W of spillway on Promised Land Road	1995	7140108	Cache	established
NE		nonspecific (probably Missouri River)	2000	10000000	Missouri	collected
SD	Yankton	James River, at the mouth [~4 mi E of Yankton, SD]	2003	10160011	Lower James	observed
SD		Missouri River below Gavins Point dam	2003	10170101	Lewis and Clark Lake	established
NE	Dodge	Elkhorn River near Dead Timber State Recreation Area [~3 mi NW of Scribner, NE]	2003	10200202	Lower Platte	collected
MO		Missouri River	1998	10300100	Lower Missouri-Blackwa	established
MO		Missouri River	1998	10300200	Lower Missouri	established

3.4.2 Narrative analysis: Aquatic invertebrates. While lists of invertebrate fauna are available for larger geographic settings (e.g., Pennak 1953, 1978; Smith 2001; Higgins and Thiel 1988; Thorp and Covich 2001), regional catalogs for aquatic invertebrates that are comparable to those available for fishes are relatively limited taxonomically, spatially, and historically (e.g., historical accounts such as Young 1924 and contemporary catalogs such as Cvancara 1983 available at http://www.npwrc.usgs.gov/resource/inverts/mollusks/mollusks.htm, and Kondratieff 2000 at http://www.npwrc.usgs.gov/resource/distr/insects/mfly/nd/toc.htm). Hence, in our current investigation the selection of zebra mussel, New Zealand mudsnail, and Asian clam clearly focused our analysis on exotics that have a history solely linked to past invasions from outside North America. As evident by the current status of these representative biota (see Appendix 3A), once established in North America, each species has followed a typical path of invasiveness, relying on diffusion and stratified diffusion processes, and their inclusion as biota of concern serves to illustrate the potential risks realized by linkages between surface waters within and between watersheds at various spatial scales.

Interpretation of risks associated with aquatic invertebrates potentially transferred collaterally with interbasin water diversion. As indicated by each species' rank score in the categorical analysis, these exotic mollusks each present a moderate risk for invasion of Red River basin, although as with the fishes, the emigration to the region need not reflect sole dependence on the realization of water diversions between the Missouri River and Red River basins. Based on their rank scores, zebra mussel and Asian clam appear to present similar invasion risks, with zebra mussel—in the absence of jump events serving to link insular occurrences of the species across a disjunct distribution—apparently nearing its northern and western distributional limit as projected by GARP (Figure 12 and Figure 13, but see Section 4, especially the analysis of uncertainty). And given the current status of the Asian clam in North America, there is little reason to minimize the interpretation of risks associated with that species dispersal and spread to surface waters of the Red River basin, provided pathways linking the basin with sources are completed (see Appendix 3A).

Although later in its arrival to North America than zebra mussel or Asian clam, New Zealand mudsnail may present greater risk of invasion to Red River basin than either of the earlier arriving mollusks, in part, because of the species' life history and capacity to reproduce parthenogenically (Winterbourn 1970a,b; Foltz et al. 1984; Hauser et al. 1992; Hughes 1996). New Zealand mudsnail has effectively spread throughout the western US via diffusion and stratified diffusion processes (see http://www.esg.montana.edu/aim/mollusca/nzms/), and has been observed in waters of the Great Lakes during its relatively short time in North America (Zaranko et al. 1997; see Appendix 3A). There is little reason to doubt its future success at establishing beachheads in other locations throughout the continent, as indicated by its projected species distribution (Figure 14 and Figure 15). Again, future expansions of the species' distribution are not reliant on interbasin water diversions between Missouri River and Red River basins, although the implementation of that transfer of water may influence the time course of invasion as witnessed by the jump events that have promoted the species' spread in the western US.

Crustaceans such as spiny water flea and others (see Appendix 3A) are categorically considered low-to-moderate risks for invasion, in part because aquatic macroinvertebrates such as these are similar to the fishes in their reliance on human agency in their emigration to unoccupied areas. At present, spiny water flea does not occur in Red River basin, although its relatively widespread occurrence in the Great Lakes basin suggests that if vectors are available, then invasion potential would be heightened, since life-history attributes of spiny water flea (and other crustaceans included in Appendix 3A) provide the capacity to establish sustainable populations.

3.4.3 Narrative analysis: Aquatic vascular plants, and wetland and riparian vascular plants. The aquatic vascular plants, and wetland and riparian vascular plants included as biota of concern for the current investigation have a long invasion history throughout North America (see Appendix 3A). Again, the availability of regional floras sufficient to the calculation of potential distributions using GARP restricted this quantitative tool to spatial analysis for tamarisk, although hydrilla, Eurasian water milfoil, and water hyacinth each present well documented occurrence data at a state and county level (see Appendix 3A). As with the aquatic invertebrates, the current investigation relied on these exotic species and subsequently minimized problems associated with incomplete catalogs of North American flora (especially for georeferenced occurrence data) or the dynamic state of species distributions, especially under conditions influencing unaided expansions and contractions of species distributions (see Scott et al. 2002; Kareiva et al. 1993). Hence, our evaluation of invasion risks potentially associated with interbasin water diversions focused on species clearly not linked to North America as indigenous species, and serve as starting points to evaluate plant species characterized by life history attributes similar to representatives on the list of biota of concern (Section 1, Table 1).

Interpretation of risks associated with vascular plants potentially transferred collaterally with interbasin water diversion. Tamarisk, whether individual species of the genus (e.g., *Tamarix chinensis*, *T. aphylla*, *T. parviflora*, *T. ramosissima*) or hybrids, has a long history of invasion throughout the western US, and has recently emigrated to the northern Great Plains, including riparian areas of North Dakota (see Appendix 3A). The categorical analysis summarized in Table 10 suggests tamarisk presents moderate risks, although its relatively recent emigration into North Dakota and the potential tolerance of northern latitudes and dry winters (see Pearce and 2002, 2003) may warrant additional analysis with respect to the species long-term sustainability. Spatial analysis derived from GARP suggests the current occurrence data support an expanded distribution including areas within the Upper Missouri River in North Dakota. Current projections do not predict expansion to the Red River basin (but see Appendix 4, especially uncertainty analysis).

Categorical outcomes suggest Eurasian (also referred to as "European") water milfoil and purple loosestrife rank as a high-risk species, primarily because populations are currently found in the Red River basin (see Appendix 3A). In the absence of effective control programs, dispersal beyond the species current distribution in the Red River basin is anticipated. As noted in Appendix 3A, the western and northern limits of distribution for hydrilla and water hyacinth may have been reached at latitudes of the northern Great Plains, which may preclude either of these species from establishing sustainable populations, since physiological constraints associated with latitudinal advance have been realized (e.g., reduced tolerance to low annual temperature). Seasonal outbreaks of either species, however, should not be ruled out in evaluating risks (see Section 4), especially given potential long-term system changes in riparian habitats and dynamic character of species distributions (Scott et al. 2002; Kareiva et al. 1993) and multiple pathways by which propagules may emigrate to the area of concern.

3.4.4 Narrative analysis: Diseases of fish and waterborne diseases. Appendix 3B provides summaries of the current status of each of the disease agents considered as biota of concern in this current investigation. To reinforce the observations in Section 1, not all these disease agents are potentially invasive species, since numerous species included as biota of concern occur in both Missouri River and Red River watersheds (see Section 1, Table 1). Serotypes of *Escherichia coli* and *Salmonella* spp. are cosmopolitan in their distribution throughout the northern Great Plains, and similarly, *Legionella pneumoniae* is tracked in Manitoba, North Dakota, and Minnesota as part of larger federal programs in Canada and US. *Cryptosporidium parvum* and *Giardia lamblia* occur in all areas of the Missouri River and Red River basins, as do the cyanobacteria included as biota of concern (*Anabaena flos-aquae*, *Microcystis aeruginosa*, and *Aphanizomenon flos-aquae*). For each of these representative biota of concern, detection of biota transfers would necessarily rely on comparisons of disease occurrence as zoonoses or diseases of wildlife "before diversion" relative to "after diversion," outcomes that would characterize shifts in metapopulations of these disease agents associated with interbasin water transfers (see §3.5).

Interpretation of risks associated with fish diseases and waterborne diseases potentially transferred collaterally with interbasin water diversion. In contrast to these disease agents potentially expressing shifts in metapopulations between Missouri River and Red River basins, linkages between interbasin water transfers and the occurrence of *Myxosoma cerebralis*, *Polypodium hydriforme*, *Yersinia ruckeri*, and infectious hematopoeitic necrosis virus (IHNV) would more closely express an invasion reflected by the emergence of a disease not previously observed in the receiving basin. The current status of each of these disease agents is summarized in Appendix 3B, including records of locations of disease occurrence. Unlike the analysis of distribution completed for fishes using GARP, the evaluation of potential locations where disease agents could occur was completed using approaches similar to those applied by Peterson et al. (2002, 2003), wherein distribution of disease host was considered as a necessary and sufficient condition for evaluating potential distribution of disease agent.

To illustrate the analytical approach, georeferenced data were available to focus on rainbow trout as host of *M. cerebralis*, the causative agent of whirling disease. Given the potential distribution of rainbow trout (Figure 19 and Figure 20), *M. cerebralis* as the causative agent of whirling disease could potentially occur throughout the Upper Missouri and Red River basins. At present, whirling disease has been recorded in Montana and other states of the western US (see Appendix 3B) but has not been observed in waters of the Missouri River basin in North Dakota or the Red River basin. However, if rainbow trout were systematically introduced in sufficient numbers throughout the surface waters of the Missouri River watershed, e.g, in North Dakota or Manitoba, or the Red River basin of North Dakota, Minnesota, or Manitoba, and if these populations became established or were actively maintained through continued stockings, then presence of the tubificid intermediate host throughout the northern Great Plains would make the occurrence of whirling disease in the area nearly inevitable. The occurrence of whirling disease would likely be projected coincident with the host species once dispersal of the disease agent was realized (Figure 19 and Figure 20). Such a scenario is not dependent on any interbasin water diversions but is more dramatically affected by independently developed natural resource management plans focused on development of rainbow trout fisheries in the northern Great Plains.

Data were not sufficient to complete a similar host-disease agent linkage for other biota of concern, but outcomes of such analyses would likely yield similar results, if widespread occurrence of hosts (primary and intermediate, as necessary) were realized for disease agents considered as biota of concern in this or any future investigation of the spread of diseases of fish and wildlife, or zoonoses involving terrestrial vertebrates.

3.5 Shifts in metapopulations associated with biota transfers associated with water diversions

Reclamation and Technical Team acknowledged the potential for interbasin water diversions to influence existing local populations in Missouri River and Red River basins—hence, the inclusion of species that currently occupy both basins on the list of biota of concern. Species invasions are not the issue in this facet of the biota transfer issue, yet mechanistically, the process of dispersal via pathways directly related to proposed water diversions are similar, if not identical, to the initial events characteristic of an invasion that results in an expanded species distribution. Extensive works have been published (see Gilpin and Hanski 1991; Hanski and Gilpin 1997; Hanski 1999; Hanski and Gaggiotti 2004; Beissinger and McCullough 2002) which highlight an increasing focus on populations—microbial, plant, and animal—and the interrelationships among local populations that are mediated by dispersal events across various spatiotemporal scales (see Colbert et al. 2001; Bullock et al. 2002).

Conceptually, Hanski and Gilpin (1997) characterized metapopulations as populations that are spatially structured; that is, there are patches of habitat in which the species can successfully growth and reproduce. From any given species' perspective, much of the landscape serves as an uninhabitable matrix, and the metapopulation consists of an assemblage of local breeding populations linked by movements of individuals, e.g., through migration between local populations. Alteration of local population dynamics and genetics results from these interactions, and as a consequence of the spatiotemporal linkage of metapopulations, local populations have the capacity, e.g., to reestablish themselves following extinction of local populations. Such a characterization of metapopulation leads to the standard definition posited by Hanski and Gilpin (1991) wherein metapopulations are considered as a "system of local populations connected by dispersing individuals" and refines the original term coined by Levins (1969).

From a practical perspective, the technical issues involved in the analysis of altered metapopulatoin dynamics directly linked to interbasin water transfers consistently outpaced the data available for analysis. Appendix 3B identifies available data and resources capable of collecting data sufficient to the analysis, if future concern warrants the design of monitoring studies to track disease occurrence. For this initial foray into the evaluation of risks potentially realized consequent to interbasin water diversions, a range of tools from statistical time-series (see Anderson 1971; Hipel 1985; Chatfield 1995; Kedem and Fokianos 2002) and disease outbreak analysis (see Woodward 1999; Diekmann and Heesterbeek 2000; Kulldorff et al. 2004) were available, but a simple analysis of graphical and summary numeric data (see Appendix 3B) was applied to this preliminary evaluation. Provided data are sufficient to more rigorous analyses, such an analysis may be indicated in future iterates of the risk analysis process.

With the exception to data collected under the auspices of public health agencies, the current review of data collections available through public domain are not sufficient for a rigorous statistical analysis required to distinguish between sources of disease agents originating in the Missouri River basin and those originating from the Red River basin. Even those data collections from public health sources that were available for this effort limited the tools for the analysis. Hence, we opted for a relatively simple assemblage of available occurrence data (see Appendix 3B) and a brief narrative interpretation of risks from a technical perspective. In general, our inability to distinguish between sources of disease agents adversely affects our ability to evaluate baseline levels and adequately characterize initial conditions in an analysis wherein projections are required to characterize how past records of disease occurrence (e.g., existing populations and outbreaks associated with disease) relate to future events such as comparisons of disease occurrence “before diversion” *v.* “after diversion.” For example, state wide and province wide data available for microbiological, e.g., *Legionella pneumoniae* and apicomplexa disease agents, e.g., *Cryptospordium parvum* suggest that data are available within-agency to conduct the necessary baseline analysis to evaluate “before diversion” status, although data resolution, e.g., at a county level, does not easily fit into the current investigation’s watershed-based analysis. Nonetheless, design of monitoring studies to evaluate “after diversion” condition could be folded into the evaluation process.

Unfortunately, one limitation to such a straightforward analysis is the characterization of source, if disease outbreaks were observed “after diversion” were realized. Misassignment of cause is a highly likely outcome of such a simple analysis. The evaluation of cause-effect relationships—whether the focus is on the assessment of species invasions or shifts in metapopulations—provides an example of how technical analysis fits into adaptive resource management (Walters 1986). Causes may be direct or indirect in their linkage to events related to biota transfers, and these linkages reflect conditions that influence the level of certainty associated with our conclusions of cause-effect relationship (see Section 4). Within an adaptive management context, characterization of cause may be captured by response and explanatory variables, and risk factors that influence the expression of response (or non-response, as it may be). Explanatory and response variables may be direct or indirect in their association with multifactorial systems being complicated by interactions among component factors that influence the expression of response (Figure 21).

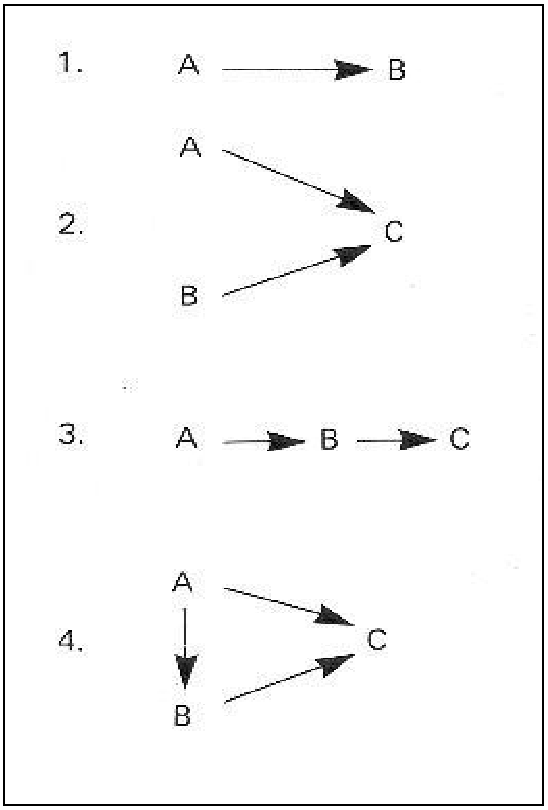


Figure 21. Simplified illustrations of direct and indirect causal relationships. In (1) A is the direct cause of B, while in (2) A and B are independent but both are direct causes of C. In (3) and (4), relatively simple multifactorial cases are illustrated. In (3) A and C are indirectly linked by B, which is the direct cause of C. A and B are direct causes of C in (4), although A may also occur as an indirect cause, if B serves as a contributing or intervening factor promoting C.

The degree of complication in multifactorial systems yields various categories of cause. For example, a frequent categorization of cause used in epidemiological studies characterizes factors as “necessary” or “sufficient.” These terms are most easily illustrated in simple systems, wherein a cause is sufficient, if it inevitably yields an effect. In multifactorial processes, such as disease, sufficient cause nearly always occurs as a set of interacting component causes, where one component is commonly described as the cause. A necessary cause must always be present to produce a specific effect (e.g., *M. cerebralis* must always be present for a diagnosis of whirling disease). In contrast to whirling disease, many infectious and noninfectious diseases may be produced by different sufficient causes that may or may not have component causes in common. Uncomplicated infectious disease is frequently characterized by a disease agent that serves as a necessary cause, and in some instances, a factor may be necessary and sufficient, depending on the specific process being considered. In multifactorial processes such as those characteristic of environmental exposures, factors may be necessary, sufficient, neither, or both.

Component causes in a multifactorial system are generally characterized as predisposing factors, precipitating factors, reinforcing factors, and enabling factors. In characterizing failures in biological systems, predisposing factors are those that increase susceptibility (e.g., of a host to a disease agent). For example, the manifestation of disease in a host is frequently influenced by its immune status. A predisposing factor might be age of exposed individuals or the nature of a stream's substrate, since these factors may be critical to the development of whirling disease. Precipitating factors are those that are associated with the definitive onset of response but are not sufficient in the absence of a necessary cause (e.g., whirling disease may be precipitated by infection with *M. cerebralis* in sensitive species of trout). Reinforcing factors are those that aggravate the expression of response, which in the case of disease agents might be repeated exposures to the causative agent or a behavioral factor that exacerbates exposure. Enabling factors tend to be less clearly characterized than other categories of component factors, since enabling factors are those components of exposure that facilitate the expression of response (e.g., dry years may enable disease outbreaks to occur in wetland habitats that usually have a low incidence of disease, or reduced prey-base may enable disease outbreaks predicated on malnutrition of host).

Epidemiological cause-effect models approach ecological complexity when disease processes are considered within a field setting where multiple factors are a common feature of exposure. In such settings, simple linear models of cause-effect may be of limited use because multifactorial systems are characterized by component factors of varying intensity that interact at various levels in the system. These multifactorial systems are adaptive and highly dynamic, yielding a "web of causation" (e.g., Grenfell and Dobson 1995; Thrusfield 1995) similar in complexity to hierarchical ecosystems (e.g., Puccia and Levins 1985). Indeed, beyond simple cause-effect analysis focused on identification of a single disease-causing agent, exposures in the field must necessarily acknowledge the ever-present role of confounding factors that inevitably produce spurious associations among variables and potentially mask real cause-effect relationships.

As the brief overviews of biota of concern (Appendix 3A and Appendix 3B) suggest, source identification of species invasions is generally fraught with complications that impact the characterization of pathways and sources, especially at the local level or along a flow of events typical of the invasion process. While the country or region of origin for an invasive species may be easily resolved for an invasive species, the proximate cause linked to the species release to previously unoccupied areas may be difficult, if not impossible, to determine. To evaluate shifts in metapopulations consequent to an interbasin water diversion would likely be more intractable, given the data presently being collected as a routine measure of public health. The identification of cause would also be highly dependent on the design of the water distribution system serving the area where outbreaks were observed. These issues related to causal analysis and the identification of source are pervasive—whether the focus is on invasive species or shifts in metapopulations—and, as such, represent a source of uncertainty that may be deferred in deference to adaptive management plans that recognize where resources (e.g., as time and financial support for monitoring programs) are best allocated.

3.6 Cited References and Bibliography

Adler, M., and E. Ziglio, 1996, Gazing into the Oracle: The Delphi Method and Its Application to Social Policy and Public Health, Jessica Kingsley Publishers, London, UK, 252pp.

American Society for Testing and Materials (ASTM)/American Water Works Association (AWWA), 2004, Compilation of ASTM Standards Relating to Wastewater and Stormwater, American Water Works Association, Denver, Colorado, 707pp.

American Water Works Association (AWWA), 2004, AWWA Standards, American Water Works Association, Denver, Colorado, multiple volumes updated annually.

Andersland, O.B., and B. Ladanyi, 2004, Frozen Ground Engineering, 2nd Edition, Co-Published by American Society of Civil Engineers and John Wiley & Sons (ASCE Press), Reston, Virginia, 363pp.

Anderson, T.W., 1971, The statistical analysis of time series, John Wiley and Sons, Inc., New York, 704pp

Andow, D. A., P. M. Kareiva, S. A. Levin, and A. Okubo, 1993, Spread of invading organisms: patterns of spread, In K. C. Kim, and B. A. McPheron (editors), Evolution of insect pests: patterns of variation, John Wiley & Sons, New York, Pp. 219-242.

Bartlett, M.S., 1955, An introduction to stochastic processes with special reference to methods and applications, Cambridge at the University Press, Cambridge, UK, 312pp.

Bartlett, M.S., 1960, Stochastic population models in ecology and epidemiology, Methuen & Co., Ltd., London, UK, 90pp.

Bernard, H.R., 1999, Social Research Methods : Qualitative and Quantitative Approaches, SAGE Publications, Thousand Oaks, California, 781pp.

Beissinger, S.R., and D.R. McCullough (editors), 2002, Population viability analysis, The University of Chicago Press, Chicago, Illinois, 577pp.

Blischke, W.R., and D.N. Parbhakar Murthy, 2000, Reliability, John Wiley & Sons, Inc., New York, 812pp.

Brown, J. H., 1989, Patterns, modes and extents of invasions by vertebrates, In J. A. Drake, H. A. Mooney, F. Di Castri, R. H. Groves, F. J. Kruger, M. Rejmanek, and M. Williamson (editors), Biological invasions: a global perspective, John Wiley & Sons, New York, New York, Pp. 85-109.

Bullock, J.M, R.E. Kenward, and R.S. Hails (editors), 2002, Dispersal ecology, Published by Blackwell Science, Ltd/Blackwell Publishing, for British Ecological Society, Oxford, UK, 458pp.

Burnham, K.P., and D.R. Anderson, 2002, Model selection and multimodel inference, Second edition, Spring-Verlag, Inc., New York, 488pp.

Cantrell, R.S., and C. Cosner, 2003, Spatial ecology via reaction-diffusion equations, John Wiley and Sons, Inc., New York, 411pp.

Carlton, J. T., 1996, Invasions in the world’s seas: Six centuries of reorganizing Earth's marine life, In Proceedings of the Norway/UN Conference on Alien Species, O.T. Sandlund, P.J. Schei, and Å. Viken (eds.), The Trondheim Conferences on Biodiversity, July 1-5, 1996. Trondheim, Norway: Directorate for Nature Management/Norwegian Institute for Nature Research.

Chatfield, C., 1996, The analysis of time series, Chapman & Hall/CRC, Boca Raton, Florida, 283pp.

Clark, J, MA Lewis, J McLachlan, J HilleRisLambers, 2003, Estimating population spread: what can we forecast and how well? Ecology 84: 1979-1988.

Clark, J., L. Horvath, L., and M. Lewis, 2001a, On the estimation of spread rate for a biological population. Statistics and Probability Letters, 51: 225–234.

Clark, J.S., M. Lewis, and L. Horvath, 2001b, Invasion by extremes: Population spread with variation in dispersal and reproduction, American Naturalist, 157, 537–554.

Colbert, J, E. Danchin, A.A. Dhondt, and J.D. Nichols (editors), 2001, Dispersal, Oxford University Press, Oxford, UK, 452pp.

Crossman, E.J., and D.E. McAllister, 1986, Zoogeography of freshwater fishes of the Hudson Bay drainage, Ungava Bay and the Arctic Archipelago, In C.H. Hocutt and E.O. Wiley, editors. The zoogeography of North American freshwater fishes, John Wiley and Sons, New York, NY, pp.53-104.

Cvancara, A.M., 1983, Aquatic mollusks of North Dakota, North Dakota Geological Survey, Report of Investigation No. 78, Northern Prairie Wildlife Research Center Online, http://www.npwrc.usgs.gov/resource/inverts/mollusks/mollusks.htm (Version 15AUG97), Jamestown, North Dakota.

D'Antonio, C. M., and P. M. Vitousek, 1992, Biological invasions by exotic grasses, the grass/fire cycle, and global change, Annual Review of Ecology and Systematics, 23:63–87.

D'Antonio, C. M., T. Dudley, and M. Mack, 1999, Disturbance and biological invasions: direct effects and feedbacks, In L. Walker, editor. Ecosystems of disturbed ground. Elsevier, Amsterdam, The Netherlands, Pp. 413-452.

D'Antonio, C. M., R. F. Hughes, and P. M. Vitousek, 2001, Factors influencing dynamics of invasive C4 grasses in a Hawaiian woodland: role of resource competition and priority effects. Ecology 82:89–104.

Deb, A.K., Y.J. Hasit, and F.M. Grablutz, 1995, Distribution system performance evaluation, American Water Works Association, Denver, Colorado, 120pp.

Diekmann, O., and J.A.P. Heesterbeek, 2000, Mathematical epidemiology of infectious disease, John Wiley and Sons, Inc., New York, 303pp.

Drake, J. A., H. A. Mooney, F. Di Castri, R. H. Groves, F. J. Kruger, M. Rejmanek, and M. Williamson (editors), 1989, Biological invasions: a global perspective. John Wiley & Sons, New York, New York, USA.

Eddy, S. and J.C. Underhill, 1974, Northern fishes, with special reference to the upper Mississippi Valley, University of Minnesota Press, Minneapolis, MN.

Eddy, S., R.C. Tasker, and J.C. Underhill, 1972, Fishes of the Red River, Rainy River, and Lake of the Woods, Minnesota, with comments on the distribution of species in the Nelson River drainage, Occasional papers: Number 11, Bell Museum of Natural History, University of Minnesota, Minneapolis, MN

Ehrlich, P.R., 1989, Attributes of invaders and the invading processes: Vertebrates. In Biological Invasions: a Global Perpective. ed. J.A. Drake, H.A. Mooney, F. diCastri, R.H. Groves, F.J. Kruger, M. Rejmánek, and M. Williamson. pp. 315-328.

Elton, C.S., 1958, The ecology of invasions by plants and animals, The University of Chicago Press, Chicago, Illinois, 181pp.

Fisher, R.A., 1937, The wave of advance of advantageous genes, Annals of Eugenics, 7, 353–369.

Fleiss, J.L,, B. Levin, and M.C. Paik, 2003, Statistical methods for rates and proportions, John Wiley and Sons, Inc., 760pp.

Foltz, D. W., H. Ochman, J. S. Jones, and R. K. Selander, 1984, Genetic heterogeneity within and among morphological types of the parthenogenetic snail, *Potamopyrgus jenkinsi* (Smith 1889), J. Molluscan Studies 50:242-245.

Fuller, P.L., L.G. Nico, and J.D. Williams, 1999, Nonindigenous fishes introduced into inland waters of the United States, American Fisheries Society, Special Publications 27, Bethesda, Maryland, 613pp.

Gilpin, M., and I. Hanski (editors), 1991, Metapopulation dynamics: Empirical and theoretical investigations, Academic Press, London, UK, 512pp.

Grenfell, B.T., and A.P. Dobson (editors), 1995, Ecology of infectious diseases in natural populations, Cambridge University Press, Cambridge, UK, 521pp.

Hanski, I., and M. Gilpin, 1991, Metapopulation dynamics: Brief history and conceptual domain, In Metapopulation Dynamics: Empirical and theoretical investigations, M. Gilpin and I. Hanski (editors), Academic Press, London, UK, pp. 3-16.

Hanski, I.A., and M.E. Gilpin (editors), 1997, Metapopulation biology, Academic Press, San Diego, California, 512pp.

Hanski, I., 1999, Metapopulation ecology, Oxford University Press, Oxford, UK, 313pp.

Hanski, I., and O.E. Gaggiotti (editors), 2004, Ecology, genetics, and evolution of metapopulations, Elsevier Academic Press, Burlington, Massachusetts, 696pp.

Hauser, L., G. R. Carvalho, R. N. Hughes, and R. E. Carter, 1992, Clonal structure of the introduced freshwater snail *Potamopyrgus antipodarum* (Prosobranchia: Hydrobiidae), as revealed by DNA fingerprinting, Proc. R. Soc. Lond. Ser. B 249:19-25.

Helsel, D.R., 2005, Nondetects and data analysis, John Wiley and Sons, Inc., New York, 250pp.

Hengeveld, R. 1989. The dynamics of biological invasions. Chapman & Hall, London, UK.

Higgins, R.P., and H. Thiel (editors), 1988, Introduction to the study of meiofauna, Smithsonian Institution Press, Washington, D.C., 488pp.

Higgins, S.I., Clark, J.S., Nathan, R., Hovestadt T., Schurr , F., Fragoso, J.M.V., Aguiar, M.R., Ribbens, E. and Lavorel, S., 2003, Forecasting plant migration rates: managing uncertainty for risk assessment. Journal of Ecology, 91: 341-347.

Hipel, K.W., 1985, Time series analysis in perspective, Water Resources (Bulletin) 21(4):95-104.

Hughes, D.M. (editor), 2002, Assessing the future: Water utility infrastructure management, American Water Works Association, Denver, Colorado, 644pp.

Hughes, R. N., 1996, Evolutionary ecology of parthenogenetic strains of the prosobranch snail, *Potamopyrgus antipodarum* (Gray) = *P. jenkinsi* (Smith), Malacol. Rev. Suppl. 6:101-113.

Huzurbazar, A.V., 2005, Flowgraph models for multistate time-to-event data, John Wiley & Sons, Inc., New York, 270pp.

Jensen, P.A., and J. F. Bard, 2002, Operations Research Models and Methods, John Wiley and Sons, Inc., New York, 700 pp.

Jordan, D.S., and Barton W. Evermann, 1896-1900, The Fishes of North and Middle America: A Descriptive Catalogue of the Species of Fish-Like Vertebrates found in the Waters of North America, North of the Isthmus of Panama, Bulletin of U.S. National Museum, no. 47, multiple volumes.

Kareiva, P.M., J.G. Kingsolver, and R.B. Huey (editors), 1993, Biotic interactions and global change, Sinauer Associates, Inc., Sunderland, Massachusetts, 559pp.

Kedem, B., and K. Fokianos, 2002, Regression models for time series analysis, John Wiley and Sons, Inc., New York, 337pp.

Koel, T.M., 1997, Distribution of fishes in the Red River of the North Basin on Multivariate environmental gradients, Ph.D. thesis, North Dakota State University, Fargo, North Dakota, Northern Prairie Wildlife Research Center Home Page, Jamestown, North Dakota available at http://www.npwrc.usgs.gov/resource/1998/norbasin/norbasin.htm (Version 03JUN98).

Kolar, C.S. and D.M. Lodge, 2002, Ecological predictions and risk assessments for alien species, Science 298:1233-1236.

Kolar, C. and D.M. Lodge, 2001, Progress in invasion biology: predicting invaders, Trends in Ecology and Evolution 16:199-204.

Kolmogorov, A., I. Petrovsky, and N. Piscounov, 1937, Etude de I'equation de la diffusion avec croissance de la quantite de matiere et son application a un problima bilogique. Univ. Bull. Ser. Int. Sect. Al: 1-25 (translation).

Kondratieff, B.C. (coordinator), 2000, Mayflies of the United States, Northern Prairie Wildlife Research Center Online at http://www.npwrc.usgs.gov/resource/distr/insects/mfly/mflyusa.htm (Version 12DEC2003), Jamestown, North Dakota.

Kot, M., M.A. Lewis, and P. van den Driessche, 1996, Dispersal data and the spread of invading organisms, Ecology 77:2027-2042.

Kulldorff, M., Z. Zhang, J. Hartman, R. Heffernan, L. Huang, and F. Mostashari, 2004, Benchmark data and power calculations for evaluating disease outbreak detection methods, MMWR 53 (Supplement):144-151.

Leung, B., J.M. Drake, and D.M. Lodge, 2004, Predicting invasions: propagule pressure and the gravity of Allee effects, Ecology 85:1651-1660.

Levins, R., 1969a, Some demographic and genetic consequences of environmental heterogeneity for biological control, Bull. Entomol. Soc. Amer. 15:237-240.

Lodge, D. M., 1993, Species invasions and deletions, In P.M. Kareiva, J. G. Kingsolver, R. B. Huey, editors. Biotic interactions and global change. Sinauer, Sunderland, Massachusetts, USA, Pp. 367-387.

Loomis, T.M., C.R. Berry, Jr., and J. Erickson, 1999, The fishes of the upper Moreau River basin, Prairie Naturalist 31:193-214, Northern Prairie Wildlife Research Center Home Page, Jamestown, ND: http://www.npwrc.usgs.gov/resource/2001/umrbfish/umrbfish.htm (Version 10JUL2001).

Manly, B.F.J., L.L.McDonald, D.L. Thomas, T.L. McDonald, and W.P. Erickson, 2002, Resource selection by animals, Second edition, Kluwer Academic Publishers, Dordrecht, The Netherlands, 221pp

Marchetti, M.P., Moyle, P.B., and Levine, R, 2004, Alien fishes in California watersheds: characteristics of successful and failed invaders, Ecological Applications, 14(2):587–596.

McKinney, M. L., and J.L. Lockwood, 1999, Biotic homogenization: a few winners replacing many losers in the next mass extinction, Trends in Ecology & Evolution, 14:450–453.

McKinney, M.L., and J.L. Lockwood, 2001, Biotic homogenization: a sequential and selective process. Pages 1–18 in J. L. Lockwood and M. L. McKinney (editors), Biotic homogenization. Kluwer Academic/Plenum, New York, Pp. 1-18.

Mooney, H. A., and J. A. Drake (editors), 1986, Ecology of the biological invasions of North America and Hawaii. Springer-Verlag, New York, New York, USA.

Moser, A.P., 2001, Buried pipe design, McGraw-Hill Companies, Inc., New York, 607pp.

Moyle, P.B. and T. Light, 1996, Biological invasions of fresh water: Empirical rules and assembly theory, Biological Conservation 78:149-161.

Nayyer, M.L. (editor), 2000, Piping handbook, McGraw-Hill Companies, Inc., New York, pagination by section.

NIST/SEMATECH, 2004, e-Handbook of Statistical Methods, available through World-wide Web http://www.itl.nist.gov/div898/handbook/, last accessed November 11, 2004.

North Dakota Game and Fish Department, 1986, Fishes of North Dakota, North Dakota Game and Fish Department, Bismarck, ND, Northern Prairie Wildlife Research Center Home Page, Jamestown, ND: http://www.npwrc.usgs.gov/resource/tools/ndfishes/ndfishes.htm (Version 02FEB98).

North Dakota Game and Fish Department, 1994, Fishes of the Dakotas, North Dakota Game and Fish Department, Bismarck, ND, Northern Prairie Wildlife Research Center Home Page, Jamestown, ND: http://www.npwrc.usgs.gov/resource/othrdata/dakfish/dakfish.htm (Version 16JUL97).

Okubo, A., and S.A. Levin (editors), 2001, Diffusion and ecological problems, Springer-Verlag, Inc., New York, 467pp.

Pearce, C.M., and D.G. Smith, 2003, Saltcedar: distribution, abundance, and dispersal mechanisms, northern Great Plains. Wetlands, v. 23, p. 215-228.

Pearce, C.M. and D.G., 2002, Introduced Saltcedar: Its distribution, abundance, and transport mechanisms in the northern Great Plains and implications for western Canada, In: Weeds Across Borders: Proceedings of a North American Conference, Barbara Tellman (editor), Tucson, Arizona, Arizona-Sonoran Desert Museum, p. 75-82.

Pennak, R.W., 1978, Fresh-water invertebrates of the United States, Second edition, John Wiley and Sons, Inc., New York, 803pp.

Pennak, R.W., 1953, Fresh-water invertebrates of the United States, The Ronald Press Company, New York, 769pp.

Peterka, J.J. 1978. Fishes and fisheries of the Sheyenne River, North Dakota. Proceedings of the North Dakota Academy of Science 32:29-44.

Peterka, J.J., 1992, Survey of fishes in six streams in northeastern North Dakota, Completion report, North Dakota Game and Fish Department, Bismarck, ND.

Peterka, J.J., and T.M. Koel, 1996, Distribution and dispersal of fishes in the Red River basin, Report submitted to Interbasin Biota Transfer Studies Program, Water Resources Research Institute, Fargo, ND. Northern Prairie Wildlife Research Center Home Page. http://www.npwrc.usgs.gov/resource/distr/others/fishred/fishred.htm (Version 29AUG97).

Peterson, A. T., V. Sanchez-Cordero, C. B. Beard, and J. M. Ramsey, 2002, Ecologic niche modeling and potential reservoirs for Chagas disease, Mexico, Emerging Infectious Diseases 8:662-667.

Peterson, A.T., D.A. Vieglais, and J.K. Andreasen, 2003, Migratory birds modeled as critical transport agents for west nile virus in North America, Vector-Borne and Zoonotic Diseases 3:27-37, Posted online on July 9, 2004 (doi:10.1089/153036603765627433).

Puccia C.J. and R. Levins, 1985, Qualitative Modeling of Complex Systems: An Introduction to Loop Analysis and Time Averaging. Harvard University Press, Cambridge, Massachusetts.

Rejmánek, M., 1996, A theory of seed plant invasiveness: the first sketch, Biological Conservation, 78, 171-181.

Ricciardi, A., and J.B. Rasmussen, 1998, Predicting the identity and impact of future biological invaders: A priority for aquatic resource management. Canadian Journal of Fisheries and Aquatic Sciences 55:1759-1765.

Ryckman, F., 1981, A revised checklist of the fishes of North Dakota, with a brief synopsis of each species distribution within the state, North Dakota Game and Fish Department, Bismarck, ND.

Schippers, J.C., J.C. Kruithof, M.M. Nederlof, and J.A.M.H. Hofman, 2004, Integrated membrane systems, American Water Works Association, Denver, Colorado, 705pp.

Scott, W.B. and E.J. Crossman, 1973, Freshwater fishes of Canada. Bulletin number 184. Fisheries Research Board of Canada, Ottawa, British Columbia.

Scott, J.M., P.J. Heglund, M.L. Morrison, J.B Haufler, M.G. Raphael, W.A. Wall, and F.B. Samson (editors), 2002, Predicting species occurrences, Issues of accuracy and scale, Island Press, Washington, D.C., 868pp.

Shigesada, N., and K. Kawasaki, 1997, Biological invasions: Theory and practice, Oxford University Press, Oxford, UK, 205pp.

Simberloff, D., 1991. Keystone species and community effects of biological invasions, In L. R. Ginzburg (editor), Assessing ecological risks of biotechnology, Butterworth-Heinemann, Boston, Massachusetts, USA, Pp. 1-19.

Simberloff, D, 1985, Predicting ecological effects of novel entities: evidence from higher organisms, In H. O. Halverson, D. Pramer, and M. Rogul, editors. Engineered organisms in the environment: scientific issues, American Society for Microbiology, Washington, D.C., USA, Pp.152-161.

Sjödin, P. I. Kaj, S. Kroney, M. Lascoux, and M. Nordborg, 2004, On the meaning and existence of an effective population size, Genetics: Published Articles Ahead of Print, published on October 16, 2004 as 10.1534/genetics.104.026799.

Skellam, J.G., 1951, Random dispersal in theoretical populations. Biometrika, 38:196-218.

Smith, D.G., 2001, Pennak's freshwater invertebrates of the United States, John Wiley and Sons, Inc., New York, 638pp.

Sokol, R.R., and F.J. Rohlf, 1981, Biometry, Second Edition, W.H. Freeman and Company, San Francisco, California, 859pp.

Speirs, D.C., and W.S.C. Gurney, 2001, Population persistence in rivers and streams, Ecology 82:1219-1237 (with supporting online appendices).

Stewart, K.W., I.M. Suthers, and K. Leavesley, 1985, New fish distribution records in Manitoba and the role of a man-made interconnection between two drainages as an avenue of dispersal. Canadian Field-Naturalist 99:317-326.

Swain, D.P., A.J. Derksen, and J.S. Loch, 1980, A literature review of life histories of some species of fish – rainbow smelt, *Osmerus mordax*; gizzard shad, *Dorosoma cepedianum*; paddlefish, *Polydon spathula*; shovelnose sturgeon, *Scaphirhynchus platorhynchus*; pallid sturgeon, *Scaphirhynchus albus*; and shortnose gar, *Lepisosteus platostomus* – that may be introduced into the Hudson Bay watershed from the Missouri River watershed as a result of the Garrison Diversion, Manitoba Department of Natural Resources, Fisheries Biological Services, Unpublished report, MS Report 80-37.

Thompson, S.K., and G.A.F. Seber, 1996, Adaptive sampling, John Wiley and Sons, Inc., New York, 265pp.

Thompson, J.R., 2000, Simulation, John Wiley & Sons, Inc., New York, 297pp.

Thorp, J.H., and A.P. Covich (editors), 2001, Ecology and classification of North American freshwater invertebrates, Academic Press, San Diego, California, 1056pp.

Thrusfield, M., 1995, Veterinary epidemiology, Second Edition. Blackfield Science Ltd., London, UK, 483 pp.

Underhill, J.C., 1989, The distribution of Minnesota fishes and late Pleistocene glaciation, Journal of the Minnesota Academy of Science 55:32-37.

Vermeij, G.J., 1996, An agenda for invasion biology. Biological Conservation 78:3-9.

Vitousek, P.M., C. M. D'Antonio, L. L. Loope, and R. Westbrooks, 1996, Biological invasions as global change. American Scientist 84:468-478.

Walters, C., 1986, Adaptive management of renewable resources, republished by The Blackburn Press, 2001, Caldwell, New Jersey, 374pp.

Williamson, M. and A. Fitter, 1996, The characteristics of successful invaders, Biological Conservation, 78: 163-170.

Williamson, M., 1989, Mathematical models of invasion. In Drake, J.A., H.A. Mooney, F. di Castri, R.H. Groves, F.J. Kruger, M. Rejmánek and M. Williamson (Eds.). Biological invasions: A global perspective. John Wiley & Sons, Ltd., New York. Pp. 329-350.

Williamson, M., 1996, Biological invasions, Population and Community Biology Series 15, Chapman & Hall. London, UK, 244pp.

Winterbourn, M. J., 1970a, The New Zealand species of *Potamopyrgus* (Gastropoda: Hydrobiidae), Malacologia 10(2): 283-321.

Winterbourn, M. J., 1970b, Population studies on the New Zealand freshwater gastropod, *Potamopyrgus antipodarum* (Gray), Proceedings of the Malacological Society of London 39: 139-149.

Woodward, M., 1999, Epidemiology: Study design and data analysis, Chapman & Hall/CRC, Boca Raton, Florida, 699pp.

Woolman, A.J., 1896, Report upon ichthyological investigations in western Minnesota and eastern North Dakota, Appendix 3, Extracted from the report to the U.S. Commissioner of Fish and Fisheries for 1893, Government Printing Office, Washington, DC.

Young, R.T., 1924, The life of Devils Lake, North Dakota, Publication of the North Dakota Biological Station, 116pp.

Zaranko, D. T., D. G. Farara, F. G. Thompson, 1997, Another exotic mollusc in the Laurentian Great Lakes: the New Zealand native Potamopyrgus antipodarum (Gray 1843) (Gastropoda, Hydrobiidae), Canadian Journal of Fisheries and Aquatic Sciences 54: 809-814.