

Viewpoint

Aquatic invasive species and emerging infectious disease threats: A One Health perspective

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Abstract

An estimated 60–75% of the world's infectious diseases of humans are zoonotic, infecting both humans and other animals. Many are vector-borne, relying on transmission by mosquitoes and biting flies that are aquatic for much of their lifespan. Others rely on aquatic molluscs, fishes, or other aquatic animals for completion of their transmission cycles, and others develop and thrive in diverse freshwater environments outside any host. While such diseases remain firmly endemic in many areas, new outbreaks of infectious diseases associated with freshwater have occurred throughout the world, and many others have spread to new locations. This may involve introduction of aquatic vectors into locations where the disease was previously unknown, as in the recent occurrences of mosquito-transmitted diseases such as West Nile Virus in North America, dengue fever in southern Europe, Chikungunya virus in the Caribbean and South America, and dirofilariasis in Central and Eastern Europe. Such a pattern is also possible with such major human pathogens as *Schistosoma* blood flukes and food-borne trematodes, through introduction of aquatic host snails from long-established foci in other areas. Alternatively, waterborne pathogens may be introduced directly, leading to disease outbreaks such as the cholera disaster still unfolding in Haiti. Accidental or intentional introduction of pathogens or their aquatic vectors and hosts are among the primary concerns that affect international trade, travel, and global health security. These concerns are compounded by the prospect of warming climate, potentially resulting in primarily tropical diseases encroaching into historically subtropical or temperate regions. Thus, we must be prepared for the possibility of geographic spread of diseases into areas where they have not occurred, or reintroduction into areas where they once occurred but have been eliminated through control measures. For example, North America and Europe are at risk for reintroduction of such major “tropical” diseases as malaria and yellow fever, and thus must come under increasing scrutiny, starting with surveillance of freshwater systems for both established and potentially invasive vector and host populations. This critical perspective paper briefly reviews selected previous cases in which aquatic invasive species have contributed to infectious disease emergence, re-emergence, or increase, and proposes One Health strategies for integrating human, animal, and environmental monitoring and surveillance to better prepare for or prevent geographic spread of major human health threats associated with aquatic systems.

Key words: climate change, yellow fever, dengue, Chikungunya, malaria, *Aedes albopictus*, *Dirofilaria repens*, water-related

Introduction

Among the many negative consequences of biological invasions, perhaps the most potentially damaging involve the introduction of new human, animal, and zoonotic (i.e., human-animal) pathogens into geographic areas that were previously free from the associated diseases (Conn 2009). Such introduced pathogens are themselves invasive species, but since infectious diseases are typically studied by a different community of scientists

than are invasive species, the bodies of literature and their associated terminology are usually different. Thus, infectious disease specialists refer to “emerging infectious diseases”, a term which encompasses diseases caused by etiologic agents including: 1) novel or newly discovered infectious agents such as the AIDS-causing human immunodeficiency virus (HIV), and new arboviruses (Carpenter et al. 2013); 2) pathogens long known to infect animals, but later discovered as human pathogens, such as human-infectious microsporidia (Graczyk et al. 2004); 3) historically well-known

pathogens such as the cholera-causing bacterium, *Vibrio cholerae*, dengue virus (Harrington et al. 2005), and the filarial nematode, *Dirofilaria repens*, which are expanding into new geographic areas (Sałamatin et al. 2013); 4) parasites such as the blood fluke worms, *Schistosoma* spp., causative agents of snail fever, protistan malaria-causing *Plasmodium* spp., or yellow fever virus (YFV), which have been eliminated from some areas, but now threaten to re-emerge, or re-invade, into areas from which they were previously eliminated through control efforts (Liang et al. 2006; Rogers et al. 2006).

When integrating the study of aquatic biological invasions with the conventionally separate field of infectious disease epidemiology, it is critical to recognize that aquatic environments play diverse roles in the transmission of infectious pathogens to humans. The broad spectrum of freshwater-associated infectious diseases has been the subject of an excellent recent review by Yang et al. (2012), who examined data on 1428 reported infectious disease outbreak events associated with freshwater between 1991 and 2008. Such diseases can be assigned to the categories of: 1) water-borne such as typhoid and cholera; 2) water-carried such as cryptosporidiosis and giardiasis; 3) water-based such as schistosomiasis and diphyllobothriasis; 4) water-related such as malaria, dengue, chikungunya, and filariasis; 5) water-washed such as trachoma and viral conjunctivitis; and 6) water-dispersed such as Legionellosis. For the bioinvasion scientist's interest, the common factor is that all involve new major incidents in freshwater systems. The cases reported by Yang et al. (2012) are a very small number of actual situations however, as this only includes reported outbreaks, and thus ignores large-scale endemic diseases, small-scale situations involving fewer patients, animal infections by known or potential zoonotic pathogens, and buildup of potential free-living stages of zoonotic or sapronotic pathogens.

This brief critical note is not intended to present a comprehensive review or analysis of these complex overlapping areas, but is intended to emphasize some general points related to the intersection between infectious disease epidemiology and invasive disease science relevant to aquatic systems, and to present a brief outline of some examples of infectious disease threats to provide a perspective on issues to be considered by aquatic bioinvasion scientists whose interests cross into biomedical and public health arenas.

Aquatic bioinvasion and climate change

In bioinvasion science, there is a tendency to concentrate work on the characteristics of invasive species that make them well suited for broad dispersal and colonization. In most cases, this involves either: 1) ability to exploit novel access to a new environment, or 2) ability to adapt to new environmental conditions (Van der Velde et al. 2010). However, it is also important to recognize that new invasions may be facilitated not by any change in the colonizing organism or development of new corridors of dispersal, but rather by change of environmental conditions in the invaded area that make an environment conducive to colonization by an organisms that previously was unable to live and reproduce there. Anthropogenic changes such as construction of new artificial lakes with resulting changes in associated wetlands have been considered by some authors (Johnson et al. 2008). Anthropogenic pollution also has been shown to have an impact on the potential for aquatic invaders to become established. One example of this is the potential for toxic antifouling paints in freshwater harbours to influence colonization by aquatic invaders (Minchin and Gollasch 2003), such that eliminating the pollution source may increase the potential for invader establishment.

Climate change is another more complicated issue that requires more attention by those who study aquatic bioinvasions (Conn 2007a). Whether by expansion, emergence, or re-emergence, the threat of new or increased infectious disease situations may be exacerbated by climate change, which may lead to both warmer temperatures and altered precipitation patterns in some areas. Both of these influence the suitability of freshwater environments for serving as disease reservoirs (Dhiman et al. 2010; Genchi et al. 2011). Since most infectious diseases of humans favor warmer climates, paralleling the generally higher biodiversity in tropical regions, potential expansion of such diseases into more temperate regions concomitant with global warming should be a major focus for bioinvasion science in coming years.

Aquatic bioinvasion by pathogens, vectors, and hosts

As with other biotic entities, the success of these infectious agents in the newly invaded region depends on other environmental conditions being met that are conducive to their survival and

continued dissemination. This may include the availability of susceptible host populations in the invaded area, as well as appropriate abiotic environmental conditions. While many human pathogens may live and accumulate in aquatic environments without any hosts, it is critical to keep in mind that approximately 61% of all known human infectious pathogens are zoonotic, and approximately 75% of emerging human pathogens are zoonotic (Taylor et al. 2001). In many cases, the host animals are aquatic or associate closely with freshwater, which may thus serve as a medium of dispersal or maintenance of the disease. Additionally, many infectious diseases require vectors or intermediate hosts that live in freshwater. Among these are some of the most important human parasites globally, such as malaria that requires water-breeding mosquito host/vectors. Similarly, schistosomiasis blood flukes require freshwater snail intermediate hosts for their larval development. Introducing a disease agent into a human population where there are no competent vectors or intermediate hosts thus poses little public health concern. However, invasion or re-invasion of a geographic region by a vector or intermediate host population itself sets the stage for introduction and emergence or re-emergence of the disease in that area, even though no human or animal cases have been detected. Of course, among human pathogens that are not zoonotic, aquatic forms may often be regarded as sapronotic, thriving in conditions where suitable organic nutrients, water, and abiotic conditions allow them to maintain populations outside any host, but with the potential of infecting humans opportunistically (Hubálek 2003). As a result of all these factors, it is important for bioinvasion scientists, and particularly those who study biotic invasions of aquatic habitats, to become increasingly aware of the potential for biotic invasions to alter the habitat and biota in ways that have the potential to increase or exacerbate threats to human health.

Bioinvasion by aquatic pathogens

Many human pathogens exist in aquatic environments either as free-living vegetative forms, actively feeding and reproducing, or as dormant spores moving between susceptible hosts. Any of these might be introduced as invasive pathogens into new aquatic environments, and thus should be subjects of study by aquatic invasion researchers. Some of these are free-living organisms

that are opportunistic, becoming infectious under certain circumstances, such as the protists *Naegleria*, *Acanthamoeba*, and *Balamuthia* that can cause primary amoebic meningoencephalitis (PAM) with an extremely high mortality rate (Lopez et al. 2012). Others include bacteria such as *Burkholderia pseudomallei*, the etiologic agent of pulmonary and cerebral melioidosis, especially in Southeast Asia and Australia, but potentially in other warm-climate areas around the globe (Meumann et al. 2012). These pathogens typically infect people who have direct contact with the water, either by swimming, wading, or other activities. Other sapronotic pathogens, such as *Legionella longbeachae* and *Legionella pneumophila*, which cause pulmonary legionellosis, may travel from water through aerosol to infect humans (Fields et al. 2002). The recent deadly outbreak of cholera in Haiti, caused by invasion by the aquatic *Vibrio cholerae* bacterium through human hosts moving from Asia, is an example of a pathogen typically acquired by drinking contaminated water (Frerichs et al. 2012).

Perhaps even more important to aquatic invasion biology are the many parasitic organisms that are active only while inside their hosts, but go through dormant dispersal stages in freshwater environments. Such pathogens may have primarily terrestrial hosts, and thus may not be regarded by many as aquatic, but nevertheless may use water as their most important medium of dispersal and transmission. Among those that have been most studied by invasion biologists are the waterborne zoonotic diarrheal protists, *Cryptosporidium* and *Giardia*, and the agents of zoonotic microsporidiosis, *Encephalitozoon* and *Enterocytozoon*. These have special relevance to invasion biology, as they can exist in their dormant oocyst, cyst, or spore forms not only in water or aquatic sediments, but sequestered within invasive molluscs such as *Dreissena* mussels and *Corbicula* clams (Conn et al. 2014; Graczyk et al. 1998a, 2003, 2004; Lucy et al. 2008). Other related pathogens responsible for recent foodborne outbreaks have been linked to introduction via field-grown produce that had been irrigated by contaminated water. Irrigation-water pathogens such as *Cyclospora cayetanensis*, causing diarrheal cyclosporiasis, have thus been implicated in movement from South America to North America, where new human populations are affected (Graczyk et al. 1998b; Ortega and Sanchez 2010). This is another mechanism for invasion by aquatic pathogens into new areas.

Bioinvasion by aquatic vectors

Despite the threat of direct invasion of new waters by infectious agents, many of the most important human pathogens require living vectors as obligate hosts or transmission vehicles. This makes colonization of new areas more difficult for the pathogen, but once the vector population is established, pathogens tend to be more difficult to eliminate or control. Examples that immediately come to mind as evidence of this include malaria, regarded by most global health experts as the world's leading disease. Malaria is caused by human *Plasmodium* spp., infectious apicomplexan protists that require both human and water-breeding mosquito hosts. Malaria, as well as other diseases vectored by mosquitoes and other biting flies, are especially complex in that they often require a particular genus or species, or at least a narrow range of genera and species as hosts for their development. Thus, it is important for invasive species biologists to be vigilant for insects that breed in various bodies of water, from flower pots to large lakes and rivers, with vehicles of invasion ranging from ballast water of large ships to rainwater in transported rubber tires and metal pipes.

Given the obligate nature of many insect vectors, it is clear that the existence of healthy vector populations is itself a pending health threat, even if the pathogen does not occur in a given area. If competent *Anopheles* vectors of malaria, or *Aedes* vectors of dengue, Chikungunya or other viruses are present in an area, new invasion of that area by the pathogen requires only the movement of infected human or animal hosts into the area. For this reason, situations such as this are regarded as major public health concerns (Rogers et al. 2006; Reiter 2010). For example both dengue fever (including deadly dengue hemorrhagic fever) and high-mortality yellow fever, both caused by viruses, can be transmitted by various species of mosquitoes. Some of these, such as *Aedes aegypti*, have been established across much of the world for centuries, while the dengue virus that it transmits to humans has been spreading at an alarming rate around the globe (Dick et al. 2012). But an even greater threat today for more temperate areas may be *Aedes albopictus*, an aggressively invasive aquatic species (Medlock et al. 2012). Both *Ae. aegypti* and *Ae. albopictus* may be responsible for the very recent introduction and spread of chikungunya virus in the Caribbean and South America (Omarjee et al. 2014). Such an invasion

was predicted and modeled before the new invasion occurred in the Western Hemisphere (Ruiz-Moreno et al. 2012). Monitoring these mosquitoes in Europe ahead of potential establishment there should be an objective of bioinvasion biologists as well as public health scientists throughout Europe (Van Bortel et al. 2014).

Of particular concern other than dengue and chikungunya is yellow fever, one of the deadliest of mosquito-borne viral diseases. This disease was once well established in the United States, with major epidemics resulting in mortalities as high as 12% of the human population in some areas. After being eliminated from temperate areas many decades ago, there is now a real possibility that yellow fever could return to temperate North America and Europe, as mosquito vector populations are already there and spreading (Reiter 2010).

Besides these ancient diseases that are subject to re-emergence, there are new threats that also depend on mosquito transmission. One emerging zoonosis that is currently among the most extensively spreading diseases in Europe (Genchi et al. 2011, Masny et al. 2013) is zoonotic dirofilariasis caused by the filarial worm, *Dirofilaria repens*. The worm causes cutaneous, mammary, genital, and conjunctival infections in people. This parasite is most often associated as a parasite of dogs, but requires freshwater for transmission by container-breeding and other mosquitoes. Almost unknown in temperate Europe a few decades ago, a recent study reported 1465 human cases in Ukraine alone within the past 16 years (Salamatina et al. 2013). Very recent reports show that it has invaded as far north as Russia (Masny et al. 2014). Clearly, as experts who continue to monitor freshwater systems for invasive mosquitoes and other insect vectors, bioinvasion scientists have a major role to play in the public health arena.

Bioinvasion by aquatic hosts

Many human pathogens, especially parasitic helminths (worms), utilize obligate aquatic hosts in developing the stages that are transmissible to humans. Most notable among these are the trematodes, which typically develop as larvae in aquatic snails and can cause serious diseases in humans when they ingest aquatic animals, or are exposed to water where infected snails live. Schistosomiasis, one of the most common, widespread and devastating human diseases globally, requires certain species of freshwater

snail hosts for its survival and reproduction. Over several centuries, one of the human-infective species, *Schistosoma mansoni*, has spread previously as an invasive disease, as its snail hosts of the genus *Biomphalaria* have invaded new environments (Morgan et al. 2001). However, biological invasion by non-host snails that compete with the schistosome host snails appears to have resulted in decline of the disease in some areas (Pointier et al. 2011). Clearly, such dynamics require further study, and should be considered by scientists interested in the study of invasive molluscs.

Other trematodes might also be implicated in the biological invasions by snail hosts (Karatayev et al. 2012). Among those that are infective to humans, trematodes of the family Echinostomatidae, and especially the genus *Echinostoma*, are worth watching. In parts of Asia, echinostomes are common and highly pathogenic human parasites (Sohn et al. 2011), while potentially human-infectious echinostomatid species also live in Europe and North America, and infect a range of native and invasive molluscan hosts (Conn and Conn 1995).

Invasive fish hosts may also serve as vehicles for introduction of human parasites into new areas. For example, Nico et al. (2011) recently began exploring the potential for imported Asian swamp eels to become pathways for human helminths into North American food markets. The invasive Asian fish tapeworm, *Bothriocephalus acheilognathi*, has been spreading actively through Europe over the past many years, and was recently confirmed to have infected a human host (Yera et al. 2013). Such situations require further monitoring by bioinvasion scientists, as international trade and thus the international movement of infective agents and their hosts increases (Conn 2009).

One Health approaches to integrative invasion science

Clearly, the foregoing discussion demonstrates that invasion science has a major role to play in defending human populations against many major threats to human health. Equally clear should be the fact that the major infectious diseases of humans are also major diseases for livestock, domestic animals, wildlife, and fish. They are therefore major problems for overall environmental health. The growing global movement frequently referred to as “One Health” involves an approach



Figure 1. Diagram showing the symmetrical relationship proposed between human, animal, and ecosystem health, to conceptualize One Health approaches.

that seeks to integrate the best of science from the human health sector, the animal health sector, and the environmental health sector (Conn 2009; Atlas et al. 2010). In this sense, One Health is seen as a natural synergism between the three formerly disparate sectors of scientific research and policy, applied such that a single health consciousness is achieved (Figure 1). The important concept presented here, is that One Health must go beyond the medical, veterinary, and traditional health communities, to incorporate those scientists who focus on the diverse biotic and abiotic components of ecosystems. In aquatic systems, nothing could be more important to such a One Health perspective than the role of invasive species research.

One Health approaches have been utilized for many years, by various names or by no name, by scientists who study parasitic and other zoonotic diseases (Conn 2009; Conn and Conn 2012). However, there is a need for more integration of scientific work on a practical level. For example, museums that serve as repositories for biological reference collections should use their extensive resources and databases from human, animal, and environmental collections to show linkages between pathogens that affect diverse sectors (Conn 2007b, 2008). Museums thus may become an important resource of diagnostics, biomonitoring, and surveillance.

One Health approaches have been successful in recent years at detecting the emergence of mosquito-borne diseases such as West Nile Virus in the United States and Rift Valley Fever in Saudi Arabia (see review by Oura 2014). One Health approaches also have applicability for detecting and preparing for potential future emerging disease outbreaks associated with

mosquito vectors. Along these lines, Ruiz-Moreno et al. (2012) have suggested strategies to monitor populations of invasive *Ae. albopictus* populations in North American freshwater systems as a means to prepare for an impending introduction of chikungunya virus into the United States.

It may be determined that in many cases, invasive species can themselves be used as monitors for pathogen invasion. This has been done at a preliminary level, primarily using the filter-feeding invasive bivalves, *Corbicula fluminea* and *Dreissena polymorpha*, as sentinels for various types of human and zoonotic pathogens in freshwater rivers and lakes (Conn 2010a, 2010b; Conn et al. 2014; Graczyk and Conn 2008; Graczyk et al. 1997, 1998a, 2003, 2004; Lucy et al. 2008). Yet, this serves as only one model that is currently still in its development phase. Bioinvasion scientists should search for other models that foster integration of invasive species studies with biomonitoring and surveillance for human and animal disease agents, thus helping to ensure One Health for all.

Conclusions

In consideration of the situations and ongoing issues outlined above, it is recommended that emerging infectious disease threats become an increasingly active area of study for bioinvasion science. It is further recommended that more effective cooperation is sought between traditional invasive species biologists and their colleagues working in the biomedical, epidemiological, animal health, and public health fields. In particular, it is recommended that bioinvasion specialists make progress in adopting the spirit and basic tenets of the One Health approaches currently being built to foster such cooperation between human, animal, and environmental health scientists. This is critical for developing and enhancing new research, monitoring, control, and remediation efforts in bioinvasion science. In particular it is crucial that the new generation of students be trained increasingly in the cross-disciplinary approaches to understanding health and disease as an all-species-all-system context through new and better One Health curricula at all educational levels. By thus integrating our research, public outreach, education, surveillance, and control efforts across the human, animal, and ecosystem health sectors, we can create synergism that will improve health across the board.

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