Jumping the Species Barrier:

By Kelly A. Reynolds, MSPH, Ph.D.

The recent emergence of H1N1 virus (aka swine flu virus) reminds us that microbes are ever-adapting to their environments. They often expand via new susceptible hosts and additional transmission routes.

Although widespread geographically, H1N1 is not the 'big one' that infectious disease experts fear will someday cause a global pandemic with extremely high mortality rates. The emergence of any new pathogen, however, provides the impetus for impact assessment, identification of exposure scenarios (including the waterborne route) and the development of risk-reduction responses.

What are emerging pathogens?

The definition of an emerging pathogen is "any new, re-emerging, or drug-resistant infection whose incidence in humans has increased within the past two decades or whose incidence threatens to increase in the future."[1] Pathogens emerge due to a variety of reasons, including: evolution of a truly new organism that is distinct from other genotypes (i.e., Ebola virus); acquisition of a new virulence factor in a previously recognized organism (i.e., a toxin-producing *E. coli* O157:H7 or antibiotic-resistant MRSA); or a newly recognized association with, or recognition of, disease (i.e., the ulcer producing *Helicobacter pylori* or community-acquired *Clostridium difficile* infections).

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Due to advances in medicine, humans are living longer with chronic infections while also presenting a more susceptible population for opportunistic microbial pathogens to invade. Routes of disease transmission for emerging pathogens may be traditionally recognized or newly discovered niches. For example, bacteria previously associated with hospital-acquired infections are now being discovered in the community (i.e., MRSA, MAC and *C. difficile*). *C. difficile* was previously a strict nosocomial infection. However, new information suggests up to 50 percent of infections are community acquired and the source of these infections is currently unknown.

Ironically, the more deadly a microbe is, the less likely it is to spread. There simply are not enough hosts living to spread the disease effectively.

Consider the highly pathogenic H5N1 influenza virus (aka avian influenza A). Cases have been reported in Asia, Africa, the Pacific, Europe and the Near East. Strains of avian influenza A virus detected in Vietnam, Thailand and Indonesia are showing resistance to two commonly used antiviral medications and have also been detected in pigs, cats, dogs, tigers, leopards and other animals (CDC, 2008. www.cdc.gov/flu/avian/outbreaks/current.htm).

With a 50-percent mortality rate, the H5N1 virus is still not able to spread from human to human and thus, has stayed relatively contained. The ever-adapting virus, however, has shown recent signs of mutation resulting in milder disease but possibly a greater transmission advantage.

In April 2009, health officials in Egypt reported an increase in cases, but as a milder disease affecting mostly children and not adults. While this may initially sound like a good thing, it may actually lead to a more globally transmissible virus among humans that even at a lower mortality rate could result in hundreds of millions of deaths worldwide.[2]

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Crossing the species barrier

Bacteria actively grow outside their host and may trade genetic information with other bacteria in the environment that have adapted to a wide range of conditions. Animal feedlots, where antibiotics are commonly used, harbor common bacterial populations with antibiotic-resistance factors. When these and other virulence factors are passed to a pathogen, a new generation of superbug can be produced. Many emerging waterborne pathogens are zoonotic, meaning they are transmitted to humans via an animal host.

Animals not only act as a vessel for transmission but may also allow for interaction and replication of microbes, leading to the development of a mutated strain. If an animal or human is co-infected with multiple strains of a pathogen, recombination events are possible, resulting in a newly evolved pathogen with elements of each individual strain.[3]

Crowded living conditions and mixing of different species in the same environment with humans increases the probability of pathogens crossing the species barrier. In other words, microbes adapt to jump from one infected species to another.

Viruses were traditionally defined as host-specific pathogens but an increasing number are now known to cross the species barrier. Examples include hepatitis E virus (HEV), SARS virus and certain rotaviruses and noroviruses.

All of these pathogens are transmitted by the fecal route and are a concern with contaminated food and water supplies. Like the H1N1 virus, HEV in swine are closely related to human strains and evidence of interspecies transmission has been reported.[4]

Although cases of HEV are rare in the US, large outbreaks in China and sporadic outbreaks in other parts of the developing world have occurred. The mortality rate of HEV in pregnant women may be as high as 25 percent.

In India, 70 percent of the HEV cases are due to contaminated water. Rapid urbanization, eutrophication of waterways, inadequate water supply and sanitation and changes in weather patterns are all key factors in global disease emergence.[5]

In developing regions and in the US, waterborne outbreaks often follow large storm events. This should remind us that water quality is dependent on a series of unpredictable events.

The waterborne route

Water, along with food, air and person-to-person contacts, is a primary route of disease transmission. According to US EPA estimates, more than a trillion gallons of sewage and storm water, including animal wastes, are discharged each year from combined sewer overflow, leading to surface water contamination.

Viruses are a concern with groundwater due to their small size and ease of transport in the subsurface. A nationwide survey in 1999 found evidence that one-third of drinking water wells used by towns and cities in the US were contaminated with human pathogenic viruses.[6]

Reoviruses, which infect both animals and humans, were also found in many of these same wells. Farming operations were the only known source in almost a third of the sites sampled.

Researchers have long recognized that HEV, found in pigs and caliciviruses of cattle and swine, are closely related to those that cause illness in man. These studies raise concern that virus transmission from animal to human by contaminated groundwater is possible.

Prevention not panic

The initial recognition of the H1N1 virus caused a low-level panic worldwide. Representatives from the pork industry lobbied for a change from the initial label of swine flu influenza to H1N1, given that there is not evidence linking the spread from pigs to humans and also to prevent a misconception that pork products could transmit the disease.

In response to the H1N1 outbreak, schools and businesses were closed in Mexico, travelers from Mexico were quarantined in China, massive amounts of funds were appropriated for vaccine development and Egypt announced they were beginning to slaughter their entire pig population (equal to approximately 250,000 pigs).

To date, 30 deaths have been reported from H1N1 in addition to 1,516 cases in 22 countries. For perspective, more than 500,000 deaths are reported each year from the typical influenza A virus worldwide.

Although the panicked response over H1N1 influenza infections may have been overstated (only time and retrospective data analysis will definitively decide), the issues of pathogen emergence are once again on the forefront of public health prevention and preparedness efforts. Scientists are not able to predict when and where the next emerging pathogen will present itself but all generally agree that more pathogens are likely to emerge and some will be spread via the waterborne route.

Just as handwashing remains an important defense against pathogens' spread from person to person, POU water treatment devices offer a consistent and reliable defense against waterborne pathogens. Conventional drinking water treatment remains effective for removal of the majority of microbial pathogens and would be expected to remove emerging pathogens as well.

Contamination in the distribution system, however, is well-documented and drinking water outbreaks continue to occur due to lack of treatment or failure in the treatment chain. While contamination sources may be from a variety of point and non-point sources, water is delivered from a distinct point source to the consumer, providing an easily controlled site for additional treatment.

Consumers can be ready for the next emerging waterborne pathogen. The best way to control contamination events at the tap is with the installation of an appropriately designed POU water treatment device for pathogen removal.

Endnotes

1. Sharma, Sachdeva, Virdi. 2003. "Emerging water-borne pathogens." *Applied Microbiology & Biotechnology*. 61:424-428.
2. *ProMED Digest*. Monday April 13, 2009 Volume 2009: No 168.
3. Gannon, Bolin and Moe, 2004. "Waterborne zoonoses: emerging pathogens and emerging patterns of infection." In: *Waterborne zoonoses: Identification, causes, and control*. WHO. IWA Publishing, London, UK.
4. Meng, 2003. "Swine hepatitis E virus: cross-species infection and risk in xenotransplantation." *Current Topics in Microbiology & Immunology*. 278: 185-216.
5. Ashbolt, 2004. "Microbial contamination of drinking water and disease outcomes in developing regions." *Toxicology.* 198: 229-238.
6. Abbaszadegan M, LeChevallier M, Gerba C (2003). "Occurrence of viruses in US groundwaters." *Journal of the AWWA.* 95:107-120.

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