One Health—Attaining Optimal Health for People, Animals, and the Environment

Adopting the One Health paradigm is crucial for understanding emerging diseases and meeting future challenges in global health

Ronald Atlas, Carol Rubin, Stanley Maloy, Peter Daszak, Rita Colwell, and Barbara Hyde

One Health is a paradigm that encompasses the health of humans, animals, and their environment, recognizing that the health of each domain is inextricably interconnected. The One Health concept is interdisciplinary, comprising, among others, public health, clinical medicine, microbiology, ecology, and geography, as well as public outreach. One Health has particularly great relevance for microbiology as a unifying discipline that connects health among humans, animals, and the environment. Given that over 60% of emerging infectious disease events are caused by the transmission of an infectious agent from animals (zoonoses), with 75% of these originating from wildlife, employing a systematic One Health approach has great potential for reducing threats to global health from infectious diseases. The One Health approach can advance health care for the 21st century and beyond by accelerating biomedical research, enhancing public health efficacy, expeditiously expanding the scientific knowledge base, and improving medical education and clinical care.

Unfortunately, practices in human and veterinary medicine and environmental management often do not recognize these links; a focus on One Health across disciplines is a strategic necessity in addressing contemporary health issues created by the convergence of these domains.

Fortunately, however, the One Health paradigm is receiving increasing attention

Summary

- Employing a systematic One Health approach has great potential for reducing threats to global health from infectious diseases.
- Modern molecular methods, especially metagenomics, are providing insights into the relationships between microorganisms and virulence genes in animal populations (both domestic and wildlife), humans, and diverse environments.
- The pattern of most of the newly emergent diseases is one of demography, human development, and anthropogenic environmental change driving repeated pathogen spillover from wildlife.
- Recent diseases and pathogens that illustrate the importance of the One Health perspective include Q fever, hantaviruses, SARS, West Nile virus, Nipah virus, cholera, malaria, and dengue.
- ASM is exploring ways of increasing communications among medical, public health, animal health, and environmental researchers and practitioners.

Ronald Atlas is Professor of Biology and Co-director of the Center for Health Hazards Preparedness at the University of Louisville, Louisville, Ky.; Carol Rubin is Chief of the Health Studies Branch, Division of Environmental Hazards and Health Effects, National Center for Environmental Health, Centers for Disease Control and Prevention, Atlanta, Ga.; Stanley Maloy is a Professor in the Biology Department and Associate Director of the Center for Microbial Sciences at San Diego State University, San Diego, Calif.; Peter Daszak is President of Wildlife Trust, New York, N.Y.; Rita Colwell is Distinguished University Professor at the University of Maryland, College Park, and Johns Hopkins Bloomberg School of Public Health; and Barbara Hyde is Director of Communications at ASM.

on a worldwide scale. In 2008, the three major international organizations charged with animal health and human health–the UN Food and Agriculture Organization (FAO), the World Organisation for Animal Health (OIE), and the World Health Organization (WHO)–collaborated with the United Nations Children's Fund, the UN System for Influenza Coordinator, and the World Bank to develop a joint strategic framework in response to the evolving risk of emerging and re-emerging infectious diseases. The document communicating this framework, *Contributing to One World, One Health—A Strategic Framework for Reducing Risks of Infectious Diseases at the Animal–Human–Ecosystems Interface*, set out specific interlinked objectives for countries to consider in their approach to infectious disease control at the animal-human-ecosystem interface.

In March 2009, the Public Health Agency of Canada, in collaboration with other Canadian ministries and the major international organizations responsible for the Strategic Framework, hosted an expert consultation titled "One World, One Health: From Ideas to Action" in Winnipeg, Manitoba. The purpose of the consultation was to discuss the Strategic Framework and to identify and shape country-level recommended actions to globally advance the framework. The *Report of the Expert Consultation* concluded that moving forward the animal, human, and ecosystem interface concepts of "One Health" required commitment at all levels–international, regional, national, and local.

Recently, OIE, FAO, WHO, and CDC convened a meeting on 4–6 May 2010 at the Stone Mountain Conference Center in Atlanta, Ga., to build upon the recommendations and conclusions drawn from the Winnipeg expert consultation. The meeting, entitled "Operationalizing 'One Health:' A Policy Perspective—Taking Stock and Shaping an Implementation Roadmap," brought together a select group of leaders, including specialists from national Ministries of Health and Agriculture, the European Commission, the UN, the World Bank, and other institutions from the academic, policy and economic sectors, including a representative from ASM, to contribute their expertise and experience to the discussion. The participants identified "critical enabling initiatives" that will promote One Health goals and that are feasible for completion over the next 18 months. Seven work groups were then formed to collaboratively develop and implement the key activities and will report their progress in September 2011.

The concept of One Health is not new. The union of veterinary and human health was both understood and widely accepted in the 19th century. Sir William Osler, a physician considered the father of modern medicine, taught in both medical and veterinary schools. But early in the 20th century, a separation developed between human and veterinary medicine and between human and animal disease research. Zoonotic diseases received increasingly less attention in medical schools, and the focus of veterinary training shifted from livestock medicine and comparative medical research to companion animal care. Both human and veterinary medicine and medical training became more specialized and compartmentalized, and environmental issues often were not considered in the context of infectious diseases.

Recent Q Fever Outbreak Illustrates Importance of One Health

Hence there are major challenges today in achieving a unified One Health approach. Some of the difficulties facing the One Health concept can be seen in the disconnect between veterinary and human health perspectives concerning a recent outbreak of Q Fever in the Netherlands.

Q Fever is an infrequent bacterial zoonosis caused by *Coxiella burnetii*. Cattle, sheep, and goats are the primary carriers of *C. burnetii*; however, other animals can also carry the bacteria. Infected animals excrete *C. burnetii* through milk, urine, and feces and during the birthing process. *C. burnetii* is resistant to heat, drying, and many common disinfectants, allowing it to survive for a long time in the environment. In animals (predominantly sheep and goats) the disease is usually minor but can result in abortions and stillbirths. Aborted goat placentas can distribute billions of the microorganism into the environment.

People can become infected with Q Fever by breathing in the *C. burnetii* bacteria, usually through contaminated barnyard dust and soil. Human illness usually manifests as pneumonia. Nearly 300 human cases of Q Fever were confirmed in the Netherlands in 2009, including 6 deaths. These cases represent an ongoing outbreak of Q Fever in the Netherlands that began in 2007; 190 cases were reported in 2007, and 1,000 cases in 2008.

From the medical and public health perspectives, the outbreak in the Netherlands in animals was not reported soon enough to prevent human infections. Although massive culling of goats was considered necessary to protect human health, it would have had a major economic impact on goat farming. From the animal health (veterinary) perspective, most animals were healthy and did not have serious disease; the increase in the number of cases was seen as a result of better diagnostic and surveillance systems rather than as a significant disease outbreak that required drastic actions by farmers.

In this case the human health perspective prevailed, and the decision was to destroy all pregnant goats. The Netherlands has begun a vaccination campaign, but *C. burnetii* will still persist in the environment and questions will remain about the role of cattle farms in the persistence of disease. The vaccine does not totally protect against infection and a recent new case of Q Fever has been detected in a herd of dairy goats that had been vaccinated, according to a posting on ProMED July 15, 2010. The outbreak of Q Fever in the Netherlands highlights the need for collaboration and a One Health approach to manage zoonotic diseases so that human outbreaks can be prevented and animal culling minimized.

Reevaluating the Concept of Zoonoses

The importance of the One Health concept was recognized in 2004 at a meeting of health experts from around the world sponsored by the Wildlife Conservation Society and Rockefeller University "One World, One Health: Building Interdisciplinary Bridges," held in New York City. A set of principles emerged from the meeting that recognizes the link between human, animal, and wildlife health and a need for holistic approaches to disease surveillance for the prevention and control of emerging infectious diseases. These principles include the following: recognize the link between human, animal, and wildlife health; devise holistic approaches for surveillance, prevention, and control of emerging infectious diseases; increase global investment in human and animal health infrastructure; form collaborative relationships among governments, local people, and the public and private sectors; provide adequate resources for implementation of these goals; invest in educating and raising awareness of the linkage between human, animal, and environmental health.

As proclaimed by the epidemiologist William Foege, who played a critical role in devising the global strategy that led to the eradication of smallpox in the late 1970s and in increasing immunization rates in developing countries in the 1980s, "You can't tell the story of human health separate from animal health or environmental health." Microorganisms circulate among human and animal hosts and environmental reservoirs. Disruption of the environment can lead to transmission to animals and humans; evolution of new microbial traits can occur in response to changes in the environment; and reservoirs of pathogens and virulence traits can persist in the environment, poised to enter the cycle at an opportune time.

Microbiologists have long recognized that pathogens can jump from one species to another. The term zoonosis was initially coined in the 19th century by the German physician Rudolf Virchow to describe the transfer of disease-causing microorganisms from vertebrate animals to humans. Virchow also initiated the concept of meat inspection to prevent human illness. According to Virchow, "between animal and human medicine there are no dividing lines—nor should there be."

Thus, although this is not a new idea, we need to reevaluate the concept of zoonosis as a unidirectional flow of pathogens from animals to humans. The flow of microbes and their genes is multidirectional and includes environmental reservoirs.

Simply consider the evolution of influenza viruses such as the H1N1 strain that emerged in 2009, which contained genes from swine, avian, and human viral lineages and was transmitted from humans to cats, dogs, and pigs. A much broader approach to the exchange of pathogens and virulence genes is needed to recognize critical molecular level exchanges that drive the emergence of new animal and human infectious diseases. The One Health concept requires us to broaden the meaning of the term zoonoses and to extend our research on emerging infectious diseases to the molecular level to understand the evolution of pathogens, environmental survival, the exchange of virulence factors, and changes in host ranges.

Fortunately modern molecular methods, especially metagenomics, are providing insights into the relationships among microorganisms and virulence genes in animal populations (both domestic and wildlife), humans, and diverse environments. Exotoxin genes have been isolated from seawater far removed from sources that could be attributed to human or domestic animal contamination. Thus gene pools of virulence factors in diverse habitats can undergo genetic exchange and contribute to the emergence of animal and human pathogens. Phages can transfer exotoxin genes between alternative bacterial hosts and transfer exotoxin genes to new hosts, thereby facilitating evolution of infectious diseases. New genomic approaches to the ecology of microbes in humans, animals, and diverse environments will allow prediction of the emergence of new pathogens.

Humans' Impact on One Health

The pattern of newly emergent infectious diseases (e.g., SARS and West Nile Fever) is one of demography, human development, and anthropogenic environmental change driving repeated pathogen spillover from wildlife and the spread of the newly evolved pathogens in dense human populations. Over the past four decades the rate of infectious disease emergence has increased—in both humans and animals. To understand the reasons for the emergence of new infectious diseases and why the rate of emergence is increasing requires an understanding of pathogen evolution, host-parasite ecology, and the broad changes that drive pathogen invasion of novel systems. A One Health approach helps bring the disciplines together to focus on this challenge and can be used to target global surveillance to the regions most likely to spawn the next SARS, coronavirus, or HIV outbreak and to the wildlife that are most likely to carry pathogens with the potential to emerge in people.

A number of factors influence a pathogen's potential spillover from wildlife to humans. As a simple case in point, rodent-borne zoonotic pathogens (e.g., hantaviruses) require the presence of rodent reservoirs. Although these animals exist throughout the world, there are certain areas where rodent abundance is greater and/or the contact with humans is more frequent. Although this does not tell us exactly where a rodent-borne pathogen will emerge, it does provide an indication of where there is a higher risk.

In the same vein, substantial molecular phylogenetic evidence points to a Central-West African origin of HIV-1 in chimpanzees, a species widely hunted for bush meat in that area. The origins of SARS and some Ebola virus outbreaks have also been linked to the consumption of wildlife. It follows that patterns of human hunting, butchering, and consumption of bush meat will likely predict patterns of the emergence of some infections. And once certain diseases like SARS emerge, they can spread globally following air travel patterns. In a very general sense, almost every emerging disease (perhaps even every one) was driven to emerge by some type of change in human behavior or demography or anthropogenic environmental change.

During the last few decades, human-wildlife contact has been associated with emergence of infectious diseases from bats. New viruses from bats in the last 15 years include Hendra virus in 1994, Australian fruit bat lyssavirus in 1997, Menangle virus in 1997, Nipah virus in 1999, SARS-like CoV in 2005, Ebola/Marburg virus in 2005/2006, and Melaka virus in 2007. What is the potential that future zoonoses will emerge from diverse animal hosts? Considering that there are 50,000 known vertebrate species and assuming each has 20 endemic viruses (likely an underestimate), then we can estimate that more than 1 million vertebrate viruses (20,000 in bats alone) exist. Only 2,000 or so viruses have been described, so 99.8% of vertebrate viruses remain to be discovered. Thus there is a large potential for future zoonotic emergence!

Wildlife is likely to be the key source of future emerging infectious disease risk: we predict that the future risk of emerging infectious diseases will be highest where mammalian biodiversity is greatest (the underlying assumption of this prediction is that each species carries a roughly equal number of new or unknown potential pathogens). While this is a very simple correlation, and the true bounds are unknown, it gives us a method to estimate the geographic origin of the next new zoonoses and the global distribution of the risk of a new zoonosis.

Consider the 1999 emergence of the Nipah paramyxovirus, which was first reported in Malaysian pig farms and was traced to an index farm with 30,000 pigs. Since then, there have been another 12 outbreaks, all in South Asia. During the initial outbreaks in Malaysia and Singapore, most human infections resulted from direct contact with sick pigs or their contaminated tissues. In infected people, Nipah virus causes severe illness characterized by inflammation of the brain (encephalitis) or respiratory diseases. It can also cause severe disease in animals such as pigs, resulting in significant economic losses for farmers. In the most recent outbreaks, Nipah virus appears to have been transmitted directly from bats (the true wildlife reservoir) to humans, and then in repeating cycles of human-to-human transmission—indeed in Bangladesh, half of reported cases between 2001 and 2008 were due to human-to-human transmission.

Fruit bats of the Pteropodidae family are the natural host of Nipah virus, but there is no apparent disease in fruit bats. In the Bangladesh and India human outbreaks of Nipah viral infection, consumption of fruits or fruit products (e.g., raw date palm juice) contaminated with urine or saliva from infected fruit bats was the most likely source of infection. The index farm and adjacent farms in Malaysia were located next to a forest that is a primary habitat for fruit bats. There were a number of adjacent pig farms with mango trees planted among the sties bringing fruit bats into direct contact with large numbers of pigs being raised intensively on these farms. Repeated introduction allowed the virus to circulate endemically in pigs, increasing the chances for its spread to surrounding farms. Understanding the origins of Nipah virus and the risk of its future emergence depend on a close collaboration among physicians, veterinarians, microbiologists, and ecologists—a true One Health approach.

The Environment as a Component of the One Health Concept

Environment impacts the emergence of some diseases. In the case of the emergence of hantavirus, a particularly wet season in the southwestern United States in 1993 led to increased vegetation, and normally brown desert areas turned green. The increased vegetation supported increases in arthropod and rodent populations—arthropods as well as vegetation are food sources for rodents. Eleven hantaviruses known to cause hantavirus pulmonary syndrome (HPS) are carried by the New World rats and mice. The virus occurs in the urine and feces of infected rodents, but it does not make the carrier animal sick. Humans are thought to become infected when they are exposed to contaminated dust from mice nests or droppings. The deer mouse (*Peromyscus maniculatus*) is the host for Sin Nombre virus (SNV), the primary causative agent of HPS in the United States. The deer mouse is common and widespread in rural areas throughout much of the United States. Although prevalence varies in time and geography, on average approximately 10% of deer mice tested throughout the range of the species show evidence of infection with SNV. As in other emerging infections, environmental change was a key factor in the outbreak of HPS in the southwestern United States in 1993.

Since 2005, the re-emergence of cholera has been noted in parallel with the ever-increasing size of vulnerable populations living in unsanitary conditions. There is evidence suggesting that global warming may change the incidence of *Vibrio cholerae* in its natural habitats and could result in an increase in the incidence of cholera in vulnerable areas. Several recent studies indicate that El Niño-Southern Oscillation (ENSO), a major source of climate variability from year to year, influences cycles of cholera. El Niño events can be monitored by satellite sensors and used to make predictions about the severity of disease outbreaks and to predict when and where major cholera epidemics are likely to occur.

Other diseases, such as malaria and dengue, may be similarly affected by climate variability. In particular, El Niño events may be responsible for changes in the prevalence and geographic distribution of various diseases. An outbreak of plague that began in central Africa in 2004 and abruptly ended in 2009 may also be related to El Niño cycles. From 2004–2009 eight countries were affected with more than 12,000 cases and more than 800 deaths attributable to plague. Then in 2009 there was a sudden dramatic decrease in the incidence in plague. According to the traditional paradigm this might have been due to improved diagnostics and control measures. But there were no new control measures implemented, and point-of-contact diagnostics were too expensive for widespread use in the affected countries. The One Health perspective would suggest that the decrease might have been due to other factors, including environmental change. The decrease coincided with the worst El Niño cycle since 1998. The wet season in Africa started late, and this might have had a significant impact on feral reservoir fecundity, movement of the reservoir rodent populations, and the abundance of fleas that transmit the pathogens. Other diseases, such as malaria and dengue, may be similarly affected by climate variability. Cases of dengue are now occurring in Key West, Fla.

Challenges to Institutions and Programs

The One Health concept has important implications for public health, interdisciplinary research, academic programs, and public outreach. In recognition of these implications, many scientific organizations have begun to focus on One Health goals. The Centers for Disease Control and Prevention (CDC), for example, has established a One Health Office aimed at enabling CDC programmatic activities to use a One Health approach. The CDC One Health Office is intended to foster leadership, investment, integration, research, and the establishment of respectful partnerships. The WHO, the OIE, the Food and Agricultural Organization of the UN (FAO), and the CDC are continuing to meet with public health and infectious disease leaders to discuss how to move forward with a global One Health agenda.

ASM has also begun a One Health Initiative that is being coordinated by the Communications Committee to increase recognition of the inter-relatedness of human, animal, and environmental health and the role that microbes play in the health of all three domains. ASM will participate in the first International One Health Congress to be held in February 2011 in Melbourne, Australia.

It is important to recognize that there are significant barriers to achieving a One Health paradigm shift, including overcoming inertia associated with change; building lines of communication between disciplines that do not currently have well-established systems for sharing information; developing professional respect among disciplines; overcoming differing mandates across agencies responsible for human, animal, and environmental health; and simultaneously being generalists and specialists. Such change requires new paradigms for communication, cooperation, and funding that crosses traditional agency and organizational lines. ASM is exploring ways of increasing communications among medical, public health, animal health, and environmental researchers and practitioners.

Integration will be a key component. It will be necessary to connect subject matter experts from different disciplines; participate in integrated national and global human and animal surveillance systems; collaborate in identifying diagnostic platforms for use in humans, animals, and the environment; and facilitate sharing of pathogen samples and information, a problem which is sometimes difficult because of fear of biopiracy. It will also be necessary to develop improved tools and models to predict where and when outbreaks are most likely to occur.

All this will require significant research activities that will involve microbiologists. It will be necessary to develop point-of-contact techniques for diagnosing and treating endemic diseases to ensure that the appropriate biologic samples are transferred to reference laboratories in a timely manner. Systems analysis will also need to be developed and applied to improve identification and movement of samples. Predictive models using human and animal biologic samples will have to be tested if we are to properly identify risk factors for zoonotic disease spread and ways to combat emerging infectious diseases.

The way forward will challenge us as microbiologists and health professionals. We will need insightful leadership from government agencies like the CDC and NIH, academic institutions, NGOs like the Ecohealth Alliance, and professional societies like ASM. We are at a crossroads between talking about One Health and truly embracing the new paradigm. The health of humans, animals, and the environment is in the balance.

This article is based in part on the symposium "One Health: Attaining Optimal Health for People, Animals, and the Environment" presented at the American Association for the Advancement of Science Annual Meeting, February 19, 2010, San Diego, California.

SUGGESTED READING

Casas, V., J. Miyake, H. Balsley, J. Roark, S. Telles, S. Leeds, I. Zurita, M. Breitbart, D. Bartlett, F. Azam, and F. Rohwer. 2006. Widespread occurrence of phage-encoded exotoxin genes in terrestrial and aquatic environments in Southern California. FEMS Microbiol Lett. **261:**141–149.

Colwell, R. 2005. Global microbial ecology of *Vibrio cholerae*. In B. Shimsho and R. Colwell (ed.), Pathogens in the marine environment, Springer US.

Daszak, P., A. A. Cunningham, and A. D. Hyatt. 2000. Emerging infectious diseases of wildlife—threats to biodiversity and human health. Science **287:**443–449.

Dinsdale, E. A., O. Pantos, S. Smriga, R. A. Edwards, L. Wegley, F. Angly, E. Brown, M. Haynes, L. Krause, E. Sala, S. Sandin, R. Vega Thurber, B. L. Willis, N. Knowlton, F. Azam, and F. Rohwer. 2008. Microbial ecology of four coral atolls in the Northern Line Islands. PloS One 3(2) e1584.

Douglass, R. J., T. Wilson, W. J. Semmens, S. N. Zanto, C. W. Bond, R. C. Van Horn, and J. N. Mills. 2001. Longitudinal studies of Sin Nombre virus in deer mouse-dominated ecosystems of Montana. Am. J. Trop. Med. Hyg. **65:**33–41.

Enserink, M. 2010. Questions abound in Q-Fever explosion in the Netherlands. *Science* 327:266–267.

Foege, W. H. 2004. "One World, One Health, Can We Muddle Through?"Online reference www.oneworldonehealth.org/sept2004/presentations/eve_foege.

Jones, K. E., N. G. Patel, M. A. Levy, A. Storeygard, D. Balk, J. L. Gittleman, and P. Daszak. 2008. Global trends in emerging infectious diseases. Nature **451:**990–994.

Monath, T. P., L. H. Kahn, and B. Kaplan. 2010. Introduction: one health perspective. ILAR J. **51:**193–198

ProMed 16 July, 2010. Q fever - Netherlands (29) Update: Archive Number 20100716.2382.

Stenseth, N. C., B. B. Atshabar, M. Begon, S. R. Belmain, E. Bertherat, et al. 2008. Plague: past, present, and future. PLoS Med 5(1): e3. doi:10.1371/journal.pmed.0050003

World Health Organization. 2010. Weekly Epidemiological Record. **85:**37–48 (5 Feb 2010).