

In This Issue

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UNTANGLING THE DISEASE WEB

Infectious disease is a complex interaction among pathogens, hosts, and external determinants, which leads to one of several possible outcomes for a host, ranging from survival to death, with various states of reduced fitness between them. **Skerratt et al.** suggest that understanding the determinant of a particular outcome cannot rely solely on deductive experiments, but involves multidisciplinary collaborations and myriad approaches, including investigating causal pathways and mechanisms of disease. The authors conclude that diagnostic investigations confirming the cause of the host's outcome are essential.

A PINCH OF POISON GOES A LONG WAY

Ancient aboriginal Australians hunted and gathered food with a level of skill and details hitherto unexplored. Some of their practices, upon scrutiny, reveal an intimate knowledge of their environment. The release of toxic phytochemicals into large and small bodies of water as part of food procurement practice is one example, which **Sadgrove** suggests actually reduced potentially dangerous cyanobacteria blooms in small bodies of water, making them safer resources for use by both humans and animals.

ALL HANDS ON DECK FOR WATER RECYCLING

The relationship between people and water has never been simple. Engaging and consulting with communities about water recycling is often fraught with conflict and polarization. Conflicting positions, discourses, and meanings attributed to water recycling present a weighty challenge to

water resource managers and governments. **Mikhailovich** discusses an ecosystem approach that not only maintains a focus on the protection of the ecosystem, but also recognizes that water management requires the involvement of multiple sectors and perspectives.

WATER, PATHOGENS, AND A WARMER FUTURE

With global climate change comes an increased risk of exposure to waterborne diseases like cholera, and diseases caused by other pathogenic *Vibrio* species. **Constantin de Magny et al.** detail their prediction system of the likelihood of *V. cholerae* in the Chesapeake Bay by exploiting what is known about the optimal physical habitat of *V. cholerae*. They back-tested 15 years of *V. cholerae* probability to explore the relationship between river flow and the likelihood of *V. cholerae* in the bay. Their approach is one of a suite of tools that can identify and predict coastal-ocean-related public health risks from pathogens.

Global warming might also create a favorable environment for *V. cholerae* incidence in Africa. **Paz** analyzes the possible association between cholera in southeastern Africa and the annual variability of air temperature and sea surface temperature (SST) at regional and hemispheric scales. The results showed a significant exponential increase of cholera rates in humans during the last decades. Additionally, air temperature and SST at both scales had significant impact on cholera incidence. Climate variability should be considered in predicting further cholera outbreaks.

The Sahel zone of West Africa is particularly vulnerable to the effects of periodic abrupt climate shifts, which have occurred several times in the last 10,000 years. The most

recent climate shift is the decades-long drought plaguing the region since the 1960s. The Sahel also suffers from one of the highest malaria burdens in the world. **Bomblies et al.** use a mechanistic modeling approach to evaluate the effects of climate shifts on malaria transmission in southwestern Niger. This approach isolates the effects of individual climate variables on vector activity and then evaluates sensitivity. The authors demonstrate the potential of mechanistic models to evaluate change scenarios at the village scale.

TO DO: STOCK UP ON ALLERGY MEDICINE

Allergies and allergy-related illnesses are not only common annoyances. They also impose substantial economic and quality-of-life burdens. Increased concentrations of CO₂ in the atmosphere—as well as climatic changes projected from such an increase—could impact the sources of seasonal allergies. While the literature does not provide definitive conclusions on how climate change might impact aeroallergens and subsequent allergic illnesses, **Gamble and Reid** demonstrate that phenologic advance, as well as changes in distribution for numerous species of plants and trees, will likely increase pollen production in most of the U.S. They also illustrate a potential for increases in aeroallergen content and potency.

PARASITIC PATCHWORK

Land use and urbanization lead to increasingly small-scale heterogeneity of cultural landscapes. Mobile organisms—humans and animals, alike—encounter variable habitat conditions. Can environmental conditions explain parasite and disease loads on the individual level? **Thamm et al.** examine the infestation patterns of hedgehogs with fleas and ticks at the individual level along a suburban–urban gradient in Germany. By estimating the underlying habitat using digital land cover data, the authors find that small-scale landscape heterogeneity, as well as the amount of particular habitats (such as arable field) in individual ranges, significantly determines flea and tick infestation levels. The findings underscore the need to understand landscape heterogeneity at various scales for animal and public health management.

ENDANGERED BANDICOOTS—WARTS AND ALL

Fewer than 1000 western barred bandicoots (WBB, *Perameles bougainville*) may remain in the wild today, persisting on two island havens off the coast of Western Australia. Conservation efforts to prevent the extinction of this Australian marsupial involve captive breeding and reintroduction programs on mainland Australia. However, efforts are restricted by a progressively debilitating papillomatosis and carcinomatosis syndrome, recently associated with a novel “papillomavirus–polyomavirus hybrid” virus: BPCV1. **Woolford et al.** examine the prevalence and distribution of BPCV1; the associated syndrome in wild, reintroduced, and captive WBB populations; and factors that may be associated with susceptibility to this syndrome.

WHAT A LITTLE BIRD TOLD ME ABOUT THE FLU

Influenza subtypes are often associated with a certain host species, the most obvious example being swine and H1N1. **Piaggio et al.** explore evolutionary relationships among H1 and N1 subtypes from various hosts, including wild birds, domestic birds, swine, and humans. The current outbreak H1 subtype arose from a swine-dominated lineage that is closely related to predominantly human H1. However, both of these lineages show multiple instances of host switching among birds, humans, and swine. The N1 subtype also arose from a swine-host lineage, but remains most closely related to N1 from bird hosts.

Meanwhile, wild migratory ducks may asymptotically carry highly pathogenic avian influenza virus (HP AIV), potentially spreading viruses over large geographical distances. In their study, **Brochet et al.** investigate the potential spreading distance of HP AIV by three common European duck species, based on capture-mark-recapture method. The study thus characterizes wintering movements from a western Mediterranean wetland, and identifies the potential distance and direction of virus dispersal. Such data may be crucial in determining higher-risk areas during this major wintering quarter, and may also serve as a valuable reference for virus outbreaks elsewhere.

CAUTION: MALFORMED TOADS

Malformed anurans raise concern among scientists, because deformities may be related to the recent global amphibian crisis. **Toledo et al.** recently discovered a toad population with more than 40% of the specimens having one or more malformations. The authors suggest that lack of predation pressure contributes to their finding. These results may inform local conservation action plans. The findings may also have implications in other parts of the world, because these and other toad species are recognized as exceptional colonizers.

AMPHIBIAN DECLINES: EXPLANATIONS, EXPERIMENTS, AND CRITIQUES

With one-third of all amphibian species threatened by extinction, worldwide amphibian decline is more than just a serious problem. In several cases, declines occur suddenly and for yet unknown reasons, termed “rapid enigmatic declines.” Testing for the hypothesis that the globally emerging amphibian chytrid fungus, *Batrachochytrium dendrobatidis* (BD) can be linked to this phenomenon, **Lötters et al.** use a GIS-based Species Distribution Model. They demonstrate that areas and species from which rapid enigmatic declines are known, significantly overlap with those of highest environmental suitability to the fungal pathogen. This connection provides one explanation for rapid enigmatic amphibian declines.

With the discovery of BD—and the use of highly sensitive molecular methods for detecting the pathogen—a dangerously single-minded approach to investigating declines and mortality has emerged. **Duffus** suggests that the swab’n’run tactics adopted to screen for BD have led to

the erosion of proper investigations into the causes of decline and mortality. As a result, infection is often misconstrued as disease. To address these issues, researchers must return to basic pathological and investigative techniques, and incorporate a multidisciplinary approach to understanding amphibian disease and decline.

Furthermore, generalizing the impacts of a pathogen or the susceptibility of a host species can have several undesirable repercussions for wildlife management and conservation. **Schock et al.** examine the importance of intraspecific differences among amphibian populations exposed to ranaviruses, a group of viruses raising alarms around the world because of their ability to cause massive die-offs. Using barred tiger salamanders and *Ambystoma tigrinum* virus (ATV) as a model system, they document large differences in mortality rates among populations of barred tiger salamanders. Mortality rates in novel pairings of salamander populations and ATV strains are not predictable, based on outcomes when salamander populations are exposed to their own ATV strain. This study highlights the need to minimize translocations of pathogens, even among conspecific host populations, and the importance of considering intraspecific variation in wildlife diseases.

Determining the dynamic relationships between host and pathogen is difficult. **Blaustein et al.** explain that well-designed experiments can help provide unambiguous answers to specific questions about host–pathogen interactions. Experiments may be especially useful for understanding the dynamics of BD. Despite the commonness of pathogens and the harmful effects that they have on their hosts, data from experimental studies—especially in amphibians—are rare. They may be necessary for a true understanding of host–pathogen interactions.

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