LETTERS

Disease transmission can occur at live animal markets, but zoonotic disease research could benefit from an emphasis on humans' and animals' shared risk of infection.

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EcoHealth reframing of disease monitoring

Decade-old (*1*) and recent warnings for coronaviruses with zoonotic epidemic potential (*2*) could have prevented the emergence of coronavirus disease 2019 (COVID-19) (*3*). We therefore agree with Watsa and colleagues ("Rigorous wildlife disease surveillance," Perspective, 10 July, p. 145) that wildlife biosurveillance should increase. However, representing animals as a threat to humans through disease transmission leads to ill-conceived reactive policies (*4*). A perspective (*5*) in which animals and humans share similar risks of pathogens and infections, making animals relevant disease models and sentinels, would be more effective. Clarifying the connection between animal and human health could increase public support for research seeking to understand host-switching in animals, such as the study of virus evolution (*6*), interactions in pathogen communities (*7*), and pathogen discovery (*8*).

A shared-risk perspective on emerging infectious diseases mirrors the field of EcoHealth, which explores the links between ecosystem, animal, and human health. Such strategies place value in healthy ecosystems through an integrative approach that considers both pathogen biodiversity and social-ecological drivers (*9*). Prevention based on understanding the transmission of pathogens through EcoHealth-based emerging infectious disease surveillance is a promising avenue for sustainability science, orders of magnitude cheaper than mitigation in response to a transfer to human hosts (*10*), and less intrusive than current crisis responses.

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Build international biorepository capacity

In their Perspective "Rigorous wildlife disease surveillance" (10 July, p. 145), M. Watsa *et al.* underscore the value of One Health approaches to stimulate integration across currently siloed efforts in zoonotic research and mitigation. To achieve comprehensive decentralized pathogen surveillance, there is an urgent need to develop environmental and biodiversity infrastructure in biodiverse countries experiencing high rates of habitat conversion, wildlife trafficking, and human-wildlife interactions.

Approximately one-third of One Health networks lack an environmental component, fewer than half are active in wildlife surveillance, and almost none is led by developing countries (*1*). International support for development of natural history museums with frozen vertebrate tissue collections remains a key component missing from the One Health equation. Most pathogens causing severe outbreaks in humans are zoonotic in origin (*2*); thus, understanding their evolution and that of their wild animal hosts is imperative.

As was the case for coronavirus disease 2019 (COVID-19) (*3*), identifying wild animal reservoirs can be challenging when biorepositories are lacking (*4*). In most countries, natural history biorepositories remain poorly supported and largely disconnected from public health initiatives. For example, most studies of bat coronaviruses to date (*5*), including the PREDICT animal surveys discussed in Watsa *et al.*, did not preserve host specimens or tissues, thus limiting the potential for molecular host identification or replication and extension of the science (*6*). Emerging infectious disease response hinges on sampling depth across space, time, and taxonomy, the very sampling enabled by museum biorepositories. As primary biological infrastructure, in-country development of museum collections that follow best practices (*7*), with specimen data freely available through the internet, should be an international imperative (*8*) for effective global surveillance and mitigation of emerging infectious diseases.

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Response

We agree with Vanhove *et al.* that wildlife conservation and emerging infectious disease screening are two sides of the same coin. Wildlife and humans can be vulnerable to spillover events by the same pathogen. For example, respiratory diseases (*1*) and Ebola virus (*2*) outbreaks have occurred simultaneously in great apes and humans. Pathogens also affect biogeographical species range expansions, contractions, and extinctions (*3*). Biosurveillance efforts should reflect that health risks are shared by humans and wildlife, a central tenet of the One Health framework (*4*). As Vanhove *et al.* point out, wildlife can serve as the source for preventive solutions that mitigate spillover risks into humans and animals.

A shared risk perspective could also combat the narratives that portray animals as dangerous pests or disposable commodities that endanger human health (*5*), as in the case of bats (*6*), many of which are likely not hosts for coronaviruses such as severe acute respiratory syndrome coronavirus 2 (SARS-CoV-2) (*7*). In addition to emphasizing shared risk, such misinformation can be countered with well-researched messaging following a zoonotic outbreak. Conservation social science has honed a suite of tools to identify the often unpredictable human motivations behind (*8*), and the possible negative consequences of, such communications (*9*).

Colella *et al.* suggest that surveillance efforts should include natural history collections. Some natural history museums and zoos archive biobanked specimens, cryopreserved viable cell cultures, disease specimen banks, and histopathology samples, but this highly effective practice (*10*) is limited by high costs. We agree that devoting funding toward biodiversity banking within countries at high risk for emerging infectious diseases would improve conservation outcomes. Taxonomically diverse biobanked tissues and live cell cultures could expand studies of host-pathogen relationships, clarifying host range or affected tissues and providing in vitro systems for infectivity and pathogenicity investigations. Such collections could allow drug development for humans to expand beyond just a few animal laboratory models, given that relatively well-studied viruses such as SARS-CoV-2 are potentially broadly infectious across taxonomic orders (*11*). Comparative genomics and transcriptomics among nonmodel species are used infrequently in biomedical research programs but hold great potential for prioritizing species and gene targets with alternative host defense mechanisms for laboratory study (*12*).

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