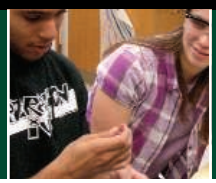
Technology reaches the classroom 1103



Star colors 1105

LETTERS

edited by Etta Kavanagh

Making Sure Public Health Policies Work

I TRUST IT WAS WITH TONGUE IN CHEEK THAT Jon Cohen, in his article on the new world of global health, referred to "an obscure 1978 health conference in the USSR" ("The new world of global health," News Focus, 13 Jan., p. 162). That "obscure conference" was the World Health Organization's Alma Ata conference on Primary Health Care.

Among its simple prescriptions was that, to ensure effective health care for people in poor communities, health structures must be built in those communities. "Smart weapons" have their limitations, in health as in the military, and the most effective medicine is invariably rooted within a society, not parachuted in from outside.

This lesson is habitually forgotten by the experts, which is why we now find that "shortages of trained health-care workers mean that those drugs that are available may not be used properly."

A Congolese child being vaccinated for smallpox in a refugee camp in Burundi.

Unfortunately, health policy in poor countries is too often directed by people who do not live in them, for whom these are academic matters. One need to look no further than rural China to understand what happens when effective community-based health care systems are allowed to collapse.

All the wonderful and worthy global health initiatives will work only if there are local systems through which they can be delivered. To achieve our goals, we need to keep a little space on the podium with all the great and the good (and some small change) for that most effective of all solutions, the well-supported primary health care worker.

MIKE MULLER

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THE NEWS SUMMARY OF THE CURRENT INTERnational efforts to control infectious diseases was both timely and interesting ("The new world of global health," J. Cohen, News Focus, 13 Jan, p. 162). There is no doubt that the agenda for improving health in poor countries is moving forward. We are concerned, however, that the approaches outlined focus on technology and research, while ignoring evidence from public health care systems. The provision of adequate health care services relies heavily on material and human infrastructure, as well as active community involvement. Evidence of an approach that works can be found in the experience from Cuba over the last four decades (*1*). With a focus on training and education, universal provision of primary care, vaccination campaigns, and community mobilization, Cuba has achieved goals that remain elusive for the countries discussed in the article. Infant mortality is currently lower in Cuba than in the United States and life expectancy is 77 years (*2*, *3*). Many infectious diseases, including polio, measles, rubella, mumps, and diphtheria, have been eliminated, and substantial progress has been made in reducing the cardiovascular disease burden (*4*). The Cuban international aid program has placed 24,000 physicians in African and Latin American countries that have seen their own health personnel leave for Europe and the United States (*5*, *6*).

Resources expended in global health could be better utilized if evidence from the Cuban health care system were incorporated into their appropriation. Unfortunately, the opportunity to learn from the Cuban model may be another of the victims of the half-century U.S. blockade of Cuba.

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Linking Bats to Emerging Diseases

A SARS-LIKE CORONAVIRUS FOUND IN 13 OF 46 horseshoe bats (genus *Rhinolophus*) ("Bats are natural reservoirs of SARS-like coronaviruses," W. Li *et al.*, 28 Oct. 2005, p. 676) led A. P. Dobson to conclude that these bats "have now been officially recorded as the natural reservoir host of the coronavirus (SARS-CoV) that causes severe acute respiratory syndrome…" ("What links bats to emerging infectious diseases?," 28 Oct. 2005, p. 628). He also said that SARS-CoV "almost brought the burgeoning

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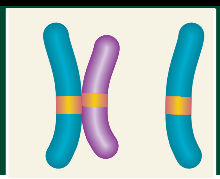
Counting X chromosomes
1107

Jurassic mammal education
1109

economy of Southeast Asia to its knees…," apparently on the basis of an unsubstantiated report (*1*). Li *et al.*'s data confirm that horseshoe bats are a reservoir for a coronavirus related to SARS-CoV found in humans and the virus isolated from palm civets, but this does not make them the reservoir for SARS-CoV.

Dobson's linking of bats to emerging diseases caused by Ebola and Marburg viruses is speculative and does not agree with published literature [e.g., (*2*)]. The assertion that direct transfer of Nipah virus from bats to humans occurred in Bangladesh and that human consumption of the pulp of fruit mouthed by bats is a route of these infections is not supported by the paper Dobson cited [i.e., (*3*)]. Ejected pellets of fruit bats consist of indigestible (by the bats) fiber and seeds with little nutritional value for animals (e.g., palm civets) unable to digest cellulose. Insectivorous bats cull indigestible insect parts, but we know of no evidence that this contaminates culled parts with bat saliva, let alone viruses.

People must be concerned about SARS and other emerging infectious diseases and the roles that bats and other animals may play in their epidemiology. When public health is the focus, however, those concerned for conservation of wildlife (including bats) must insist on careful consideration of documented facts rather than speculation and unsubstantiated statements.

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Response

FENTON AND COLLEAGUES RAISE SOME INTEResting points in their Letter. The fact that 13 of 46 horseshoe bats are seropositive to SARS certainly convinced me that horseshoe bats are likely to be an important reservoir of SARS. There are numerous economic analyses of the impact of SARS on the economy of Southeast Asia and Canada; I cited the most comprehensive of several possible references. There have now been outbreaks of Nipah virus in Bangladesh in each of the last 5 years—since detailed surveillance began. In all cases, fruit bats are implicated as the natural reservoir (*1*).

When we have visited the primary sites for the outbreaks of Nipah virus in Ipoh, Malaysia, the ground under the fruit trees shading the pig farms was littered with partially eaten fruit often bearing bat teeth marks. We also found similar partly eaten fruits under colonies of fruit bats south of Cairns, the site of a more recent Hendra virus outbreak. All of this makes me think it likely that bats do occasionally drop partially eaten food to the ground and that this food is occasionally eaten or ingested by other species: palm civets, pigs, horses, foxes, etc. I agree with Fenton *et al.* that rejected, or accidentally dropped, food items are unlikely to be major items in the diets of these novel host species, but interspecific transmission of most pathogens is a rare event. A recent paper partially confirms that bats are the likely reservoir hosts for Ebola virus (*2*). A similar mechanism can be postulated for the route of transmission of Ebola from bat to fruit to primate.

The main point of my Perspective is that I think it is crucial that we understand a lot more about the way that bats manage the interesting pathogens that infect them. This wish extends to a diversity of other hosts harboring pathogens that have a distant possibility of entering either human populations or our domestic livestock. Bats have many adaptations that have allowed them to adapt to a completely novel life-style when compared with other mammals (*3*). Adaptations such as torpor, a highly venous alimentary canal, flight, and a reduced skeleton provide important and different selection pressures on the pathogens that have to persist in populations of bats. The fruit-eating bats implicated as the reservoirs of SARS and Ebola have diets that are very low in nitrogen. Does this have any bearing on their inability to withstand infection by these pathogens? The major bat radiations occurred around 50 to 60 million years ago (*4*, *5*), significantly earlier than those of the other mammalian groups from which most pathogens of humans and domestic livestock evolved. This suggests there is a great need to search for novel regions in the immunological genes of the major bat families and to better understand the natural dynamics of infectious diseases in bats.

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SARS has been found in horseshoe bats.

Voucher Specimens for SARS-Linked Bats

WE READ WITH INTEREST THE REPORT "BATS are natural reservoirs of SARS-like coronaviruses" by W. Li *et al.* (28 Oct. 2005, p. 676). These authors and others (*1*) have identified bats in three genera as reservoirs of SARS-like coronaviruses (SL-CoVs), raising the possibility that SARS-CoVs arose among these or other bats. An omission in these papers is that no systematic attempt was made to preserve voucher specimens (*2*).

Properly vouchered specimens of reservoir hosts are a sine qua non in a research program whose goals are the accurate understanding of disease emergence and the ability to forecast disease risk (*3*, *4*). In the present instance, this basic standard was not followed and, thus, there is little that can be done to verify species identifications; this is especially troublesome when new data indicate that in SARS and other diseases, some individuals transmit more infection than predicted by homogeneous null models (*5*, *6*). Bat systematics is a dynamic area of research, and classifications change accordingly. This is especially the case in *Rhinolophus*, a group where species identification cannot be based solely on external morphological characters (*7*). Voucher specimens and associated data could be used for genetic validation of species identification and comparison to other forms

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from Africa, Europe, and the Southwest Pacific. This would provide the potential for global prediction of SARS-like viruses.

We submit that work in epidemiology of infectious zoonotic disease is strengthened by following four steps: (i) depositing voucher specimens of all collected species in a local or international museum of natural history; (ii) preserving skin snips from all individuals, in alcohol or other preservative; (iii) identifying these samples by numbers so they can be cross-referenced to individual vouchers; and (iv) reporting these numbers in print.

JORGE SALAZAR-BRAVO,[1]* CARLETON J. PHILLIPS,[1] ROBERT D. BRADLEY,[1] ROBERT J. BAKER,[1] TERRY L. YATES,[2] LUIS A. RUEDAS[3]

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References and Notes

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Response

WE THANK SALAZAR-BRAVO *ET AL.* FOR RAISING the important issue of accurate species identification in studying wildlife reservoirs for emerging infectious diseases. We agree that the collection and deposit of voucher specimens is extremely important in biological studies, including those of wildlife epidemiology. Our group has done the following to ensure that specimens were archived and that the bats captured were correctly identified: (i) We deposited specimens of each species (morphological type) captured during this study in the Institute of Zoology, Chinese Academy of Sciences, Beijing. (ii) In addition to morphological characterization, the identification of *Rhinolophus* species was supported by DNA sequence phylogeny. (iii) In a paper currently submitted to a peer-reviewed journal, we describe the DNA sequence phylogeny of this group of bats in China. The molecular data support our morphological identification. (iv) We have undertaken a long-term study of the diversity of bats in China as part of a Darwin Initiative–funded project. (v) We did not submit each individual bat that tested positive because of conservation and biosecurity issues; however, samples of blood from each bat are deposited at the Institute of Virology, Wuhan, China, as well as at the Australian Animal Health Laboratory, CSIRO, Australia. These institutions are able to safely store samples that potentially contain lethal infectious agents.

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Letters to the Editor

Letters (~300 words) discuss material published in *Science* in the previous 6 months or issues of general interest. They can be submitted through the Web (www.submit2science.org) or by regular mail (1200 New York Ave., NW, Washington, DC 20005, USA). Letters are not acknowledged upon receipt, nor are authors generally consulted before publication. Whether published in full or in part, letters are subject to editing for clarity and space.

TECHNICAL COMMENT ABSTRACTS

Comment on "On the Regulation of Populations of Mammals, Birds, Fish, and Insects" I

Wayne M. Getz and James O. Lloyd-Smith

Sibly *et al*. (Reports, 22 July 2005, p. 607) concluded that density dependence acts far below the carrying capacity in most animal populations. We argue that the authors confused discrete and continuous models, that their best-fit models cannot explain observed oscillations, and that their estimation procedures appear biased. They also neglected trophic and migratory processes, which we demonstrate could underlie their empirical findings.

Full text at www.sciencemag.org/cgi/content/full/311/5764/1100a

Comment on "On the Regulation of Populations of Mammals, Birds, Fish, and Insects" II

Joshua V. Ross

Sibly *et al*. (Reports, 22 July 2005, p. 607) recently estimated the relationship between population size and growth rate for 1780 time series of various species. I explain why some aspects of their analysis are questionable and, therefore, why their results and estimation procedure should be used with care.

Full text at www.sciencemag.org/cgi/content/full/311/5764/1100b

Comment on "On the Regulation of Populations of Mammals, Birds, Fish, and Insects" III

C. Patrick Doncaster

Stochasticity in time series explains concave responses of per capita growth rate to population size. The gradients with the natural log of population size have more biological importance because they measure strength of density compensation. Its weakening with increasing body size across taxa (Sibly *et al*., Reports, 22 July 2005, p. 607) is consistent with slower responses in ascent than descent toward carrying capacity.

Full text at www.sciencemag.org/cgi/content/full/311/5764/1100c

Response to Comments on "On the Regulation of Populations of Mammals, Birds, Fish, and Insects"

Richard M. Sibly, Daniel Barker, Michael C. Denham, Jim Hone, Mark Pagel

The technical comments by Getz and Lloyd-Smith, Ross, and Doncaster focus on specific aspects of our analysis and estimation and do not demonstrate any results opposing our key conclusion—that, contrary to what was previously believed, the relation between a population's growth rate (*pgr*) and its density is generally concave.

Full text at www.sciencemag.org/cgi/content/full/311/5764/1100d

CORRECTIONS AND CLARIFICATIONS

News Focus: "A timely debate about the brain" by Y. Bhattacharjee (3 Feb., p. 596). The story did not mention Matthew Matell's affiliation; he is a researcher at Villanova University in Villanova, Pennsylvania. Also, Matthew Leon was Michael Shadlen's postdoc, not his graduate student.

News Focus: "China: healing the metaphorical heart" by G. Miller (27 Jan., p. 462). The Chinese characters depicted in the illustration on page 462 were identified in the caption as yiyuzheng, a technical term for depression, but they actually represent youyuzheng, a more commonly used term for depression.

Editors' Choice: "The grandmother effect" (20 Jan., p. 305). The last sentence of this item is incorrect and should have been deleted.

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