uted to the scope of the 2010 pertussis outbreak, according to Witt. That vaccine schedule should be re-evaluated, but “better evidence” is needed before it is changed, he says.

Officials also are considering whether adult pertussis vaccine “boosters” should be recommended more generally, Witt adds. Currently, boosters are given to limited numbers of adults, including health care workers or others who work with infants and very young children, the population group most vulnerable to the disease. The main goal is to reduce the likelihood that those children will be infected by ill adults or those unwittingly carrying the responsible bacterial pathogen, Bordetella pertussis.

During the outbreak last year, the “attack rate” of pertussis was the highest seen in many decades, according to Witt. Although the risk for infection and severity of symptoms was greater among unvaccinated children, many children who were vaccinated against pertussis nonetheless became ill, as did some adults. However, the fatalities were seen only among infants, who begin the standard five-dose vaccine series at 2 months of age but do not immediately develop a full immune response. According to the Centers for Disease Control and Prevention in Atlanta, Ga., all five doses are required for “maximum protection.” The vaccine is administered as a combination product that also protects against diphtheria and tetanus.

Vaccine refusal—California law, for example, allows families to opt out of pertussis and other vaccination requirements for their children—complicates but does not fully account for the 2010 pertussis outbreak, Witt says. One oddity is that California rules require all families in which one child develops pertussis to treat siblings with antibiotics before they are allowed to return to school. Thus, even families that kept their children from being vaccinated were required last year to administer antibiotics prophylactically to them when at least one in the family was sick with pertussis. In some of those cases, he says, parents were eager for their children to have those antibiotics. “We had a huge spike in azithromycin use from families getting it for prophylaxis,” he says. “The politics of vaccine refusal are] truly complicated.”

Jeffrey L. Fox

Artemisinin Resistance in Thailand; Carbapenem Resistance Spreading

Artemisinin-resistant malaria, seen along the border between Thailand and Cambodia, is “very worrying” and, if it spreads, could lead to a “disaster,” says Arjen Dondorp of the Mahidol-Oxford Research Unit in Bangkok, Thailand. Similarly, widespread resistance to carbapenems among gram-negative bacterial pathogens is a “hydra-headed threat,” says David Livermore of HPA Microbiological Services Colindale in London, United Kingdom. They and others described problems from widening antimicrobial drug resistance during the Interscience Conference on Antimicrobial Agents and Chemotherapy (ICAAC), held in Chicago, Ill., last September.

Partial resistance to artemisinins among malaria patients along the Thai-Cambodian border could be a “step toward failing combination therapy,” says Dondorp, who spoke during the ICAAC symposium “Emerging Issues in Infectious Diseases.” Officials of the World Health Organization already established a three-tiered program along the border to “contain this resistance.” Even so, there are “signs” that this resistance might also be spreading to the border between Thailand and Myanmar, where it could prove even more difficult to control.

“Partial resistance” means it takes about twice as long as expected for malaria patients to respond to combination artemisinin treatment, Dondorp explains. To determine what this means in terms of mechanism, a large-scale effort is under way to sequence

Smallpox Vaccine and Plague Pathogen: Fresh Thoughts on Early Samples

English physician Edward Jenner is credited with first using cowpox to vaccinate children against smallpox in the late 19th century, presumably relying on local cattle for his source. However, new evidence suggests the source of modern-era smallpox vaccines—based on the cowpox virus—instead traces to central or eastern Europe, according to Norbert Nowotny at the University of Veterinary Medicine in Vienna, Austria, and his collaborators. Details appear on 14 September 2011 in PloS One. Separately, the remains of victims of the plague, or “Black Death,” from 14th-century Europe yielded enough DNA in dental pulp to determine the genome sequence of the responsible bacterial pathogen, and it appears to be only slightly changed from the Yersinia pestis strains now causing bubonic disease, according to Johannes Krause of the University of Tübingen in Germany, Hendrik Poinar of McMaster University in Hamilton, Ontario, Canada, and their collaborators. Details appear online 12 October 2011 in Nature [doi:10.1038/nature10549].
Another Giant Virus, but with a Bigger Genome than Its Mimivirus Relative

The latest installment of an declared contest to identify large-scale viruses brings us the largest member, so far, of the group, being called Megavirus chilensis to refer to Chile, where it was found living off the coast, according to Jean-Michel Claverie of Institut de Microbiologie de la Méditerranée in Marseille, France, and his collaborators. Although found in a marine habitat, the new virus, like its smaller Mimivirus relative, is capable of replicating in a freshwater acanthamoeba. The 1.2-million-base-pair genome of M. chilensis can encode about 1,120 proteins, 141 more than its smaller relative. Both viruses contain “cellular-like” genes, reinforcing the view of these researchers that these large viruses emerged from ancestral cells via “reductive evolution.” Details appear in the October 12, 2011, Proceedings of the National Academy of Science.

the genomes of about 1,500 Plasmodium falciparum isolates from the region to identify which genes are responsible. One thought is that resistance traces to a period in which malaria patients in Cambodia were treated inadequately, either with single-drug artemisinin therapy or with counterfeits, he says.

With resistance to a formerly effective drug chloroquine nearly global, artemisinin antimalarial drugs are about all that remain for treating this disease. “I want to stress the urgency of this problem,” Dondorp says. “We don’t want to repeat what happened with chloroquine resistance in Africa, where a lot of kids died from malaria.”

Carbapenem resistance in gram-negative pathogens can also prove deadly, particularly for patients in hospital settings, according to Mitchell Schwaber of the Israel Ministry of Health in Tel Aviv, who spoke during the ICCAC symposium “Control of Carbapenem-Resistant Enterobacteriaceae in Health Care Settings.” Although aware of an outbreak of carbapenem-resistant Klebsiella pneumoniae infections in New York hospitals, Israeli health officials were not well prepared when similar cases began to appear in Tel Aviv and elsewhere throughout the country during 2005, he says. That outbreak traced to the same version of K. pneumoniae circulating in New York. The pathogen is clonal and carries a gene encoding a potent carbapenemase, known as KPC, that inactivates such drugs. “This clone is extremely efficient at spreading in health care settings, and KPCs are on the march,” he says.

In response, Israeli health officials established a country-wide program to control the KPC outbreak, Schwaber continues. A task force was authorized to develop, implement, and enforce “compulsory guidelines” for health care workers to follow, establishing strict measures for dealing with patients with symptomatic infections but also for screening others to determine whether they might be carriers of the KPC strain. Although health care workers “continue to fight this every day,” those measures enabled Israel to “put a halt to the [KPC] rise by 2007,” he says.

KPC resistance “is spreading widely,” as are other mechanisms rendering gram-negative pathogens resistant to carbapenem and other antibiotics, and “there is little in the pipeline for the next few years,” says Livermore who spoke during several sessions, including the ICAAC “Opening Keynote Session.” “We live in an evolving genetic soup. Antibiotic resistance is a part of the landscape, and we have to brace ourselves to deal with it at every level.”

Jeffrey L. Fox

Genomic Analysis Traces Cholera in Haiti to Strains from Nepal

Robust genomic sequencing analysis greatly bolsters the case that the cholera epidemic in Haiti that began late in 2010 was caused by a strain of Vibrio cholerae from Nepal, according to a team of Danish, American, and Nepalese investigators. These findings “highlight how rapidly infectious diseases might be transmitted globally through international travel and how public health officials need advanced molecular tools along with standard epidemiological analyses to quickly determine the sources of the outbreak,” note Frank M. Aarestrup of the Technical University of Denmark in Lyngby, Paul Keim of Northern Arizona University in Flagstaff, and their collaborators at those institutions and at the National Public Health Laboratory in Kathmandu, Nepal. Their report appears in the July-August 2011 mBio (doi:10.1128/mBio.00157-11).

The cholera epidemic that began late in 2010 in Haiti was “far larger than other recent outbreaks... and arguably one of the best managed,” says Scott Dowell of the Centers for Disease Control and Prevention (CDC) in Atlanta, Ga. It led to approximately 450,000 cases, more than 6,000 of which proved fatal. The epidemic marked the first time that cholera was documented in Haiti, he says. Based on epidemiological evidence, its arrival in Haiti was traced tentatively to emergency workers from Nepal, who traveled from there to help re-