

infection, underlying disease(s), the medical setting in which the infection occurred, the appropriateness of antibiotics prescribed, the age and sex of the patients, no increased death was associated with MRSA, although inappropriate therapy was associated with a poorer outcome. In contrast, for bone infections and mediastinitis, MRSA may increase the risk of death.

The complete results of standard antimicrobial susceptibility tests are not generally available to the prescriber before at least 48–72 hours. The initial regimen prescribed may be not adequate during the first 2 to 3 days of treatment. This may impact death or illness attributable to multi-resistant bacteria. Shortening this interval, rapid diagnosis techniques based on molecular identification of resistance mechanisms could improve outcome. For example, methicillin resistance in *S. aureus* colony is detectable within 6 hours. Studies on clinical specimens showed that resistance-detection techniques, coupled with DNA identification of the bacterium, gave an excellent concordance to discriminate MRSA and MSSA and for MDRTB. Advances in the field of DNA microchips might soon improve the clinical impact of these techniques.

With more clinical failures, more expensive alternative regimens, the cost-effectiveness ratio of the treatment of antimicrobial bacterial resistant infections will inevitably rise. However, very few studies have addressed this issue; it requires precise and documented scenarios based on close collaboration between clinicians, microbiologists, epidemiologists and economists. Proposing prospective scenarios and foreseeing all the public health consequences of antimicrobial bacterial resistance is difficult. Although the impact on life expectancy should remain relatively limited in western nations, this will not be the case in developing countries where alternative regimens are

usually either not available or too costly.

Quantifying the consequences of antimicrobial bacterial resistance is a key element for allocating resources for public health programs. Some evidence exists of such consequences on illness and death, most of which appear to be associated with inappropriate or delayed therapy. Nevertheless, more studies which take into account the specific methodologic difficulties mentioned above are needed to better convince policy makers.

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**Reference**

1. Helms M, Vastrup P, Gerner-Smidt P, Molbak K. Excess mortality associated with antimicrobial drug-resistant *Salmonella typhimurium*. *Emerg Infect Dis* 2002; 8:490-5

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## Vets, Meds, and Zoonotic Threats

The fourth international conference on emerging zoonoses (September 18–21, Ames, Iowa, USA) brought together 180 scientists and healthcare specialists from 18 countries working to control diseases transmitted from animals to humans. The meeting took place under the auspices of the Center of Food Security and Public Health, USA, and the Institute for International Cooperation in Animal Biologics (a collaborating center of the World Animal Health Organisation [OIE]).

A multidisciplinary and global approach shed new light on both old and new zoonoses. For example, brucellosis topics covered a wide range of material, from economic aspects of control in Mongolia to characterization of *Brucella* isolates from feral swine in coastal South Carolina. Another presentation concerned the increasingly appreciated role of wildlife in the dynamic epidemiology of other zoonotic infections, such as tuberculosis. Scientists also explored the intricate routes prions follow between wildlife and domestic animals; between sheep, cattle, and humans; and between the tongue and brain of infected animals.

Since most agents of bioterrorism potential are zoonotic, a full session was dedicated to bioterrorism and biodefense. It included a global view, a report on national preparedness by Israeli hospitals, and examples of research that may eventually help experts coping with bioterrorism but would also unfortunately be accessible to persons with malicious intent.

Innovative methods for preventing spread of foodborne pathogens were presented, including the use of fluorescence spectroscopy to detect fecal contamination on animal carcasses or the use of vaccination to reduce transmission of zoonotic pathogens and drug-resistant nonpathogens through the food chain to humans. In the field of xenotransplantation, key components of a source-animal production facility were described. The feasibility of breeding pigs free of designated pathogens offers hope for wide use of xenotransplantation in the near future.

Participants also discussed current trends and challenges of protozoan parasitic zoonoses, including cryptosporidiosis, toxoplasmosis, African and Latin American trypanosomiasis, and leishmaniasis. Controversial zoonotic viruses were given an important place in the conference. These included hepatitis E virus, with similar strains causing liver disease in

swine and humans; Borna disease virus, causing neurologic disease in various species of animals as well as, debatably, psychiatric disorders in humans; and the recently discovered severe acute respiratory syndrome-associated coronavirus and its yet-undefined animal reservoir. The recent mapping of the genome of *Mycobacterium avium* subspecies paratuberculosis, the etiologic agent of Jhone's disease in cows, brought some hope in solving the long-lasting dispute on its role in the pathogenesis of Crohn's disease in humans.

The value of using a global, multi-disciplinary approach was highlighted in studies on the flow of genes among avian, swine, and other influenza viruses and on the ongoing interconti-

mental spread of arboviruses, exemplified by the evolving epizootic of equine West Nile encephalitis in the United States. Several papers dealt with the epidemiology of Nipah, Ebola, monkeypox, rabies, and Hantaan viruses.

A series of presentations demonstrated how genomic fingerprinting and other sophisticated molecular biology techniques allow exceptionally fast development in understanding the epidemiology and pathogenesis of many zoonotic infections, such as those caused by *Escherichia coli* O157:H7 or by species of *Anaplasma*, *Bartonella*, *Borrelia*, *Campylobacter*, *Coxiella*, *Francisella*, *Pasteurella*, and *Salmonella*.

The "one-track" meeting, by avoiding parallel and superspecialized sessions, gave an opportunity for fruitful and inspiring interactions among experts from multiple disciplines with a shared goal of mitigating human disease from emerging infections. More details on the meeting can be viewed online (available at: <http://www.zoonoses2003.com>).

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#### Correction, Vol. 10, No. 3

On p. 519, in the table entitled "Characteristics of enterotoxigenic *Escherichia coli* (ETEC) outbreaks, United States, 1996–2003," the serotype of the strain associated with outbreak number 16 was O169:H41 not O169:H49.

#### Emerging Infectious Diseases Policy on Corrections

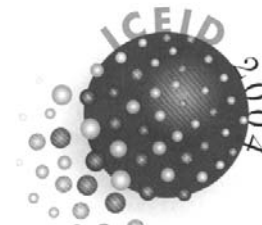
The Emerging Infectious Diseases journal wishes error-free articles. To that end, we

1) Make corrections as quickly as we become aware of errors

2) Publish corrections online and in print. Online, we correct the error in the article it occurred with a note that the article was corrected and the date of correction. In print, we prominently publish a full correction, printing all needed information, and provide the URL of the corrected online article for reprints.

For additional information on corrections, send e-mail to [eideditor@cdc.gov](mailto:eideditor@cdc.gov).

## Conference Presentations Online and on CD-ROM



Webcasts—some enhanced by the visual presentations—of the International Conference on Women and Infectious Diseases (February 27 - 28, 2004) and the International Conference on Emerging Infectious Diseases (February 29 - March 3, 2004) are now available.

Online access to the presentations is available to conference attendees. A username and password are required, previously emailed to all registrants. The online sessions are accessible for a limited time only.

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