In response: Watson et al. stressed some points that may be important determinants in assessing the risk for epidemics following natural disasters (*1*). We agree that large-scale population displacement, with overcrowding and water disruption, is clearly a risk factor for disease transmission. This factor was probably the main cause of the measles and diarrhea outbreaks that occurred in the temporary settlements created after the eruption of Mount Pinatubo in the Philippines, as mentioned in our previous article (*2*). However, by studying >600 geophysical disasters (earthquakes, volcano eruptions, and tsunamis) that occurred in the last 20 years, we found that deleterious conditions such as large-scale population displacement with overcrowding and water disruption were uncommon and that epidemics were the exception, not the rule. We agree that some epidemics, especially if they are limited and develop well after the disaster, may remain undetected, as was discussed in our paper (*1*).

However, we do not concur with the opinion expressed by Watson et al. that the incidence of postdisaster infectious diseases is more related to the characteristics of the displaced population than to the precipitating event. Our findings are just the opposite. In contrast to the situation seen with flooding and cyclones, which are sometimes followed by outbreaks of waterborne diseases, such as cholera or leptospirosis, and vectorborne diseases (*3*–*6*), the study we carried out on geophysical disasters did not detect any notable outbreak except for the above-mentioned measles outbreak. Watson et al. illustrated their statement by referring to outbreaks following floods and hurricanes, and not earthquakes, tsunamis, or volcano eruptions. Further work must be carried out on epidemics after floods provoked by heavy rains and hurricanes.

Renaud Piarroux,*†
Nathalie Floret,*†
Jean-François Viel,*†
Frédéric Mauny,*†
and Bruno Hoen*†

*University Hospital of Besançon, Besançon, France; and †University of Franche-Comté, Besançon, France

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Address for correspondence: Renaud Piarroux, Service de Parasitologie, Hôpital Jean Minjoz, 25000 Besançon, France; email: renaud.piarroux@ufc-chu.univ-fcomte.fr

Community-associated Methicillin-resistant *Staphylococcus aureus*

To the Editor: Community-associated (CA) methicillin-resistant *Staphylococcus aureus* (CA-MRSA) is a global emerging threat (*1*–*7*). Accurate measures of the extent of CA-MRSA are critical to allocate resources, guide control measures, and inform prescribing practices (*8*). We assessed the utility of administrative databases, a computerized clinical data repository, and an electronic rule to enhance surveillance for CA-MRSA at Stroger (Cook County) Hospital, a 464-bed public safety net hospital in Chicago, and its associated clinics—all part of the Cook County Bureau of Health Services (CCBHS).

Using data collected within the Chicago Antimicrobial Resistance Project computerized clinical data repository (*9*) from September 1, 2001, to August 31, 2004, we developed an electronic rule to define persons with CA infection with *S. aureus*. This rule used the electronic records of all persons from whom MRSA or methicillin-susceptible *S. aureus* (MSSA) had been identified in cultures of soft tissue, pus, bone, or joints. Infections from patients who met the following electronic case definition were designated CA: 1) culture obtained as an outpatient or within the first 3 days of hospitalization, 2) no clinical culture with MRSA in the last 6 months, 3) no hospitalization or surgeries within 1 year, and 4) no hemodialysis. All other infections were defined as healthcare associated. Data for microbiology results, demographics, and recent surgery or hospitalization were linked by a unique patient identification number. Dialysis use was detected by the use of biochemical tests obtained around the time of dialysis or of hemodialyis-related ICD-9 procedure codes (39.27, 90945, 39.95, 90935, 54.98, 39.43, 39.42, or 38.95). Because the electronic data sources were complete for the period specified, absence of data for a patient was considered to be due to the absence of exposure, not missing data.

Using the electronic case definition and data repository, we randomly selected 100 patients with putative CA- and 100 with putative healthcare-associated *S. aureus* infections. The paper charts for these 200 patients were reviewed to validate the designa-

tions of CA- or healthcare-associated infection, by using the same criteria as for the electronic rule. To ensure blinding for manual chart reviews, all references to results of the electronic rule were removed from data collection instruments. Using information obtained from chart review as the standard, we determined sensitivity and specificity of the electronic rule and calculated agreement (κ statistic) between manual and electronic reviews. To ascertain data sources of most value in detecting healthcare exposures, we examined data tables required for each type of exposure and for coincident exposures to develop more parsimonious data requirements.

During the study period, 714 (386 MSSA and 328 MRSA) healthcare-associated and 1,222 (518 MRSA and 704 MSSA) CA infections occurred; all electronic data elements were available for all patient encounters that occurred within CCBHS. Sampling yielded 47 CA- and 52 healthcare-associated MRSA infections and 53 CA- and 48 healthcare-associated MSSA infections.

The electronic case definition performed well when compared with chart review. All 100 healthcare-associated infections identified electronically were confirmed by manual chart review as classified correctly. Among the 100 community-associated infections identified electronically, 3 (3%) were determined by chart review to have been misclassified: 2 patients had been hospitalized, and a third had surgery within the previous year, all outside CCBHS. The sensitivity of the electronic case definition for community association was 100%; specificity was 97%. The κ statistic was 0.97 (confidence interval [CI] 0.83–1.00), which indicated superior agreement between chart review and electronic rule. For misclassified cases, 1 infection was due to MRSA, and 2 were due to MSSA. The performance characteristics of the rule for CA-MRSA were sensitivity 100%, specificity 98.1%, and $\kappa = 0.98$ (CI 0.78–1.00).

The Table describes data elements required to detect healthcare exposures. The most data-intensive exposure to detect was hemodialysis, which required a search of laboratory and discharge diagnosis databases. Isolates of MRSA were designated healthcare-associated most commonly because of prior hospitalization (523 [73%] of 714) and date of culture (i.e., >3 days after hospital admission) (259 [36%] of 714). With the use of only admission/discharge and microbiology data, 28 patients (90%) who had undergone dialysis and 23 (85%) who had undergone surgery were identified. The use of only admission/discharge and microbiology data would have detected 707 patients, 99% of those who would have been detected by the full algorithm.

Our study had limitations. Chart review may have undercounted healthcare-associated factors and is dependent on clinician histories and documentation. However, retrospective review of paper charts is the principal method that infection control practitioners use to gather information. Also, this study was conducted at a single center that served a population that may have had difficulty seeking care elsewhere. For single hospitals or systems with a less captive population, electronic measures may not function as well until disparate systems can be integrated, i.e., at the level of health departments or through data sharing among regional health information organizations.

In conclusion, using easily accessible data from a computerized clinical data repository, we readily classified *S. aureus* and MRSA infections as CA or healthcare associated. Comparison of the electronic method with manual paper chart review demonstrated high agreement for MRSA ($\kappa = 0.98$). Additional review suggested that use of only 1 or 2 data sources efficiently detected prior healthcare exposures. A major dividend of increased use of information technology in healthcare is application of electronically stored data to improve public health surveillance.

Bala Hota*†
and Robert A. Weinstein*†

*Rush University Medical Center, Chicago, Illinois, USA; and †John H. Stroger Jr. (Cook County) Hospital, Chicago, Illinois, USA

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Table. Data sources for healthcare exposures

Healthcare exposure	Databases needed	Comments
Isolate obtained >3 d after admission	Microbiology laboratory	Microbiology table must contain patient registration date to compare with culture date
Hemodialysis	Discharge diagnoses, biochemistry laboratory	Biochemistry laboratory table must contain location of test to identify dialysis clinic
Prior hospitalization (within 1 y)	Admission, discharge, and transfer data	Query must be able to compare individual patients across admissions
Prior surgeries (within 1 y)	Operating room schedules	May not be readily available in many institutions
Prior isolation of MRSA* (within 6 mo)	Microbiology laboratory	Query must be able to compare individual patients across admissions

*MRSA, methicillin-resistant *Staphylococcus aureus*.

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Address for correspondence: Bala Hota, John H. Stroger Jr. (Cook County) Hospital; 637 S. Wood St, Chicago, IL 60612, USA; email: Bala_N_Hota@rush.edu

Cryptosporidium felis Infection, Spain

To the Editor: Coccidian protozoans that belong to the genus *Cryptosporidium* frequently cause gastrointestinal infection in humans and animals and are distributed worldwide. *Cryptosporidium hominis* and the cattle genotype of *C. parvum* are responsible for most human infections. However, other species and genotypes of *Cryptosporidium*, such as *C. felis*, *C. muris*, *C. meleagridis*, *C. canis*, *C. parvum* pig genotype, and *C. parvum* cervine genotype, have also been detected in stool samples of immunosuppressed and immunocompetent patients (*1*). Since 1999, when Pieniazek et al. described 3 cases of *C. felis* infection in HIV-positive patients (*2*), several studies have confirmed that this species can infect humans. Recently, Muthsusamy et al. described *C. felis* infections in 5 HIV-positive persons in southern India (*3*). In this article, we describe our experience with an imported case of *C. felis* infection in Spain.

A pediatrician requested a parasitologic study for an immunocompetent, 4-year-old boy with diarrhea. The child came from an orphanage in Calcutta, India; he had arrived in Spain 10 days earlier after having been adopted by a Spanish family. Stool specimens were tested for a wide panel of enteric pathogens, including bacteria, viruses, and parasites. *Cryptosporidium* oocysts were detected by direct microscopic visualization of the samples, which had been concentrated by formalin–ethyl acetate sedimentation and stained with a modified Ziehl-Neelsen stain. Results were also positive for *Cryptosporidium* for samples tested by using an immunochromatographic (Crypto-Strip, Coris Bioconcept, Gembloux, Belgium) (*4*) and an immunofluorescent assay (Merifluor *Cryptosporidium/Giardia*, Meridian Diagnostics, Cincinnati, OH, USA).

DNA was extracted as described elsewhere (*5*), purified with polyvinyl-pyrrolidone, and stored at –20°C in Tris-EDTA buffer. After DNA extraction, PCR–restriction fragment length polymorphism (RFLP) analysis was performed by using previously described protocols based on the small subunit (SSU) rRNA gene (*6*), with digestion of the amplicon by the restriction enzymes *Ssp*I for species diagnosis or *Vsp*I for *C. parvum* genotype identification. For DNA sequencing, PCR products of the 18S rRNA gene fragments were purified and used for direct sequencing in an ABI377 automated sequencer (Applied Biosystems, Foster City, CA, USA).

RFLP analysis showed a profile distinct from those of *C. hominis* and *C. parvum* cattle genotype and consistent with the published patterns for *Cryptosporidium felis*: 426 and 390 bp with *Ssp*I digestion; 476, 182, and 104 bp with *Vsp*I (*6*). The sequence of the PCR product was determined, and a comparison with all SSU rDNA *Cryptosporidium* sequences available in databanks showed 100% similarity with the homologous fragment of *C. felis* (GenBank accession no. AF112575).

To date, >30 cases of human infection by *C. felis* have been reported in the literature. Only 3 of them have occurred in immunocompetent patients: 2 in the United Kingdom (*7*) and 1 in Peru (*8*). To our knowledge, this is the first case of human *C. felis* infection diagnosed in Spain. The child had been in Spain for only 10 days, no pet animals lived in his new home, and he had not gone to kindergarten. Consequently, the infection was likely acquired in India.

The transmission route for the unusual *Cryptosporidium* species is unclear. In the study by Matos et al., only 1 of 4 immunocompromised patients with *C. felis* had been in close