

always the reason for admission," this rise could represent altered disease manifestation, severity, or virulence.

In summary, the previously noted rate of growth in CDAD-related hospitalizations in US adults appears to have slowed somewhat in 2006. The encouraging downward trend in CDAD in the Northeast requires further exploration. Of concern is the increasing proportion of CDAD-related hospitalizations coded as the primary reason for admission because this may signal a change in characteristics of the disease. Given that the new data represent only 1 year, and the difference between the raw numbers from 2005 through 2006 did not reach statistical significance, these findings need to be interpreted with caution and monitored annually. In general, although helpful, most nationwide data have a considerable lag time. In this and other resistant diseases sweeping the US hospitals, real-time surveillance data are needed for more prompt and actionable policy development.

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References

- Zilberberg MD, Shorr AF, Kollef MH. Increase in adult *Clostridium difficile*-related hospitalizations and case fatality in the US, 2000–2005. *Emerg Infect Dis*. 2008;14:929–31.
- O'Brien JA, Lahue BJ, Caro JJ, Davidson DM. The emerging infectious challenge of *Clostridium difficile*-associated disease in Massachusetts hospitals: clinical and economic consequences. *Infect Control Hosp Epidemiol*. 2007;28:1219–27. DOI: 10.1086/522676
- Kyne L, Hamel MB, Polavaram R, Kelly CP. Health care costs and mortality associated with nosocomial diarrhea due to *Clostridium difficile*. *Clin Infect Dis*. 2002;34:346–53. DOI: 10.1086/338260
- Healthcare Cost and Utilization Project, Agency for Healthcare Research and Quality. Nationwide inpatient sample (NIS) [cited 2008 Jun 1]. Available from <http://www.hcup-us.ahrq.gov/nisoverview.jsp>
- Agency for Healthcare Research and Quality. Welcome to H-CUPnet [cited 2008 Jun 1]. Available from <http://hcupnet.ahrq.gov>
- US Census Bureau [cited 2008 Jun 1]. Available from <http://www.census.gov>

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Pulmonary Tuberculosis and *Mycobacterium bovis*, Uganda

To the Editor: In 2005, prevalence of human tuberculosis (TB) in Uganda was 559 cases/100,000 population (1). In 2002, the average number of extrapulmonary TB cases in humans, considered a crude indicator of the level of bovine TB, was 7.5% of TB cases for Uganda and 6% for Mbarara district, the main Ugandan milk basin (2). Worldwide, the proportion of human cases caused by *Mycobacterium bovis* has accounted for 3.1% of all forms of TB (3). Although zoonotic TB is more often reported as an extrapulmonary disease, recent publications report that 0.4%–10% of sputum isolates from patients in African countries are *M. bovis* (3). These studies, however, give little information about the cattle environment. A 2002 survey of dairy cattle in Mbarara district reported that 74% of herds and 6% of individual animals were reactive to the single tuberculin test (4). However, this test does not differentiate between *Mycobacterium* species involved. We therefore explored whether *M. bovis* might be a major threat to human health in this region.

From September 2004 through January 2005, we surveyed 658 pa-

tients who had been admitted to the Mbarara University Teaching Hospital TB ward after positive bacterial findings for at least 3 sputum smears or positive chest radiographs for smear-negative patients. Of 90 randomly selected patients, only 70 samples were available for analysis to differentiate the species in the *M. tuberculosis* complex; the other samples were excluded because of contamination, lack of mycobacteria growth on culture, or postal delay in transportation of sample. The questionnaire asked about patients' demographic data (including occupation), association with cattle, and milk consumption habits. Genomic DNA was extracted from the pellet culture of Middlebrook 7H9 broth (Difco; Cergy, France) as described previously (5). DNA samples were used to carry out PCRs and hybridization processes; we used the GenoType MTBC kit (Hain Lifescience GmbH; Nehren, Germany) for differentiation in the *M. tuberculosis* complex, especially between *M. tuberculosis* and *M. bovis* species (6).

Questionnaire responses showed that 27/64 (42.2%; 6 did not answer) patients had a history of raw milk consumption; nevertheless, 20/24 (83%; 3 did not answer) reported that they boiled fresh milk before consuming it, as did 54/60 (90% of all patients; 10 did not answer). Eating undercooked or raw meat was reported by 91% of the patients. Most patients were adult males (ratio 2.14:0.97 male:female for the district population); 8.6% were <18 years old (56% in the district); and average number of persons in household was 5.7 vs. 4.8 for the district (7). Of the samples, 8.6% were from extrapulmonary sites.

After amplification and hybridization of sample DNA, 69 samples were found to be *M. tuberculosis*, and 1 was not a *Mycobacterium* species. Our sampling method would detect at least 1 case of *M. bovis* in *n* patient specimens if the prevalence of bovine TB was $\geq p(0.033\%)$ according to the

formula in which a is the first order error (5%):

$$n = \frac{\log a}{\log(1-p)}$$

Because of the change in sample size, the limit prevalence was redetermined by using the inverse of the formula above:

$$p = 1 - \sqrt[n]{a}$$

If at least 1 sample was positive for *M. bovis*, the prevalence of bovine TB among patients would be $\geq 4.2\%$. However, the prevalence of *M. bovis* was $< 4.2\%$ and confirmed the low-level involvement of *M. bovis* in human TB in Mbarara district. These findings are consistent with previous work in Uganda's capital, Kampala, and in other African or Asian countries (2,8,9). The estimation of extrapulmonary cases among all TB cases (95% confidence interval 2%–15.2%) did not differ from the official estimate. We can add, using the second formula shown above, that among the 6 extrapulmonary TB cases, the prevalence of *M. bovis* is $< 39.3\%$. Our results come from a population in a highly rural area (91.5% of the population in Mbarara district) (7), where the high prevalence of animal TB has been reported.

These results could be explained by the patients' consumption habits, which reduce the risk for contamination. Even if bovine TB could also be found in other farm or wild animals, it seems to have a minor effect on public health. Zoonotic TB appeared to not be a major public health problem in Mbarara district. However, this finding could also result from underdiagnosis of extrapulmonary TB, from prevalence of *M. tuberculosis* being so high that in proportion *M. bovis* is a minor problem, or from rural populations' difficult access to TB diagnosis (directly observed therapy case detection rate in Uganda in 2005 was 37%) (1).

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References

1. World Health Organization. WHO Report 2007, global tuberculosis control, Uganda. WHO/HTM/TB/2007.376 [cited 2008 Apr 9]. Available from http://www.who.int/tb/publications/global_report/2007/pdf/uga.pdf
2. STD/AIDS Control Programme Ministry of Health. STD/HIV/AIDS surveillance report, June 2003, Kampala, Uganda [cited 2008 Apr 9]. Available from <http://www.health.go.ug/docs/hiv0603.pdf>
3. Cosivi O, Grange JM, Daborn CJ, Raviglione MC, Fujikura T, Cousins D, et al. Zoonotic tuberculosis due to *Mycobacterium bovis* in developing countries. *Emerg Infect Dis.* 1998;4:59–70.
4. Faye B, Cassel V, Lesnoff M, Rutabinda D, Dhalwa J. Tuberculosis and brucellosis prevalence survey on dairy cattle in Mbarara milk basin (Uganda). *Prev Vet Med.* 2005;67:267–81. DOI: 10.1016/j.pvetmed.2004.11.002
5. van Soolingen D, de Haas PE, Hermans PW, van Embden JD. DNA fingerprinting of *Mycobacterium tuberculosis*. *Methods Enzymol.* 1994;235:196–205. DOI: 10.1016/0076-6879(94)35141-4
6. Richter E, Weizenegger S, Rusch-Gerdes S, Niemann S. Evaluation of genotype MTBC assay for differentiation of clinical *Mycobacterium tuberculosis* complex isolates. *J Clin Microbiol.* 2003;41:2672–5. DOI: 10.1128/JCM.41.6.2672-2675.2003
7. Uganda Bureau of Statistics. 2002 Uganda population and housing census main report. 2005, Kampala, Uganda [cited 2008 Mar 11]. Available from <http://www.ubos.org>
8. Jou R, Huang WL, Chiang CY. Human tuberculosis caused by *Mycobacterium bovis*, Taiwan. *Emerg Infect Dis.* 2008;14:515–7. DOI: 10.3201/eid1403.070058
9. Niemann S, Rusch-Gerdes S, Joloba ML, Whalen CC, Guwatudde D, Ellner JJ, et al. *Mycobacterium africanum* subtype II is associated with two distinct genotypes and is a major cause of human tuberculosis in Kampala, Uganda. *J Clin Microbiol.* 2002;40:3398–405. DOI: 10.1128/JCM.40.9.3398-3405.2002

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Vertical Transmission of *Pneumocystis* *jirovecii* in Humans

To the Editor: Currently, animal and human studies favor an airborne transmission pattern for *Pneumocystis* pneumonia (1). However, the early age of acquisition of *Pneumocystis* spp. in different mammals, including humans, warrants study of vertical/transplacental transmission as an additional route of transmission of this stenoxenic microorganism.

Available studies on transplacental transmission of *Pneumocystis* spp. suggest that it varies among mammal species on the basis of the type of placenta (2). Transplacental transmission of *Pneumocystis* spp. has been demonstrated in rabbits (2,3), but it