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Increasing Incidence of Nontuberculous Mycobacteria, Taiwan, 2000–2008

To the Editor: Lai et al. (1) reported an increase in the number of nontuberculous mycobacteria (NTM) isolates and patients with pulmonary NTM diseases after implementation of the BACTEC system (Becton Dickinson, Sparks, MD, USA) late in 2001. These authors also reported that the increase was mainly in persons infected with *Mycobacterium avium* complex (MAC) and *M. abscessus*. They stated that diseases caused by NTM were defined according to current diagnosis criteria published in 2007 (2). This finding suggests that Lai et al. were able to review the clinical and radiologic information for all patients.

We wonder whether they were also able to identify and exclude people with NTM colonization, i.e., persons with positive cultures for NTM who did not meet the American Thoracic Society disease criteria. It would have been interesting to know the trend in colonized persons. In a previous study from British Columbia (3), we found an increase in the number of NTM isolates mostly in persons with MAC colonization. This finding coincided with implementation of a new laboratory technique in 2000, which suggested that the new technology is more sensitive in detecting MAC. In contrast with the findings of Lai et al., our study from British Columbia

showed that the incidence in patients treated for NTM pulmonary disease (the group used as a surrogate of NTM disease) has been decreasing over time, which is reassuring.

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In Response: We thank Hernández-Garduño and Elwood for drawing attention to the issue of nontuberculous mycobacteria (NTM) colonization (1), which was not described in our study (2). Among 4,786 patients with NTM isolates treated at our hospital during 2000–2008, colonization was found in 76.9% (3,681), and only 23.1% (1,105) had NTM diseases according to the criteria of the American

Thoracic Society and Infectious Diseases Society of America (3).

Annual proportions of NTM isolates causing colonizations ranged from 29.2% in 2001 to 19.8% in 2007. During the study period, annual incidences of NTM colonization and disease increased from 6.6/100,000 inpatients and 2.7/100,000 outpatients in 2000 to 34.5/100,000 inpatients and 10.2/100,000 outpatients in 2008. *Mycobacterium avium* complex (MAC) was the most prevalent species, colonizing 1,282 (34.8%) of 3,681 patients. Annual proportions of MAC isolates causing colonization ranged from 20.0% in 2000 to 12.6% in 2006. Annual incidence of MAC colonization increased from 1.9/100,000 inpatients in 2000 to 12.3/100,000 inpatients in 2008; incidence of MAC disease also increased from 0.5/100,000 inpatients in 2000 to 2.1/100,000 inpatients in 2008. *M. abscessus*, the second most common species in our study (2), caused colonization and disease in 669 and 155 patients, respectively. Annual incidence of *M. abscessus* colonization and infection also increased from 1.49/100,000 inpatients and 0.3/100,000 outpatients in 2000 to 7.0/100,000 inpatients and 1.9/100,000 outpatients in 2008.

Our study and a previous study in British Columbia (4) suggest that improvement in diagnostic methods would detect increased incidence of NTM, especially of MAC; most isolates identified in these studies were associated with colonization. We also demonstrated a gradual increase in the incidence of all NTM, MAC, and *M. abscessus* over time in Taiwan, which may be attributable to increasing vigilance and awareness of these bacteria as human pathogens and the increased population of immunocompromised patients. Thus, clinicians should consider diagnosing NTM diseases with sensitive and advanced laboratory methods because of the increasing population of patients at risk.

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Food Reservoir for *Escherichia coli* Causing Urinary Tract Infections

To the Editor: We read with interest the article by Vincent et al. that compared *Escherichia coli* isolates from 3 sources (human urinary tract infections [UTIs], retail meat, and restaurant/ready-to-eat foods) by multiple molecular typing methods (1). This study has to be considered in the context of the larger debate about the possible animal origin of *E. coli* isolates that cause extraintestinal infections in humans (2–5), and the same authors (Vincent et al.) have declared, in the introduction, that their efforts were directed toward investigating the hypothesis that retail chicken is the main reservoir for extraintestinal *E. coli*.

We strongly appreciate the amount of the experimental data and some interesting findings, but we are not totally convinced of the authors' conclusions, particularly the assumption that the study strongly supports the preliminary hypothesis. First, the observation that only a low proportion (73/844, 8.6%) of the *E. coli* isolates analyzed belonged to clonal groups (defined as ≥ 2 *E. coli* isolates that had indistinguishable multilocus variable number tandem repeats and enterobacterial repetitive intergenic consensus 2 patterns), including members from >1 source, suggests an overall high degree of genetic heterogeneity among isolates from different sources. Second, looking at the single isolates within clonal groups reported in Table 2, twelve (2.9%) of the 417 isolates from retail meat shared multilocus variable number tandem repeats, enterobacterial repetitive intergenic consensus 2, and multilocus sequence types with some human UTI isolates; however, only 1 isolate (strain EC01DT06–1737–01) was also found to be indistinguishable from a human isolate (strain MSHS 161) by pulsed-

field gel electrophoresis, indicating that identical genotypes (between isolates from retail meat and human infections) were observed only once.

Although we agree that the finding of a partial overlap between multilocus sequence types of isolates from retail meat and from human UTI isolates is noteworthy (especially recovery of an ST131 isolate of avian origin), the emphasis posed for the role of food transmission in the dissemination of the *E. coli* strains that cause community-acquired UTIs, in our opinion, does not seem strongly supported by the experimental data. Nevertheless, the topic is relevant, and we would highlight the importance of further research on this issue.

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