netilmicin increased the coverage to 65% among noncolistin-based regimens. Although colistin-based combinations provided the broadest coverage for infection with *A. baumannii*, colistin has recognized adverse effects and low tissue penetration in lower respiratory tract infections.[7] The triple noncolistin-based regimens provided broader coverage than the dual noncolistin-based regimens for MDR–*A. baumannii* infections. These results were not substantially different when the analysis was repeated for the following subgroups: (1) isolates recovered from sites other than the urinary tract, (2) isolates recovered from the urinary tract, (3) isolates recovered from patients in the intensive care unit, and (4) isolates recovered from patients outside the intensive care unit.

Although antibiograms are often used by clinicians to assess local antimicrobial susceptibility rates, as an aid in selecting empirical antibiotic therapy, and in monitoring resistance trends over time in an institution, antibiograms do not reveal additional information concerning microbial isolates, such as the time the isolate was obtained relative to the time of the patient's hospital admission (to determine whether an infection was community acquired or healthcare acquired). In addition, an antibiogram cannot be used to select empirical therapy for a patient who develops an infection subsequent to a previous one, because a patient's particular infection history, including past antibiotic use, must be considered.

Limitations of our study include the restricted analysis of *A. baumannii* isolates, instead of an effort to empirically target a variety of gram-negative pathogens. Our findings would require modification if the process was repeated in other institutions, given the wide local and regional variations in antimicrobial susceptibility data. In addition, the ultimate choice of empirical antimicrobial regimen will also rest on other factors, such as suspected pathogens, likely site of infection, drug allergies and intolerance, drug penetration into different tissue sites, and drug toxicities. Nonetheless, the selection of empirical dual or triple combinations via antibiogram provides a useful tool to guide physicians in their initial decision making when MDR–*A. baumannii* infection is suspected in at-risk patients in endemic settings.

ACKNOWLEDGMENTS

Potential conflicts of interest. Both authors report no conflicts of interest relevant to this article.

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Infect Control Hosp Epidemiol 2008; 29:678–679

 0899-823X/2008/2907-0018$15.00. DOI: 10.1086/588681

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Relationship Between Pathogenic and Colonizing Microorganisms Detected in Intensive Care Unit Patients and in Their Family Members and Visitors

To the Editor—Recent data have demonstrated the usefulness of an unrestricted visiting policy in the intensive care unit (ICU), the so-called "open ICU."[1-4] One of the most frequent objections to the open ICU, despite the lack of empirical evidence, is an increased risk of patient infection.[2,3,5] It is generally argued that the transmission of microorganisms responsible for infections—so-called "cross-pollination" from visitors[2]—results from the presence of relatives in the ICU. Visitors and relatives also run the risk of acquiring infection.[5]

We designed a prospective, observational, pilot study to test the hypothesis that patients' family members are healthy carriers (reservoirs) of pathogens, which are, in turn, transmitted to patients, causing colonization or nosocomial infection. This study was conducted in an 8-bed, mixed medical-surgical ICU, with a nurse-to-patient ratio of 1:2. Patients in this ICU were treated in 1 room with 4 beds and in 2 rooms with 2 beds.

Family members (2 visitors per patient) were admitted in the afternoon from 12:30 pm–2:00 pm and from 6:30 pm–8:00 pm. If the patient awakened or regained consciousness, the second afternoon visit can be extended from 4:00 pm–8:00 pm. For pediatric patients, an unrestricted visiting policy was applied.

The visitors were required to wash their hands and wear a disposable gown; shoe-covers, gloves, and masks were not required. Another hand washing was required on departure.

Using Margherita software (Istituto Mario Negri),[6] we per-

TABLE 1. Microbiological Data for Patients With Intensive Care Unit (ICU)–Acquired Infection and for Their Family Members and Other Visitors

	Patients		Family members		
Patient	Type or site of infection	Causative organism	Culture results	Site of colonization	Bacteria
1	Pneumonia	MRSA	1 positive, 5 negative	Skin	MSSA
2	Peritoneum, CVC	*Enterobacter cloacae, Pseudomonas aeruginosa, Acinetobacter baumanii, Klebsiella* species	14 negative	None	None
3	Pneumonia, BSI, Skin	*A. baumanii, Klebsiella* species, *Escherichia coli*	2 negative	None	None
4	Urinary tract	*Klebsiella* species	1 positive, 3 negative	Skin	MSSA
5	Pneumonia	*Klebsiella* species, *A. baumanii*	1 positive, 3 negative	Skin	*A. baumanii*[a]
6	Pneumonia, CVC	*E. coli, Klebsiella* species	1 positive, 1 negative	Skin	MSSA
7	Pneumonia	*Klebsiella* species	2 positive, 4 negative	Skin, nares	MSSA from both sites
8	Pneumonia, CVC	MSSA, *Stenotrophomonas* species	2 negative	None	None
9	Pneumonia, fever of unknown origin	*Klebsiella* species	2 positive, 6 negative	Skin, nares	CoNS from skin; MSSA from nares
10	Pneumonia	*Proteus* species	2 positive, 8 negative	Skin, nares	CoNS and *A. baumanii*[a] from skin; CoNS from nares
11	Skin	*A. baumanii*	4 negative	None	None
12	Pneumonia	*Klebsiella* species	1 positive, 7 negative	Nares	MSSA
13	Pneumonia	*Klebsiella* species	6 negative	None	None
14	Cerebrospinal fluid	MSSA	4 negative	None	None

NOTE. BSI, bloodstream infection; CoNS, coagulase-negative staphylococci; CVC, central venous catheter (infection due to central venous catheter without bacteremia); MRSA, methicillin-resistant *Staphylococcus aureus*; MSSA, methicillin susceptible *S. aureus*.

[a] *A. baumanii* detected at departure from ICU, prior to hand washing.

formed routine surveillance of infections already present at the time of ICU admission as well as ICU-acquired infections. Routine surveillance of tracheobronchial tree colonization by culture of an unprotected tracheal aspirate sample obtained from intubated patients and/or those with tracheotomies was performed twice weekly, even if clinical signs of pulmonary infection were absent. If clinical signs of infection were present, diagnostic culture samples were collected from all possible sites of infection prior to beginning empirical antibiotic therapy.

From May through August 2007, patients' family members and other visitors were screened for bacterial and fungal contamination or colonization on entry to the ICU and following hand washing. Swab samples from the nares and palmar skin were obtained. Family members and other visitors were screened only for patients who stayed in the ICU for more than 6 days. Each day, according to a bed rotation, samples from 1 family member or visitor (always the same person for each patient) of each of 2 different patients were obtained. Once a week, samples from 2 family members or visitors were obtained prior to departure and before hand washing to see if cross-contamination had occurred between the patients and their family members and visitors. We collected all microorganisms recovered from routine surveillance cultures of tracheal aspirate samples and samples from other sites (urine, skin, cerebrospinal fluid from ventricular devices, and wound drainage) and from clinical cultures performed for ICU patients.

Overall, 180 swab samples were obtained from 90 family members and visitors; a total of 16 nasal swab samples and 20 skin swab samples were positive for pathogens. Twenty isolates were recovered from 90 skin swab samples (13 coagulase-negative *Staphylococcus* isolates, 5 methicillin-susceptible *Staphylococcus aureus* isolates, and 2 *Acinetobacter* species isolates). Sixteen isolates were collected from 90 nasal swab samples (7 coagulase-negative staphylococci, 8 methicillin-susceptible *Staphylococcus aureus*, and 1 *Aspergillus* species). During that period, 19 ICU-acquired infections and 1 fever of unknown origin occurred in 14 patients who stayed in the ICU for longer than 6 days.

The site(s) of the patients' infections and the contamination and/or colonization status of family members and visitors is detailed in Table 1. None of the microorganisms responsible for infection in patients was found on the skin or in the nares of

family members or visitors. No correlation was found between isolates recovered from routine surveillance cultures done for patients and isolates found to be colonizing or contaminating patients' family members or visitors.

The duration of family visits in our ICU (3 or more hours per day) is no shorter than the visiting times reported in other countries.[5,7,8] In addition, 18 of 33 patients had a length of stay of 15 days or more. Thus, limited exposure time is not a good explanation for the lack of correlation between isolates recovered from patients and isolates recovered from their respective family members and visitors.

Hand washing is recommended as the most effective means to prevent transmission by direct contact, because it reduces the concentration of contaminants on the skin.[9] We did detect contamination with *A. baumanii* on the hands of visitors prior to hand washing at departure, an organism that was also isolated from the patients that they visited. After that, these visitors were monitored for the presence of *A. baumanii* prior to entry to the ICU and after hand washing; *A. baumanii* was not isolated again from these individuals. We believe the lack of correlation between the isolates recovered from patients and those recovered from family members may relate to our hand washing policies.

Fumagalli et al.[4] have shown that an unrestricted visitation policy, despite imposing a greater microbial burden and greater environmental contamination, does not increase the risk of infectious complications in cardiac ICU patients. Potential pathogens isolated from patients do not appear to be the same as those carried by their family members and visitors, nor does exposure to these pathogens increase the risk of infection in the ICU if appropriate hand hygiene is enforced.

ACKNOWLEDGMENTS

Potential conflicts of interest. All authors report no conflicts of interest relevant to this article.

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Infect Control Hosp Epidemiol 2008; 29:679–681

 0899-823X/2008/2907-0019$15.00. DOI: 10.1086/588703

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Whole-Blood Interferon-Gamma Release Assay for Baseline Tuberculosis Screening of Healthcare Workers at a Swiss University Hospital

To the Editor—In countries with low tuberculosis incidence rates, such as Switzerland,[1] targeted testing for latent tuberculosis infection (LTBI) among risk groups such as healthcare workers (HCWs) is an important measure for preventing tuberculosis disease.[2-4] We studied the prevalence of LTBI and its risk factors among hospital employees at the University Hospital of Berne, Switzerland, in a retrospective cohort study using a whole-blood interferon-gamma release assay (IGRA).[5]

From June 1, 2005, through May 31, 2006, we screened 777 employees for tuberculosis infection with an IGRA on commencement of employment. The following data were collected for each HCW: age, sex, bacille Calmette-Guérin (BCG) vaccination status (documented or reported), country of origin, place of work, and profession. The mean age of subjects was 32 years (75% were aged 20–40 years). The majority (70.8%) of employees were female (Table). The overall BCG vaccination rate was 87.4% (90.4% among employees of Swiss origin, of whom 12.1% had multiple BCG vaccinations). The IGRA used for screening (QuantiFeron-TB Gold In-Tube assay; Cellestis) was performed according to the manufacturer's instructions.[6] Data were evaluated by univariate analysis as well as multiple logistic regression analysis. GraphPad Prism 4, version 4.01 (GraphPad Software), and StatView, version 5.0 (SAS Institute), were used for all data evaluations.

A positive IGRA result was found for 59 (7.6%) of the 777 participants (Table). Tuberculosis disease was ruled out in each case by a careful consideration of the medical history, the symptoms, and the chest X-ray findings. The overall rate of LTBI in our study population was 7.6%, which concurs with