Nosocomial Outbreak of *Microbacterium* Species Bacteremia among Cancer Patients

Juan Alonso-Echanove,1,2 Samir S. Shah,2,3
August J. Valenti,1 Sheri N. Dirrigl,1 Loretta A. Carson,2
Mathew J. Arduino,2 and William R. Jarvis2

To date, only 6 sporadic *Microbacterium* species (formerly coryneform Centers for Disease Control and Prevention [CDC] groups A-4 and A-5) infections have been reported. The source, mode of transmission, morbidity, mortality, and potential for nosocomial transmission of *Microbacterium* species remain unknown. From 26 July through 14 August 1997, 8 episodes of coryneform CDC group A-5 symptomatic bacteremia occurred in 6 patients on the oncology ward at the Maine Medical Center. One patient died. All isolates were identified at CDC as *Microbacterium* species and had identical DNA banding patterns by pulsed-field gel electrophoresis. To assess risk factors for *Microbacterium* species infection, a retrospective cohort study was conducted. The presence of a central venous catheter was the strongest risk factor (66 vs. 22/48; relative risk, 3.2; *P* < .0001). This outbreak demonstrates significant *Microbacterium* species–associated morbidity and mortality in immunocompromised populations and confirms the potential for epidemic nosocomial transmission.

*Microbacterium* species is in the genus of gram-positive rods generally identified as coryneform Centers for Disease Control and Prevention (CDC) groups A-4 and A-5. Little is known about the epidemiology of *Microbacterium* species. It has been isolated from a variety of environmental sources, including soil, sewage, corn steep liquor, and dairy products and from humidifiers and air samples in hospitals [1]. Although rare, *Microbacterium* species infections are being reported more frequently and include 6 recent sporadic infections of blood, wounds, or vitreum [2–7]. The source, mode of transmission, morbidity, mortality, and potential for nosocomial transmission of *Microbacterium* species remain unknown.

From 26 July through 14 August 1997, 8 episodes of coryneform CDC group A-5 bacteremia and 1 cerebrospinal fluid (CSF)–positive culture were detected in patients on the oncology ward at the Maine Medical Center. One patient died. All isolates were identified at the MMC but is re-identifying as *Microbacterium* species infection; a retrospective cohort study was conducted. The presence of a central venous catheter was the strongest risk factor (66 vs. 22/48; relative risk, 3.2; *P* < .0001). This outbreak demonstrates significant *Microbacterium* species–associated morbidity and mortality in immunocompromised populations and confirms the potential for epidemic nosocomial transmission.

Materials and Methods

Our investigation had 3 components. First, we evaluated secular trends in *Microbacterium* species infection to confirm and describe the outbreak. Second, to assess risk factors for *Microbacterium* species infection, we conducted a retrospective cohort study among all patients hospitalized on the oncology ward at the MMC from 26 July through 2 August 1997 (epidemic period). Third, we performed health care worker and environmental culture surveys, to assess the potential role of these 2 factors in the transmission of *Microbacterium* species.

Case definitions and ascertainment. *Microbacterium* species is not identified routinely to the genus level at the MMC but is reported as Corynebacterium species or coryneform CDC group A-4 or A-5. Thus, to determine the extent of possible *Microbacterium* species bacteremia at the MMC, we used a nonspecific case definition. A “case culture” was defined as any blood sample obtained at the MMC from 1 July 1995 through 1 October 1997 that was culture positive for Corynebacterium species (including coryneform CDC group A-4 or A-5).

To determine risk factors for *Microbacterium* species bacteremia, we used a more specific case definition. A case patient was defined as any patient hospitalized on the oncology ward at the MMC with coryneform group A-4 or A-5 isolated from ≥ 1 blood culture sam-
ple during the epidemic period. Case patients and case cultures were identified by review of the MMC’s clinical microbiology laboratory and infection control records.

Determination of existence of an outbreak and descriptive epidemiology. To determine whether an outbreak had occurred, we compared the cumulative incidence rates of case cultures (i.e., coryneform species-positive and coryneform CDC group A-4–or A-5–positive blood cultures) for the entire hospital and the oncology ward during the pre-epidemic (i.e., 1 July 1995 through 25 July 1997) and epidemic periods. To determine and describe characteristics for case patients, we examined their medical records and abstracted demographic, clinical, and laboratory data. To assess the possibility of pseudobacteremia, we evaluated the potential for cross-contamination in the laboratory by reviewing processing procedures for microbiology specimens, interviewing laboratory personnel, and examining processing dates for positive-culture specimens; then we reviewed policies and procedures used by the oncology ward staff for obtaining blood culture samples and for care and access of central venous catheters (CVCs). Finally, to evaluate a potential point source of contamination in the pharmacy or ward, we interviewed nurses and pharmacy personnel, observed medication admixture practices, and reviewed pharmacy records.

Cohort study. To identify a possible common source of infection and potential risk factors for Microbacterium species infection, we compared attack rates among all patients hospitalized on the oncology ward at the MMC during the epidemic period. For case patients, we defined day 1 as the day the first Microbacterium species–positive blood culture sample was obtained. For non–case patients, we defined day 1 as the third day after admission, a time determined on the basis of the median length of time from admission to the first Microbacterium species–positive blood culture sample among case patients (2.8 days). Data were collected for the 3 days preceding day 1, a time determined on the basis of the longest length of time that it took Microbacterium species isolates to grow (<3 days). We hypothesized that the exposure to any potential source of infection most likely happened during that period. Risk factors that were assessed included the following: demographics, underlying disease and tumor stage, chemotherapy, signs and symptoms of infection, severity of illness, as measured 72 h before day 1 by the Acute Physiology and Chronic Health Evaluation (APACHE II) [8] and the Intermediate Therapeutic Intervention Scoring System (Intermediate TISS) [9] scoring systems, location of patient on the oncology ward during recent and current hospitalizations, laboratory and microbiological data, receipt of blood products, intravenous medications, and infusions prepared in the pharmacy (“partial fills”) and received during the hospitalization or in the recent outpatient clinic visits, presence of CVC, and exposure to contaminated nurses or nurse assistants.

Microbiological and environmental studies. Microbacterium species was identified from case cultures by use of a combination of conventional tests along with the Gram-Positive Identification Panel (BiologC) and the API Corynezyme (bioMérieux). Susceptibility testing was done for penicillin, ceftiazone, vancomycin, ciprofloxacin, and chloramphenicol. Isolate relatedness for Microbacterium species was assessed by pulsed-field gel electrophoresis (PFGE), using enzymes XbaI and SpeI. Agarose plugs were prepared from 18-h cultures in heart infusion broth (35°C), according to the procedure of Maslow et al. [10]. Agarose slices were digested with restriction endonucleases XbaI and SpeI, and PFGE was carried out with a CHEF-DR II apparatus (BioRad) at 14°C for 20 h at 20 V, with pulse-time ramps of 0.1–20 and 1–60 s, respectively. Gels were interpreted according to the criteria of Tenover et al. [11]. To ensure that the PFGE patterns were species specific, we used PFGE to compare the epidemic isolates with representatives from the gram-positive non–spore-forming coryneform CDC groups A-4 and A-5, which were obtained from the CDC collection.

To assess for potential environmental sources of Microbacterium species, we interviewed MMC architects and physical plant and engineering employees. Selected environmental samples from the rooms of case patients were obtained, including samples from sinks, toilets, telephones, sharps containers, sills, and bed rails.

To assess for health care worker carriage, we obtained hand, nares, axilla, and perineal samples from 10 nurses and nurse assistants who cared for ≥3 case patients during the 72-h period preceding the onset of their symptoms. To obtain samples from hands, we used the wipe rinse technique [12]. Personnel being sampled were asked to scrub their hands up to the wrist, using a sterile, premoistened (0.02% Tween 80) Handi Wipe (First Brands). The wipe then was placed in a sterile specimen cup and was shipped to the CDC for processing. At CDC, 120 mL of sterile 0.02% Tween 80 was added to the wipe container and was shaken for 15 min. The fluid then was cultured on tryptase soy agar and Columbia nutrient agar (containing 5% sheep blood) plates, using the membrane filtration technique [13]. Next, plates were incubated at 36°C for ≥7 days, and colonies were counted and isolated for identification. Finally, to identify possible patient colonization with Microbacterium species from November through December 1997, we obtained culture specimens from 20 consecutive hospitalized oncology patients with CVCs. The sites sampled included nares, axilla, perineum, vagina, rectum, wounds, CVC entry site, and huber needle.

Statistical methods. Standardized forms were used for collection of data, which were analyzed by use of Epi Info software (version 6.04; CDC) [14]. Categorical variables were compared by use of χ² or Fisher’s exact test. Continuous variables were compared by using the Student’s t or Kruskal-Wallis test. To control for confounding, we performed stratified analysis, using the method of Mantel-Haenszel.

Results
Case ascertainment and characteristics. A total of 8 episodes of Microbacterium species bacteremia were identified in 6 case patients (5 female), 1 of whom died. All case patients had fever (oral temperature, ≥38.2°C), 5 had prior bacteremia with a different organism within 2 weeks of the Microbacterium species bacteremia, 4 had diarrhea, 3 had severe neutropenia (<500 cells/mm³), and 2 had vomiting. The length of time from admission to first positive blood culture for Microbacterium species varied from 2 h to 7 days (median, 2.9 days). Underlying disease, severity of illness, and laboratory data varied among case patients (tables 1 and 2).

Of the 6 case patients, 3 (patients 2, 4, and 5) had fever not attributable to any other cause, and Microbacterium species was isolated in both of 2 blood samples obtained from different
sites. One of these patients died with a possible central nervous system (CNS) Microbacterium species infection (patient 4). This case patient had fever, confusion, agitation, and generalized myoclonus, and Microbacterium species grew in a CSF sample from the patient. However, the patient had no meningismus or increase in CSF protein and had a normal CSF glucose level. Gram’s staining results for the patient’s CSF sample were negative. Unfortunately, a CSF cell count was not done. The patient was treated with tobramycin and nafcillin but died 50 h later. No other acute infectious or noninfectious cause of death was identified.

Another patient (patient 1) had Microbacterium species isolated on 2 different days from 1 of 3 and 1 of 2 blood culture samples, but a-hemolytic Streptococcus species also was isolated in the first set of blood culture samples. Both samples were obtained ≥24 h after starting empiric therapy with vancomycin, tobramycin, and ceftazidime. The patient remained febrile for 7 days, and the fever abated 36 h after the CVC was removed. Cultures of samples from the CVC tip were negative.

The other 2 case patients (patients 3 and 6) had other infectious conditions that could explain the febrile illness, and, for each patient, Microbacterium species grew in only 1 of 2 blood culture samples.

**Determination of existence of an outbreak and procedure review.** On the oncology ward, the mean number of Corynebacterium species–positive blood culture samples per 1000 patient days during the epidemic period was significantly higher than that in the pre-epidemic period (27.0 vs. 0.4, \( P = .006 \)). All Corynebacterium species isolated from case patients were identified as Microbacterium species. The median number of blood samples obtained per 1000 patient days on the oncology ward and the entire hospital was not significantly different in the epidemic versus pre-epidemic periods (data not shown).

The Bactec 9240 (BD Diagnostic Systems) was the routine blood culture system in use during the period studied. For culturing in this system, a minimum of 2 blood samples are obtained ordinarily 3–5 min apart. At the MMC, a phlebotomy team obtains 1 sample from a peripheral vein, and the attending nurse obtains 1 from the CVC. No standard method for preparing the venipuncture site or for obtaining blood from the CVC was used by ward nurses. Also, no quantitative or semi-quantitative cultures were done routinely on blood or exit-site skin samples, respectively. Single-dose povidone-iodine or 70% alcohol preparations were used to prepare skin and CVC sites before obtaining blood. Bottles with blood samples were sent to the laboratory and were placed in an incubator for 5 days.

**Table 1. Characteristics of case patients with Microbacterium species bacteremia, Maine Medical Center, 1997.**

<table>
<thead>
<tr>
<th>Case patient</th>
<th>Age, in years/sex</th>
<th>Underlying neoplasia</th>
<th>Metastasis</th>
<th>Admitting diagnosis</th>
<th>Symptoms 72 h before bacteremia</th>
<th>Time to bacteremia positive</th>
<th>CVC type</th>
<th>Prior bacteremia</th>
<th>ANC, cells/mm³</th>
<th>No. of platelets, ×10⁰/mm³</th>
</tr>
</thead>
<tbody>
<tr>
<td>1</td>
<td>50/F</td>
<td>Non-Hodgkin’s lymphoma</td>
<td>Yes</td>
<td>Fever, neutropenia</td>
<td>Fever, chills</td>
<td>12 h</td>
<td>Medi-port</td>
<td>α-Hemolytic streptococci</td>
<td>50</td>
<td>27</td>
</tr>
<tr>
<td>2</td>
<td>31/F</td>
<td>Pheochromocytoma</td>
<td>Yes</td>
<td>Pain control</td>
<td>Vomiting, back pain</td>
<td>78 h</td>
<td>Port-a-cath</td>
<td>None</td>
<td>6127</td>
<td>90</td>
</tr>
<tr>
<td>3</td>
<td>64/M</td>
<td>Pancreatic adenocarcinoma</td>
<td>Yes</td>
<td>Dehydration, pain control</td>
<td>Fever, diarrhea, vomiting</td>
<td>60 h</td>
<td>Port-a-cath</td>
<td>Flavobacterium meningosepticum</td>
<td>3975</td>
<td>99</td>
</tr>
<tr>
<td>4</td>
<td>49/F</td>
<td>Non–small cell lung carcinoma</td>
<td>Yes</td>
<td>Pain control</td>
<td>Fever, diarrhea, menorrhagia</td>
<td>7 days</td>
<td>Medi-port</td>
<td>Staphylococcus epidermidis</td>
<td>5200</td>
<td>131</td>
</tr>
<tr>
<td>5</td>
<td>48/F</td>
<td>Acute myelocytic leukemia</td>
<td>No</td>
<td>Chemotherapy</td>
<td>Diarrhea</td>
<td>6 days</td>
<td>Triple lumen</td>
<td>S. epidermidis</td>
<td>14</td>
<td>1.8</td>
</tr>
<tr>
<td>6</td>
<td>77/F</td>
<td>Non-Hodgkin’s lymphoma</td>
<td>No</td>
<td>Fever, neutropenia</td>
<td>Fever, diarrhea, hypotension, petechiae</td>
<td>2 h</td>
<td>Medi-port</td>
<td>Escherichia coli</td>
<td>28</td>
<td>24</td>
</tr>
</tbody>
</table>

**NOTE.** A case patient was defined as any patient hospitalized on the oncology ward at the Maine Medical Center with coryneform Centers for Disease Control and Prevention group A-4 or A-5 isolated from 1 blood culture sample from 26 July through 1 August 1997. ANC, absolute neutrophil count; CVC, central venous catheter.

\* From admission to first Microbacterium species–positive blood culture sample.

\*\* Medi-Port and Port-a-cath (Sims-Portex [now Deltec] and Bard, respectively); Triple lumen (Bard).

\* Bacteremia with a different organism in the 14 days before the Microbacterium species bacteremia episode.

\* Case patient 4 had cerebrospinal fluid culture-positive Microbacterium species.

**Table 2. Comparison of clinical and laboratory characteristics for case patients and non–case patients, Maine Medical Center, 1997.**

<table>
<thead>
<tr>
<th>Categorical variables</th>
<th>Case patients (n = 6)\a</th>
<th>Non–case patients (n = 48)\b</th>
<th>OR (95% CI)</th>
<th>( P )</th>
</tr>
</thead>
<tbody>
<tr>
<td>CVC</td>
<td>6 (100)</td>
<td>22 (46)</td>
<td>Undefined</td>
<td>&lt;.0001</td>
</tr>
<tr>
<td>Temperature</td>
<td>( &gt;38^\circ C ) (83)</td>
<td>11 (23)</td>
<td>16.8 (1.6–425)</td>
<td>.007</td>
</tr>
<tr>
<td></td>
<td>3 (50)</td>
<td>2 (4)</td>
<td>23 (2–58)</td>
<td>.007</td>
</tr>
<tr>
<td></td>
<td>4 (67)</td>
<td>7 (15)</td>
<td>11.7 (1.4–118)</td>
<td>.01</td>
</tr>
<tr>
<td></td>
<td>3 (50)</td>
<td>5 (10)</td>
<td>8.6 (1–81)</td>
<td>.04</td>
</tr>
<tr>
<td></td>
<td>2 (33)</td>
<td>2 (4)</td>
<td>11.5 (0.8–176)</td>
<td>.05</td>
</tr>
</tbody>
</table>

**NOTE.** A case patient was defined as any patient hospitalized on the oncology ward at the Maine Medical Center with coryneform Centers for Disease Control and Prevention group A-4 or A-5 isolated from 1 blood culture sample from 26 July through 1 August 1997. CI, confidence interval; CVC, central venous catheter; OR, odds ratio.

\a Data are no. (%) of patients with variable.

\b Neutrophil count <500 cells/mm³.
No other manipulation of the bottles was done, unless the automatic fluorometric optic-reading system detected a suspected positive culture. In such cases, Gram’s staining and non-quantitative subculture on standard media were performed.

During the pre-epidemic and epidemic periods, there were no changes in procedures for obtaining, handling, or processing blood samples, and there were no changes in the culture media or the methods of organism identification used. At least 4 different people obtained samples from case patients; however, it was not possible to identify all personnel responsible for obtaining the 10 case cultures. The origin (sites from which the blood was drawn) and timing of case culture also varied. All positive blood culture samples had gram-positive rods on Gram’s staining. In addition, there was no clustering of blood culture samples from case patients to nurses.

Eighteen (68%) of the 28 CVCs in the cohort were totally implantable devices (Port-a-Cath and Medi-port catheters). In most cohort patients, a CVC was recommended at the time of admission. All CVCs were placed in the operating room and were accessed routinely through needleless devices that were covered with antimicrobial patches for a maximum of 7 days. There was no standard procedure for CVC care or replacement of the administration set. Catheters were flushed with heparin from multidose vials or with saline from single-dose vials. There was no change in CVC or needleless device brands or insertion or care procedures used during the epidemic and pre-epidemic periods.

Pharmacy procedures were reviewed and observed. In the oncology ward, the same shift prepared all intravenous antibiotics from multidose vials in partial-fill bags containing 50–100 mL of saline. For the oncology ward, these admixtures were prepared in a laminar flow hood. There were no records to trace which vials were used for which patient. However, there was a rapid turnover of vials, and none lasted >2 days. No total parenteral nutrition or chemotherapy was administered to case patients during the epidemic period.

**Cohort study.** From 26 July through 2 August 1997, 54 patients were admitted to the oncology ward, and 6 (11%) met the case definition. Case patients were more likely than were non-case patients to have tachycardia, fever, diarrhea, vomiting, neutropenia, or presence of a CVC (table 2). In univariate analyses, age, sex, stage of underlying malignancy, severity of illness, as measured by the APACHE II or TISS, levels of hemoglobin, albumin, or creatinine, and intravenous products were not associated with *Microbacterium* species bacteremia. Since having a CVC was a risk factor and all case patients had a CVC, we next limited our analyses to all patients with a CVC (*n* = 28). Among these patients, significant risk factors for *Microbacterium* species bacteremia included a TISS score $\geq$15, presence of metastasis, diarrhea, prior bacteremia with a different organism in the 14 days preceding day 1, receipt of bupivacaine, or contact with nurse A or B (table 3). Prior bacteremia was the risk factor most strongly associated with *Microbacterium* species bacteremia (relative risk, 17.5; 95% confidence interval, 2.5–122.5; *P* = .0004), and this factor remained significantly associated when we controlled for each of the other significant variables in a stratified analysis. Factors not associated with an increased risk for *Microbacterium* species bacteremia were sex, age, type of malignancy, APACHE score, neutropenia, or receipt of blood products, intravenous antibiotics, granulocyte colony-forming stimulating factor, heparin flushes, morphine from mono- or multidose vials, or partial fills.

**Environmental and microbiological studies.** All isolates from case cultures were small, irregularly shaped, gram-positive, non-acid-fast “diphtheroid” bacilli. All isolates were motile, esculin positive, yellow pigmented, urea negative, catalase positive, and nitrate positive and produced acid in glucose, maltose, sucrose, and mannitol. Isolates did not ferment either xylose or lactose. These diphtheroids were identified as coryneform bacilli.
Clinical Microbiology

CDC group A-5 (*Microbacterium* species) [15–17]. Cultures of specimens from the hands of nurses, nurse assistants, environmental sources, and the cohort of consecutively admitted oncology patients with a CVC were negative for coryneform CDC group A-5 (*Microbacterium* species).

All case patient isolates had an identical DNA banding pattern, as determined by use of *XbaI* and *SpeI* digests, and were different from those of coryneform CDC groups A-4 and A-5 isolates from the CDC collection. Furthermore, all group 4 and 5 isolates from the CDC collection showed marked variability (table 4). All case patient isolates were susceptible to third-generation cephalosporins, vancomycin, and chloramphenicol; were intermediately susceptible to penicillin (MIC, 0.5); and were resistant to ciprofloxacin.

**Discussion**

*Microbacterium* species is in the genus of gram-positive rods generally identified as coryneform CDC group A-4 or A-5, according to the scheme of Hollis and Weaver [17]. This is a heterogeneous group of bacteria that most likely contains different genera [1] that are not identified at the genus level on a routine basis in many clinical microbiology laboratories, and they usually are considered to be contaminants when isolated from clinical samples. As a result, the identification of clusters or sporadic episodes of infection caused by these bacteria may be missed. Only sporadic *Microbacterium* species infections have been reported in the literature; these include infections in 1 patient with native-valve endocarditis [2], 2 patients with CVC-associated sepsis [3, 4], 1 patient with a surgical-site infection and secondary mixed endocarditis [5], and 2 patients with endocarditis after a penetrating eye injury [6, 7]. Most *Microbacterium* species from clinical specimens have been recovered from blood [1]. Although *Microbacterium* species have been recovered from different environmental sources [1], the source and mode of transmission for all infections reported to date are unknown. In addition, in all but 3 reports, *Microbacterium* species have been regarded as contaminants or have not been identified to the genus level [2–4].

Our investigation documented that there was a significant increase in the rate of *Microbacterium* species bacteremia in oncology ward patients at the MMC during the epidemic period. Also, PFGE results support the epidemic nature of the *Microbacterium* species infections. To our knowledge, this is the first report of an outbreak of *Microbacterium* species infections. On the basis of several factors, the possibility that these epidemics of bacteremia were true bacteremia, as opposed to pseudobacteremia, is very high. First, contamination of blood culture samples in the laboratory was very unlikely, since there was no manipulation of the blood sample bottles during processing of samples, all Gram’s stains were positive in all case cultures, and there was no clustering of *Microbacterium* species-positive blood culture samples in the laboratory. Second, in 4 of 6 case patients, *Microbacterium* species was isolated from ≥2 blood samples obtained from different sites (a peripheral vein and the CVC). Third, different personnel obtained blood samples that, after culturing, were determined to be case cultures, making repeated contamination of the blood sample bottles very unlikely. Fourth, 1 case patient had recurrent *Microbacterium* species bacteremia; and fifth, 3 of 6 case patients had clinical findings consistent with symptomatic bacteremia.

The source of *Microbacterium* species in this outbreak was probably a contaminated product. The PFGE results, the short time period in which case patients developed their infections, and the spontaneous end of the outbreak without any infection-control interventions are very suggestive of a common source of infection. The limited number of case patients and the location of these patients being limited to 1 hospital ward suggests extrinsic product contamination rather than intrinsic contamination. Multidose vials were used routinely at this hospital to admix infusates for our cohort. However, all admixtures were prepared in the pharmacy, according to CDC guidelines for the prevention of intravascular device–related infections [18]. Unfortunately, it was not possible to trace back whether any of these multidose vials were used for all case patients or to determine the sequence in which they were used. Furthermore, our investigation was initiated 2 months after the onset of the last case patient’s infection; thus, the common source could have been used or discarded by that time. Bupivacaine, although significantly associated with a higher risk of infection, was used in only 2 of 6 case patients and would not explain the infections in the remaining case patients. No other specific product was epidemiologically associated with a higher risk of *Microbacterium* species bacteremia.

**Table 4.** Pulsed-field gel electrophoresis (PFGE) patterns of *Microbacterium* species isolates from case patients and coryneform Centers for Disease Control (CDC) groups A-4 and A-5 from the CDC collection, Maine Medical Center, 1997.

<table>
<thead>
<tr>
<th>PFGE type</th>
<th>Outbreak isolates (Microbacterium species)</th>
<th>Coryneform CDC group</th>
</tr>
</thead>
<tbody>
<tr>
<td>A</td>
<td>X</td>
<td>A-4&lt;sup&gt;a&lt;/sup&gt;</td>
</tr>
<tr>
<td>B</td>
<td>X</td>
<td>A-5&lt;sup&gt;b&lt;/sup&gt;</td>
</tr>
<tr>
<td>C</td>
<td>X</td>
<td></td>
</tr>
<tr>
<td>D</td>
<td>X</td>
<td></td>
</tr>
<tr>
<td>E</td>
<td>X</td>
<td></td>
</tr>
<tr>
<td>F</td>
<td>X</td>
<td></td>
</tr>
</tbody>
</table>

<sup>a</sup> 3 Isolates.

<sup>b</sup> 2 Isolates.
not available in the identification charts for *Microbacterium* species [15], none of our isolates fermented lactose.

This outbreak also illustrates the value of molecular subtyping in the investigation of nosocomial outbreaks. PFGE results demonstrated that all case cultures were linked by a common strain and pointed to a common-source outbreak.

Having a CVC in place was associated strongly with being a case patient, and all case patients had a CVC at the time of the *Microbacterium* species bacteremia. *Microbacterium* species have been reported to cause CVC-associated bacteremia [3, 4]. CVCs or needless devices used during case patients’ hospital stays could become contaminated from solutions or colonized from the exit-site skin or from hands of health care workers. Unfortunately, no quantitative blood cultures or semiquantitative CVC exit-site skin cultures or cultures from needless devices were done at the time of these infections. Such cultures would have helped confirm the diagnosis of CVC-associated infection. However, it is unlikely that the source for *Microbacterium* species was the patients’ or health care workers’ skin (with secondary contamination of catheters or associated devices), because none of the case patients had local signs of infection. Moreover, no changes in antimicrobial therapy were made in those case patients already receiving antibiotics, and the outcome was favorable.

Finally, none of the culture specimens from other patients, health care personnel, or the environment yielded *Microbacterium* species to support the hypothesis of skin colonization or health care worker transmission; however, these cultures were obtained 3 months after the end of the outbreak.

When we evaluated other risk factors for CVC-associated blood-stream infection (BSI), having a prior bacteremia with a different organism in the 14 days preceding the onset of infection was significantly associated with an increased risk for *Microbacterium* species bacteremia. Although we could not demonstrate the independence of this association in the multivariate model, it remained significantly associated after stratifying for the other significant risk factors. Previous studies have demonstrated that a CVC left in place after a BSI increases the risk of further BSIs with the same or a different organism [19] (CDC unpublished data, 1997). This increased BSI risk may reflect an actual increase in the risk of the CVC becoming colonized again or that a prior bacteremia may intrinsically predispose to another bacteremia; it also may reflect an increased severity of illness. Regardless, an increased risk of exposure to a contaminated product remains speculative. It is difficult to interpret the significance of the other risk factors. Metastatic disease and diarrhea are probably indicative of the severity of illness. Case patients were sicker and, thus, probably more likely to receive medications, including a potentially contaminated product. Confounding bias would explain the association of nurse A or B, because nurses were not assigned randomly to patients each day.

*Microbacterium* species bacteremia had associated morbidity. In 3 of the 6 case patients, the infection clearly caused symptoms and, although the overall outcome was favorable, it is likely that in 1 case patient the infection contributed to death. Moreover, this patient probably had a CNS *Microbacterium* species infection, although there were insufficient data to confirm this. To our knowledge, no previous death or CNS infection attributed to *Microbacterium* species has been reported.

Our investigation had several limitations. First, no samples of potentially contaminated products were available, since the outbreak ended spontaneously ~2 months before our investigation. Second, no records were available to accurately trace CVC manipulation or multidose vial use in each patient. Third, since the investigation was initiated 2 months after the end of the outbreak, other potential unusual common sources could have been discarded, used, or forgotten and therefore could not be investigated.

In conclusion, to our knowledge, this is the first reported outbreak of *Microbacterium* species that confirms the potential for its epidemic nosocomial transmission. Although no specific source could be implicated, an extrinsically contaminated product was the most likely cause. Furthermore, our investigation demonstrated significant morbidity associated with this organism in immunocompromised populations. In addition, having a CVC and a previous bacteremia with a different organism in the 14 days preceding day 1 of the current infection while the same CVC was in place were significant risk factors. We recommend that any coryneform bacteria isolated from a sterile body site of an immunocompromised patient and considered to be a potential pathogen should be identified at least to the genus level, especially when a cluster of such infections occurs.

Acknowledgments

We thank the following persons from the Maine Medical Center for their invaluable help during the investigation: Nancy M. Young and Gwen M. Rogers (Infection Control Department); Don Piper and Cathy Dragni (Microbiology Laboratory); William Gousse (Pharmacy); Doris Skarka (Nursing); and health care workers from the Oncology Ward. We also thank Kathleen F. Gensheimer, State Epidemiologist, Maine, for her collaboration.

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