

***Leptotrichia trevisanii* Sepsis after Bone Marrow Transplantation**

To the Editor: *Leptotrichia* spp. have been identified as the cause of various infections. However, the most commonly reported infection is bacteremia in the setting of chemotherapy for hematologic malignancies (1,2). Only recently has *L. trevisanii* emerged as a cause of infection; case reports are rare (3–5). We recently observed 3 cases of *L. trevisanii* bacteremia in patients who had recently undergone peripheral blood stem cell transplantation (SCT.) Our goal was to identify possible causes of these infections.

The patients were 2 men and 1 woman (ages 53, 56, and 63 years, respectively) who had received myeloablative chemotherapy. The 2 men had multiple myeloma and relapsed follicular non-Hodgkin lymphoma and had neutropenic fever 5 and 4 days post-SCT, respectively. The woman had acute myelogenous leukemia that had arisen from a myelodysplastic syndrome after matched sibling donor SCT failure. She had neutropenic fever on day 13 of induction therapy.

Multiple blood cultures from >1 site (peripheral and central venous catheter [CVC] or 2 separate CVCs) obtained from each patient during the initial febrile episode grew *L. trevisanii*. For the 2 patients with positive cultures for peripheral blood and CVC sites, the peripheral culture was reported as positive before the CVC culture but not before use of the CVC. All subsequent blood cultures and catheter tip cultures from these patients had negative results for bacteria.

All organisms were cultured by using the Bact/ALERT 3D blood culture instrument (bioMérieux, Durham, NC, USA) and standard aerobic and anaerobic media. Times to positivity were approximated (range 28–58 hours). Gram staining of isolates from

culture media showed large, fusiform gram-negative rods. One isolate had gram-positive beading and was reported as gram variable. A second isolate grew anaerobically from initial subculture on 5% sheep blood agar but grew aerobically in chocolate agar in 5% CO₂ on second subculture. A third isolate showed pinpoint growth on initial aerobic culture on sheep blood agar. No isolates were identified by using the RapID ANA II System (Remel, Lenexa, KS, USA).

One organism was identified as *Sphingomonas paucimobilis* by Vitek 2 (bioMérieux), but this result was inconsistent with results of other biochemical tests. The 3 organisms were sent to the Mayo Medical Laboratories (Rochester, MN, USA) for anaerobic bacteria identification and speciation by 16S rRNA gene sequencing. All catheter tips were cultured by rolling a 1-inch segment of the catheter on sheep blood agar and incubating them aerobically in 5% CO₂ for 5 days.

The reason *L. trevisanii* has only recently been identified as a cause of bacteremia in neutropenic patients is likely multifactorial. Our findings suggest routine use of 16S rRNA gene sequencing and increased numbers of bone marrow transplants as the major reasons.

L. trevisanii was discovered in 1999. More than a decade had passed between the availability of 16S rRNA sequencing and discovery of this bacterium. (5). Some authors suggested that previous lack of recognition may have been caused by fastidious growth requirements, inconsistent staining, or misidentification (3,4,6). No recent major changes in instrumentation, subculture algorithm, or solid media had been made before we isolated this organism, and we had not previously isolated any unidentified organisms with similar appearance and growth patterns typical of *L. trevisanii*. Unlike some species of *Leptotrichia*, *L. trevisanii* grows readily on solid media when subcultured (3). This finding

indicates an emergent pathogen rather than a previously undiagnosed cause of bacteremia.

We have seen an increase in the number of bone marrow transplants performed, but there has been no major change in myeloablative regimens. We observed 1 case of *L. trevisanii* bacteremia in each year during 2009–2011, in which our institution performed 185, 189, and 215 transplants, respectively (overall incidence 0.5 cases/100 transplants). This finding might explain why no cases were seen previously. All 3 patients had grades 1–2 mucositis, which in the presence of neutropenia, is a known risk factor for anaerobic bacteremia in patients undergoing chemotherapy for hematologic malignancies (3,7,8).

Bacteremia developed in the 3 patients while they were treated with levofloxacin. The 56-year-old man responded to a cephalosporin. The 63-year-old woman did not respond to a carbapenem or vancomycin but did respond to a second carbapenem. The 53-year-old man did not respond to a cephalosporin or metronidazole but became afebrile after treatment with vancomycin. These inconsistencies did not enable us to make specific therapeutic recommendations for treatment of *L. trevisanii* infection other than to report clinical resistance to levofloxacin.

Currently recommended treatment regimens for neutropenic fever do not include treatment for anaerobic infections. Some institutions have altered treatment regimens to include antimicrobial drugs, such as meropenem, because of increases in anaerobic bacteremias (3,9). We do not believe that the number of cases of anaerobic bacteremia at our institution warrants a change in treatment policy.

On the basis of our findings, we expect an increase in the number of cases of anaerobic bacteremia after an expected increase in the number of bone marrow transplants performed. Future policies include improved

treatment or prevention of mucositis, earlier detection and identification of isolates, and revision of current antimicrobial drug protocols for empiric treatment of neutropenic fever.

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**Jennifer M. Schrimsher,
Joseph P. McGuirk,
and Daniel R. Hinthorn**

Author affiliations: University of Kansas Medical Center, Kansas City, Kansas, USA (J.M. Schrimsher, J.P. McGuirk, D.R. Hinthorn); and University of Kansas Cancer Center, Kansas City, (J.P. McGuirk)

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Address for correspondence: Jennifer M. Schrimsher, Department of Internal Medicine, University of Kansas Medical Center, 3901 Rainbow Blvd, Mailstop 1028, Kansas City, KS 66160, USA; email: jschrimsher@kumc.edu

Clinical Profile of Children with Norovirus Disease in Rotavirus Vaccine Era

To the Editor: After the substantial decrease in acute gastroenteritis (AGE) in children caused by rotavirus after introduction of 2 rotavirus vaccines (1), norovirus has become the leading cause of medically attended AGE in US children <5 years of age (2). We describe the clinical characteristics of norovirus disease and assessed whether rotavirus vaccine protected against norovirus AGE.

During October 2008–September 2010, the New Vaccine Surveillance Network enrolled 1,897 children <5 years of age with symptoms of AGE (≥ 3 episodes of diarrhea or any episodes of vomiting within 24 hours lasting ≤ 10 days) who came to hospitals,

emergency departments, and outpatient clinics in Cincinnati, Ohio; Nashville, Tennessee; and Rochester, New York, USA, as described (2).

Epidemiologic, clinical, and vaccination data were systematically collected. Whole fecal specimens were obtained within 14 days of the date of visit and tested for rotavirus by using a commercial enzyme immunoassay (Rotaclone; Meridian Bioscience, Inc., Cincinnati, OH, USA) and for norovirus by using real-time reverse transcription quantitative PCR, followed by sequence analysis of positive samples (3,4). Clinical severity was assessed by using a 20-point scoring system (5), which was modified to use behavior as a proxy for dehydration. Odds ratios used to calculate vaccine effectiveness (VE) were adjusted for race and insurance status (online Technical Appendix, wwwnc.cdc.gov/EID/article/19/10/13-0448-Techapp1.pdf).

Inclusion criteria for this study corresponded with criteria used in previous New Vaccine Surveillance Network studies (2,6). Children were age eligible for pentavalent rotavirus vaccination (RV5), had a fecal specimen tested for norovirus and rotavirus, and had complete vaccination and AGE symptom information (online Technical Appendix Figure 1). Children who received a dose of monovalent rotavirus vaccine or vaccine of unknown type or were positive for rotavirus and norovirus were excluded from analyses. Only unvaccinated rotavirus-positive children ($n = 69$, 72%) were used in severity score analyses because RV5 is known to attenuate rotavirus illness (6).

Of the enrolled children, 574 met the inclusion criteria; 144 (25%) norovirus-positive case-patients, 96 (17%) rotavirus-positive case-patients, and 334 (58%) patients negative for norovirus and rotavirus (control patients with AGE) (online Technical Appendix Figure 1). Of 144 norovirus-positive specimens, 10 (7%) could not be genotyped, 4 (3%) were positive