for designated use, treatment of VRE infection, surveillance of colonized patients, and the hidden social costs of patient isolation and the emotional impact on family members. Colonization with VRE predisposes to VRE infections, including bacteremia. One study found that the mean duration of hospitalization for patients with nosocomial enterococcal bacteremia was 83 days compared to 44 days for matched control.[20] The cost saving in the prevention of an episode of VRE bacteremia makes the $10,000 in extra expense in barrier precautions seem insignificant.

In summary, VRE poses serious therapeutic problems, and, once it has spread beyond a geographically isolated group of patients, eradication becomes difficult, labor intensive, and expensive. Control of VRE may require the cooperation of an interdisciplinary group to improve continually compliance with good infection control practices.

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Staphylococcus schleiferi Outbreak

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Within a 1-year period, six surgical-site infections caused by *Staphylococcus schleiferi* were observed in the department of cardiac surgery of Ignatius Hospital, Breda, The Netherlands. Because outbreaks caused by this species of coagulase-negative staphylococci have not been described before, an extensive environmental survey and a case-control study were performed in combination with molecular typing of the causative microorganism to identify potential sources of infection. Variability, as detected by four different genotyping methods (random amplification of polymorphic DNA [RAPD], conventional and polymerase chain reaction (PCR)-mediated ribotyping, and pulsed-field gel electrophoresis [PFGE] of DNA macro restriction fragments), appeared to be limited both among the clinical isolates and among several control strains obtained from various unrelated sources. Among unrelated strains, RAPD and PCR-mediated ribotyping identified two types only, whereas seven different types were identified in a relatively concordant manner by conventional ribotyping and PFGE.

The latter two procedures proved to be the most useful tools for tracking the epidemiology of *S schleiferi*. Four of the outbreak-related strains were identical by both methods, and two isolates showed limited differences. In the search for a potential source of *S schleiferi* infection, two slightly different PFGE types were encountered on several occasions in the nose of a single surgeon. These strains were, however, clearly different from the outbreak type. In contrast, *S schleiferi* cultures remained negative for two persons identified on the basis of case-control analysis. It was demonstrated that surgical-site infection caused by *S schleiferi* had a clinical impact for patients comparable to that of a wound infection caused by *Staphylococcus aureus*. A source of the outbreak was not detected.

FROM: Kluytmans J, Berg H, Steegh P, Vandenesch F, Etienne J, van Belkum A. Outbreak of *Staphylococcus schleiferi* wound infections: strain characterization by randomly amplified polymorphic DNA analysis, PCR ribotyping, conventional ribotyping, and pulsed-field gel electrophoresis. *J Clin Microbiol* 1998;36:2214-2219.

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