Staphylococcal prosthetic joint infections: similar, but still different

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Staffan Tevell

Akademisk avhandling

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Opponent: Professor Annelies Zinkernagel
Division of Infectious Diseases and Hospital Epidemiology
University Hospital Zürich
Schweiz
Abstract

Staphylococci constitute a major part of our commensal flora but are also the most common bacteria causing prosthetic joint infections (PJIs), a dreaded complication of arthroplasty surgery. However, not all staphylococci are the same. The virulent *Staphylococcus aureus* has the ability to cause severe disease such as bacteremia and infective endocarditis in previously healthy people, while the coagulase-negative staphylococci *Staphylococcus epidermidis* and *Staphylococcus capitis* rarely act as pathogens unless the patient is immunocompromised or has an implanted medical device, such as a prosthetic joint. This thesis accordingly explores similarities and differences between these three staphylococci in PJIs.

*S. capitis* can cause early postinterventional and chronic PJIs, a finding that has not previously been described. Furthermore, its nosocomial NRCS-A outbreak sublineage, recently observed in neonatal intensive care units, is also present in adult PJIs. When comparing nasal and PJI isolates, the patterns differed between staphylococcal species. In *S. capitis*, the commensal and infecting strains were separated phylogenetically, while they clustered together for *S. aureus*. This may indicate diverse reservoirs and acquisition routes in PJIs caused by different staphylococcal species.

Outcomes in early postinterventional PJIs were similar in *S. capitis* and *S. aureus* infections, with 70–80% achieving clinical cure. In *S. aureus* infections, no virulence genes were significantly associated with outcome. Although multidrug resistance (MDR) was rare in *S. aureus*, inability to use biofilm-active antibiotics was a risk factor for failure. However, in *S. epidermidis* and in the NRCS-A sublineage of *S. capitis*, MDR and glycopeptide heteroresistance were widespread, highlighting the challenge of antibiotic resistance in the treatment of PJIs.

Keywords: Prosthetic joint infections, staphylococcal infections, nasal carriage, *Staphylococcus aureus*, *Staphylococcus epidermidis*, *Staphylococcus capitis*, NRCS-A, antibiotic resistance, heterogeneous glycopeptide resistance, whole-genome sequencing

Staffan Tevell, Department of Infectious Diseases, Region Värmland, SE-651 82 Karlstad, and Center for Clinical Research and Education, Region Värmland, Sweden and School of Medical Sciences, Faculty of Medicine and Health, Örebro University, SE-701 82 Örebro, Sweden, staffan.tevell@regionvarmland.se