



Polymicrobial *Staphylococcus aureus* bacteremia: Frequency, distinguishing characteristics and outcome



Riad Khatib ^{a,*}, Mamta Sharma ^a, Leonard B. Johnson ^a, Kathleen Riederer ^b, Laurence Briski ^c

^a Department of Medicine, St John Hospital & Medical Center, Grosse Pointe Woods, MI, USA

^b Department of Medical Education, St John Hospital & Medical Center, Grosse Pointe Woods, MI, USA

^c Department of Pathology, St John Hospital & Medical Center, Grosse Pointe Woods, MI, USA

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ABSTRACT

Staphylococcus aureus bacteremia (SAB) is usually monomicrobial (M-SAB). We reviewed SAB in adults (≥ 18 years old) over a 13 year-period and compared polymicrobial (P-SAB) and M-SAB. We encountered 93 P-SAB among 1537 SAB cases (6.1%). The source distribution was comparable; however, source-specified differences were apparent. P-SAB was noted in 12/58 (20.7%) necrotizing soft tissue infections/sacral decubiti and foot gangrene vs. 1/122 (0.8%) cellulitis/abscesses ($P < 0.001$), in 7/64 (10.9%) femoral intravascular catheters (IVC) vs. 16/376 (4.3%) IVC in other sites ($P = 0.03$) and 15/134 (11.2%) healthcare-associated pneumonia (HAP) vs. 1/33 (3.0%) community-associated cases ($P = 0.1$). Methicillin-resistance frequency was similar but community-associated SCCmec types (IV/V) were infrequent (17.9% vs. 34.2%; $P = 0.04$). P-SAB was associated with higher mortality (50.5% vs. 24.2%; $P < 0.001$) across nearly all sources. In summary, P-SAB is infrequent, usually encountered in necrotizing soft tissue infections/decubiti, femoral IVC and possibly HAP. The actual incidence of *S. aureus* in these infections should be defined.

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1. Introduction

Staphylococcus aureus causes a wide spectrum of mild superficial to invasive life threatening infections (Noskin et al., 2007). It possesses numerous virulence factors and usually causes infection as a single pathogen (Diep et al., 2006; Kong and Jabra-Rizk, 2015; Li et al., 2012; Malachowa et al., 2015; McGavin and Heinrichs, 2012; Rozemeijer et al., 2015). Other organisms may be recovered from the implicated source but their actual role is uncertain except when cultures are obtained from a sterile body site. Therefore, the frequency of mixed *S. aureus*-other pathogens infection and their characteristics are not clearly defined. For a more accurate assessment, comparison of monomicrobial and polymicrobial infections is better carried out in patients with a non-ambiguous microbiology, such as bacteremia. Polymicrobial bacteremia accounts for 5–20% of blood stream infection, often in patients with an intraabdominal focus, complicated urinary tract infection or an intravascular catheter; and, it is associated with a worse outcome (Kiani et al., 1979; Rello et al., 1993; Reuben et al., 1989; Roselle and Watanakunakorn, 1979; Weinstein et al., 1986). The usual microbiology is determined by the source of infection and the type of patient (Rello et al., 1993; Reuben et al., 1989; Weinstein et al., 1986). The majority of polymicrobial bacteremias are caused by *Enterobacteriaceae*, anaerobes, non-group A streptococci and yeasts (Rello et al., 1993; Reuben

et al., 1989). *S. aureus*, group A *Streptococcus* and *Streptococcus pneumoniae* are uncommon (Kiani et al., 1979; Rello et al., 1993; Reuben et al., 1989). We looked at our patients with *S. aureus* bacteremia (SAB), determined the frequency of polymicrobial (P-SAB), and defined the distinguishing characteristics from monomicrobial (M-SAB).

2. Material and methods

Facility: Our hospital is a 772-bed teaching hospital in Detroit, Michigan.

Patients' selection: Patients were identified by a review of blood culture (BC) results. All adult patients (18 years or older) with *S. aureus* in one or more BCs were considered for inclusion. Cases from 1/1/2002–6/30/2003, 10/1/2005–12/31/2006, 1/1/2008–12/31/2009 and 12/1/2010–12/31/2012 were followed prospectively during earlier studies (Khatib and Sharma, 2013; Khatib et al., 2013, 2015). Cases from 1/1–11/30/2010 and 1/1/2013–1/31/15 were identified retrospectively. A patient was considered to have true SAB if one or more BC was positive in association with clinical evidence of infection (fever, leukocytosis and/or a source of bacteremia). The source of bacteremia was determined according to the Centers for Disease Control and Prevention definitions of nosocomial infections, the presence of clinical signs with isolation of *S. aureus* from the presumed source and Duke criteria for endocarditis (Garner et al., 1988; Li et al., 2006). Additional positive BC separated by ≥ 100 days were counted as a new bacteremia.

* Corresponding author. Tel.: +1-313-3437837; fax: +1-313-3437840.

E-mail address: riad.khatib@stjohn.org (R. Khatib).

Severity of illness and comorbidity scores were predetermined in the prospectively included cases. Severity of illness score was calculated based on mean arterial pressure, heart rate, respiratory rate, peripheral oxygen saturation, Glasgow Coma Scale score and age (REMS) (Sharma et al., 2013). Comorbidity score was calculated according the modified Charlson's weighted index of comorbidity (Quan et al., 2011).

The following information was gathered: patient' demographics, underlying conditions, source of infection, mode of onset, and 100-day all-cause mortality.

2.1. Definitions

The onset of SAB was classified into 3 mutually exclusive categories according to the Centers for Disease Control and Prevention (Kallen et al., 2010). Hospital onset: SAB after 3 days of inpatient hospitalization.; health care-associated community-onset: SAB within 3 days of admission in patients with invasive devices or exposure to a health care setting within the preceding 12 months; community-associated: SAB within 3 days of admission without invasive devices or health care exposure during the preceding 12 months. Polymicrobial bacteremia: the presence of another pathogen(s) in one or more BC obtained during the first 2 days of admission. Detection of other pathogens after 2 days of hospitalization in patients with persistent SAB was considered to represent an unrelated nosocomial infection. Commensal organisms detected along with *S. aureus* in one BC were presumed contaminants.

2.2. Microbiology determination

Blood culture isolates were identified by standard tests. *S. aureus* isolates were identified by Staphaurex latex agglutination test (Remel, Lenexa, KS). Methicillin susceptibility was determined using the VITEK-2 bacterial identification system (bioMérieux, Durham, NC) and verified by the oxacillin agar screening test (Remel). SCCmec type was previously determined for all saved methicillin-resistant isolates (Ganga et al., 2009). Isolates from 2010 and 2013–15 were not saved.

2.3. Statistical methods

Chi square test, student t-test and the Extended Mantel–Haenszel chi square test for linear trend were used to assess the significance of differences in categorical variable, continuous variables and the trends respectively, utilizing the computer software SPSS release 19. $P < 0.05$ was considered to indicate statistical significance.

The study was approved by the St John Hospital and Medical Center Institutional Review Board.

3. Results

We encountered 1787 instances of SAB, 1537 cases were selected. The remainder consisted of 229 duplicate patients and 21 patients without adequate medical records for assessment. Other organisms were detected in 185 instances, 93 (6.1%) were considered P-SAB. The remainder consisted of 87 BCs mixed with commensal organisms which were considered contaminants and five BCs from patients with persistent SAB who acquired an unrelated nosocomial infection. The additional organisms (110 in 93 BCs) were predominantly gram-negative bacilli (Fig. 1).

Patient characteristics are shown in Table 1. Patients with P-SAB were less likely to be hemodialysis-dependent and were more likely to have a respiratory or urinary tract source of bacteremia compared with M-SAB. No difference in the frequency of methicillin-resistance was noted but SCCmec types tended to be different with more frequent healthcare-associated (II, III) types in P-SAB.

3.1. Soft tissue related bacteremia

We encountered 221 patients with SAB secondary to soft tissue infections including 57 cellulitis (25.8%), 65 abscesses (29.4%), 41 postoperative wounds (18.6%) and 58 necrotizing infections (26.2%) that included 30 sacral decubitus ulcers, 24 foot gangrene and four miscellaneous locations. P-SAB was noted in 15 (6.8%) instances. Stratifying cases according to the type of soft tissue infection revealed that P-SAB

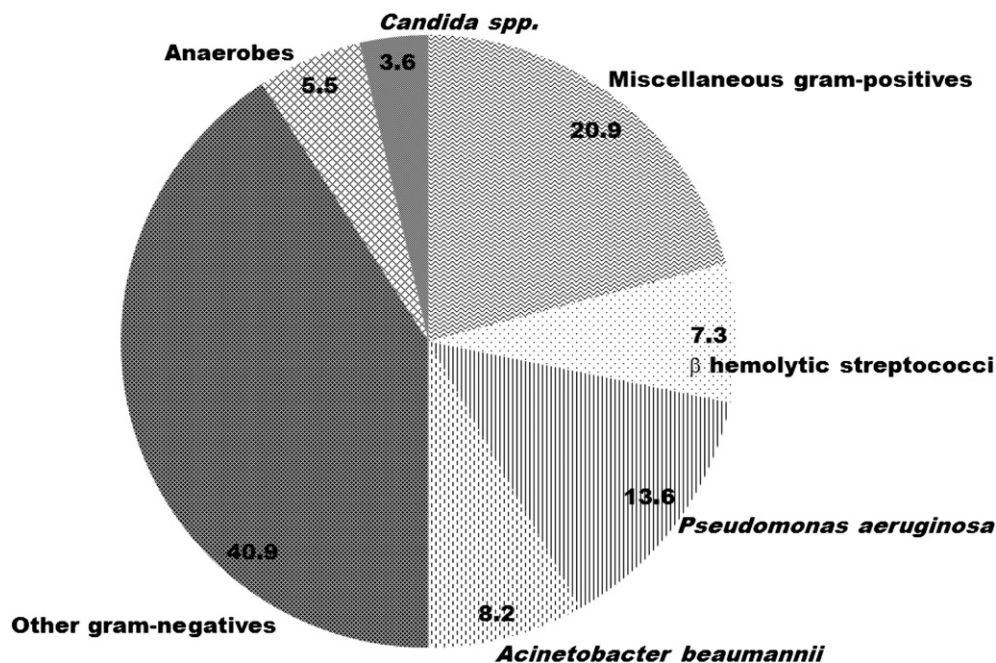


Fig. 1. Distribution of the additional organisms detected in polymicrobial *Staphylococcus aureus* bacteremia.

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