

Brief History of *Staphylococcus aureus* and Diagnosis, Treatment

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Abstract

Staphylococcus aureus is a gram-positive bacterium that causes a wide variety of clinical diseases. Infections caused by this pathogen are common both in community-acquired and hospital-acquired settings. MRSA (Methicillin-Resistant *Staphylococcus aureus*). *S. aureus* does not normally cause infection on healthy skin; however, if it is allowed to enter the internal tissues or bloodstream, these bacteria may cause a variety of potentially serious infections.

1. Describe the workup of a patient with staphylococcus infection.
2. Outline the importance of improving care coordination among the interprofessional team members to educate patients about hand hygiene to prevent transmission of infection to others.
3. Summarize the treatment options for staphylococcus infections.
4. Review the pathophysiology of *S. aureus* infections.

This activity describes the evaluation and treatment of *Staphylococcus* infections and reviews the role of the interprofessional team in managing patients with these diseases.

Keywords: Vancomycin-resistant *Staphylococcus aureus*; Resistant *Staphylococcus aureus*; *S. aureus*; Antibiotic resistance

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Introduction

History and physical will vary greatly depending on the type of infection; however, an accurate history and physical is often required for diagnosis and treatment [1].

Staphylococcus aureus is Gram-positive bacteria (stain purple by Gram stain) that are cocci-shaped and tend to be arranged in clusters that are described as “grape-like.” On media, these organisms can grow in up to 10% salt, and colonies are often golden or yellow (aureus means golden or yellow). *Staphylococcus aureus* (including drug-resistant strains such as MRSA) are found on the skin and mucous membranes, and humans are the major reservoir for these organisms [2].

S. aureus is found in the environment and is also found in normal human flora, located on the skin and mucous membranes (most often the nasal area) of most healthy individuals. *S. aureus* does not normally cause infection on healthy skin; however, if it is allowed to enter the bloodstream or internal tissues, these bacteria may cause a variety of potentially serious infections [3, 4].

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by Gram stain) that are cocci-shaped and tend to be arranged in clusters that are described as “grape-like.” On media, these organisms can grow in up to 10% salt, and colonies are often golden or yellow (aureus means golden or yellow) [5].

Methods

This study was conducted on 236 *S. aureus* isolates. All isolates were subjected to antimicrobial susceptibility testing by using a standard microbroth dilution method [6]. The Polymerase Chain Reaction (PCR) was performed to identify genes encoding the β -lactams resistance (*blaZ*, *mecA*), macrolides (*Erma*, *ermB*, *ermC*) and aminoglycosides (*aacA*-*aphD*). The molecular structures and genomic relatedness of MRSA isolates were determined by staphylococcal chromosome cassette *mec* (SCC*mec*) typing and pulsed-field gel electrophoresis (PFGE), respectively [7].

Diagnosis of *S. aureus*

Presence of *S. aureus* in culture is normally insignificant since this bacteria is normally present on the skin, nose and pharynx of many humans and animals. The organism is readily cultured

from nasopharynx or skin, or by culture of suspicious lesions [8].

On culture the bacterial colonies a characteristic glistening, opaque, yellow to white appearance on blood agar.

1. Impetigo
2. Bacteraemia
3. Chemical Burns
4. Pediatric Bacterial Endocarditis
5. Juvenile Idiopathic Arthritis
6. Kawasaki Disease
7. Leptospirosis
8. Parvovirus B19 Infection
9. IBS
10. Pediatric Osteomyelitis
11. Pediatric Serum Sickness

Treatment of *Staphylococcus aureus*

Treatment of *S. aureus* infections depends largely on the type of infection as well as the presence or absence of drug resistant strains. When antimicrobial therapy is needed, the duration and mode of therapy are largely dependent on the infection type as well as other factors. Prevention of *S. aureus* infections remains challenging. Despite many efforts, a routine vaccination for *S. aureus* infections has remained elusive [9]. As a result, efforts have relied on infection control methods such as hospital decontamination procedures, handwashing techniques, and MRSA transmission prevention guidelines. Topical antimicrobials such as mupirocin can be used to eliminate nasal colonization in some nasal carriers [10]. However, usage is controversial.

Conclusion

In conclusion, *S. aureus* bacteremia represents a serious infection, associated with significant both early and late mortality. Methicillin resistance is associated mostly to nosocomial and health-care associated infections and may be a risk factor for mortality in patients with SAB. First, its retrospective, observational nature

can limit the considerations on patient treatments. Second, we considered overall mortality rather than SAB-related mortality. We tried to overcome this bias using two timepoints for mortality, assuming that early mortality could have been more likely associated with SAB. Third, while not specific criteria for requesting an ID consultation have been established and followed, this option could be more likely requested in patients with more severe infections. Clinicians should be aware of the severity of patients with *S. aureus* bacteremia, and infectious disease consultation should be always considered to improve patients' outcomes.

Staphylococcus aureus (*S. aureus*), especially methicillin-resistant *Staphylococcus aureus* (MRSA), is considered a common zoonotic pathogen, causing severe infections. The objective of this study was to investigate the antimicrobial susceptibility, resistance genes and molecular epidemiology among MRSA and methicillin-susceptible *Staphylococcus aureus* (MSSA) isolated from food animals in Sichuan Province, China. The *S. aureus* isolates from food animals in Sichuan province of China have severe antimicrobials resistance with various resistance genes, especially MRSA isolates. Additionally, the genetic pool of MRSA isolates is diverse and complex, and further investigation is necessary.

The global threat of a VRSA epidemic is a public health problem that is currently quiet but perhaps brewing. Unlike *S. aureus* resistance to other antibiotic classes, there has been a prolonged interval between vancomycin use and VRSA development and disease has occurred in selected patients with co-morbidities, prolonged vancomycin use and co-infection with VRE. There are limited choices of available drugs effective against VRSA; several promising therapeutic options are in research or development phases. Assessment of the actual effectiveness of these antimicrobials would need full-scale use during an epidemic, an event of global catastrophic proportions that we all hope will not occur.

Acknowledgement

None

Conflict of Interest

None

References

- 1 Ghebremedhin B, Layer F, König W, König B (2008) Genetic classification and distinguishing of *Staphylococcus* species based on different partial gap, 16S rRNA, hsp60, rpoB, sodA, and tuf gene sequences. *J Clin Microb* 46: 1019-25.
- 2 Matthews KR, Roberson J, Gillespie BE, Luther DA, Oliver SP, et al. (1997) Identification and Differentiation of Coagulase-Negative *Staphylococcus aureus* by Polymerase Chain Reaction. *J Food Prot* 60: 686-8.
- 3 Jin M, Rosario W, Watler E, Calhoun DH (2004) Development of a large-scale HPLC-based purification for the urease from *Staphylococcus leei* and determination of subunit structure. *Protein Expression and Purification* 34: 111-7.
- 4 Becker K, Heilmann C, Peters G (2014) Coagulase-negative staphylococci. *Clin Microb Reviews* 27: 870-926.
- 5 Chan CX, Beiko RG, Ragan MA (2011) Lateral transfer of genes and gene fragments in *Staphylococcus* extends beyond mobile elements. *J Bact* 193: 3964-77.
- 6 Kloos WE (1980) Natural populations of the genus *Staphylococcus*. *Annual Review of Microbiology* 34: 559-92.
- 7 Pantůček R, Sedláček I, Indráková A, Vrbovska V, Mašlaňová I, et al. (2017) mecC gene and genomic islands with suspected role in adaptation to extreme environment. *Applied and Environmental Microbiology* 84: 1746-17.
- 8 Harris LG, Foster SJ, Richards RG (2002) An introduction to *Staphylococcus aureus*, and techniques for identifying and quantifying *S. aureus* adhesins in relation to adhesion to biomaterials: review. *Eur Cell Mater* 4: 39-60.
- 9 Takahashi T, Satoh I, Kikuchi N (1999) Phylogenetic relationships of 38 taxa of the genus *Staphylococcus* based on 16S rRNA gene sequence analysis. *Int J Bacteriol* 49: 725-8.
- 10 Kloos WE, Ballard DN, George CG, Webster JA, Hubner RJ, et al. (1998) Delimiting the genus *Staphylococcus* through description of *Macrocooccus caseolyticus* gen nov, comb Nov and *Macrocooccus equiperficus* sp nov, and *Macrocooccus bovicus* sp no and *Macrocooccus carouselicus* sp nov International. *Int J Bacteriol* 48: 859-77.