



Patients with Methicillin-Resistant *Staphylococcus aureus* Nasal Carriage and Antibioqram

Vargas Georges *

Department of Microbiology, University of Rouen Normandy, Pasteur, Rouen, France

DESCRIPTION

Staphylococci are spherical bacteria with a diameter of 0.5 to 1.8 μ m and are members of the Micrococcaceae family. Gram-positive cocci, catalase-positive, oxidase-negative, and forming minute clusters when stained, these bacteria are also Gram-positive cocci. Staphylococci are non-spore-forming, non-motile bacteria that can survive in salty environments and derive their energy from aerobic respiration or fermentation. Although they have a variety of dietary requirements, they typically need an organic source of nitrogen, five to twelve essential amino acids, and B vitamins. A frequent bacterium found in both strong and weak hosts is *S. aureus*. It may persist on the biofilm on the inert surface or long-term, asymptomatic colonization of human tissue.

Moreover, it can invade the host fulminant and present with a variety of symptoms. *S. aureus* may endure harsh environmental and animal conditions in addition to human hosts. There has been a worldwide pandemic of Methicillin-Resistant *Staphylococcus aureus* (MRSA) in hospitals and community settings since *S. aureus* developed resistance to methicillin as soon as the antibacterial antibiotic was used clinically in 1961. Its high morbidity and mortality rates, as well as their complete immunity to all penicillin's and the majority of other beta-lactam drugs. The bacterial cell wall contains penicillin-binding proteins (PBPs), which serve as an enzyme in the production of peptidoglycan. PBPs frequently have a poor affinity for beta-lactam antibiotics, in contrast to MRSA, which results in antibiotic resistance. *MecA*, a structural gene on the *S. aureus* chromosome, identifies MRSA, while the *femA* and *femB* genes encode proteins that influence how resistant *S. aureus* is to methicillin. PBP2a, a PBP with reduced antibiotic affinity, is encoded by the *mecA* gene in MRSA.

One of the main reasons why hemodialysis patients pass away is due to bacterial infections. Because of their weakened immune systems and the nature of the hospital environment used for the

dialysis session, hemodialysis patients are actually more likely to contract an infection. *S. aureus* is the most prevalent bacterial infection in hemodialysis patients, according to recent data. Normal flora of the body can lead to more severe problems such as bacteremia, osteomyelitis, necrotizing pneumonitis, infective endocarditis, and Toxic Shock Syndrome (TSS) from this infection.

Clinically, the main issue with *S. aureus* is the significant level of antibiotic resistance that has developed, making treatment challenging. In the *S. aureus* resistance appeared two years after penicillin was first introduced. Many infections in humans may be brought on by *S. aureus*. Based on where the infection originated, *S. aureus* clinical infections are divided into nosocomial and community-based groups. Infections with *S. aureus* are, however, becoming more common. During weeks or months, the bacterium can stay in the anterior nares in a carrier state without producing any illnesses. The colonization advances to infection when specific predisposing factors, such as prolonged hospitalization, immune suppression, procedures, the use of invasive medical equipment, and persistent metabolic diseases, take place. Among the clinical infections brought on by *S. aureus* include bacteremia, osteoarticular infections, infective endocarditis, pleuropulmonary infections, and wound infections.

Other clinical infections include epidural abscesses, urinary tract infections, and meningitis. This microorganism has the ability to enter the bloodstream and spread widely to several organs, leading to sepsis. *S. aureus* releases enterotoxins into food to produce food poisoning, whereas super antigens released into the bloodstream to cause toxic shock syndrome. MRSA was discovered in cattle rose using various techniques. However, compared to veal calves, the estimated prevalence was lower in nasal isolates from dairy and beef cows. The two isolation techniques under test showed no discernible difference. Despite the animals being collected appearing to be in good health, a high degree of multi-resistance was discovered along with a wide range of antibiotic resistance and virulence genes.

Correspondence to: Vargas Georges Department of Micro biology, University of Rouen Normandy, Pasteur, Rouen, France, E-mail: Georgesv@gmail.com

Received: 02-Feb-2023, Manuscript No. JMBT-23-20298; **Editor assigned:** 06-Feb-2023, Pre QC No. JMBT-23-20298 (PQ); **Reviewed:** 20-Feb-2023, QC No. JMBT-23-20298; **Revised:** 27-Feb-2023, Manuscript No. JMBT-23-20298 (R); **Published:** 06-Mar-2023, DOI: 10.35248/1948-5948.23.15:545

Citation: Georges V (2023) Patients with Methicillin-Resistant *Staphylococcus aureus* Nasal Carriage and Antibioqram. J Microb Biochem Technol. 15:545.

Copyright: © 2023 Georges V. This is an open access article distributed under the terms of the Creative Commons Attribution License, which permits unrestricted use, distribution, and reproduction in any medium, provided the original author and source are credited.