Methicillin-resistant *Staphylococcus aureus* (MRSA)

Mona Z Zaghloul

Microbiology Unit, Department of Clinical Pathology, Ain Shams University Hospitals, Cairo, Egypt

**Corresponding author:** Zaghloul MZ, Microbiology Unit, Department of Clinical Pathology, Ain Shams University Hospitals, Cairo, Egypt. Tel: 02-24023494; E-mail: monazaki_810@hotmail.com

**Rec date:** Apr 07, 2016; **Acc date:** Apr 08, 2016; **Pub date:** Apr 16, 2016

**Copyright:** © 2016 Zaghloul MZ. 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.

**Citation:** Zaghloul MZ (2016) Methicillin-resistant *Staphylococcus aureus* (MRSA). J Med Microbiol Diagn 5: e131. doi:10.4172/2161-0703.1000e131

**Editorial**

Methicillin-resistant *Staphylococcus aureus* (MRSA) infections have become a global health problem particularly in hospital setup causing simple skin infections to life-threatening infections. It may lead to serious complications, such as pneumonia, septicemia, arthritis and osteomyelitis [1].

MRSA was isolated from pus, urine, breast discharge, blood culture, cerebrospinal fluid, and ascetic fluid [2]. The extensive use of antibiotics over the last 50 years has led to the emergence of bacterial resistance and to the dissemination of resistance genes among pathogenic organisms [3]. In addition, since few cells in a population might actually express resistance, these heterogeneous strains can evade detection in standard susceptibility test systems [4,5].

During the 1980s, MRSA started to constitute a wide spread human health concern [6] besides its importance as a nosocomial pathogen [7-9].

MRSA is primarily mediated by the over production of penicillin-binding protein 2a (PBP2a) with low affinity for beta-lactam antibiotics [10]. The mecA gene is part of a 21 kb to 60 kb staphylococcal chromosome cassette mec (SCCmec), a mobile genetic element that may also contain genetic structures as Tn554, PUB110, and pT181 which encode resistance to non-β-lactam antibiotics [11]. The mecA gene which encodes PBP2a is considered a useful molecular marker of putative methicillin resistance in *S. aureus*. *S. aureus* strains have a tendency to accumulate additional resistance determinants, resulting in the formation of multiple-antibiotic resistant MRSA strains which are creating therapeutic problems and limiting the choice of therapeutic options [12].

Accurate and rapid identification of MRSA is essential for effective antimicrobial chemotherapy. Numerous approaches that improve turnaround time for the identification of MRSA have been described such as: fluorescence tests [13], PCR assays [14], or penicillin-binding protein 2a (PBP2a) antibody agglutination tests [15]. Molecular methods for detecting resistance valuable infection-control tools by rapid and accurate identification of Staphylococci and their resistant types. Thus help in confirming patients infected by resistant bacteria. Clearly rapid detection of a specific resistance mechanism in a molecular test would allow clinicians initially to avoid potentially inappropriate treatment options [16]. In recent years, detection of mecA by PCR is considered the gold standard for identification of MRSA [17].

**References**


2. Green-top Guideline No.64h-The Royal College of Obstetricians and Gynaecologists. Bacterial sepsis following pregnancy, April 2012


