Methicillin Resistant Staphylococcus Aureus (MRSA), A Challenge and an Opportunity!

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**Article ID:** WMC001996

**Article Type:** Review articles

**Submitted on:** 19-Jun-2011, 03:19:26 PM GMT    **Published on:** 20-Jun-2011, 05:43:49 PM GMT

**Article URL:** http://www.webmedcentral.com/article_view/1996

**Subject Categories:** PUBLIC HEALTH

**Keywords:** CA-MRSA, HA-MRSA, Zoonotic MRSA, Libya

**How to cite the article:** Ahmed M. Methicillin Resistant Staphylococcus Aureus (MRSA), A Challenge and an Opportunity! . WebmedCentral PUBLIC HEALTH 2011;2(6):WMC001996
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Review

Methicillin-resistant Staphylococcus aureus (MRSA), often described as superbug, is a serious health and global issue that is evolving to a general concern and deserves continues attention (Ahmed et al., 2010a; Klevens et al., 2007). Staphylococcus aureus, the most pathogenic species of staphylococci, is found almost everywhere, particularly on the skin of animals, including humans (Mathanraj et al., 2009). It is estimated that about 60% of human population are colonized by S. aureus and 20% of humans are persistent carriers. The nose is a favourite site (Zorgani et al., 2009a) but it can also survive on skin and in the environment for long time. Whether S. aureus is susceptible or resistant to antimicrobials (i.e. MSSA, MRSA), it can cause skin infections, gastroenteritis and on occasion can cause serious complications (Tiemersma et al., 2004; Lewis & Jorgensen, 2005). As is the case with most of the common bacterial pathogens, animals including humans with compromised immunity are much more susceptible to the invasive form of infection.

Staphylococcus aureus unique nature and its ability to adapt and survive in the environment has made it one of the most successful pathogen known to man (de et al., 2007). The genetic plasticity of S. aureus has resulted in the emergence of varying degrees of antibiotic resistance and virulence patterns (de et al., 2007). The major problem of S. aureus being resistant to multiple drugs (i.e. MRSA) has been recognized and considered in human medicine to be primarily a problem of hospitals, until recently (Ahmed et al., 2010a; Palavecino, 2007). The problem of antibiotic resistance associated with S. aureus and how resistant strains are spreading outside the hospital setting is a new concern of public health today (Barber, 1961; Brown et al., 2005; Robinson et al., 2009). Methicillin resistant S. aureus has been evolving since the 1960s. Many MRSA resistant phenotypes with multi resistance characteristic have been described and reported worldwide e.g.MRSA-MLSB phenotypes. The MLSB resistance phenotypes (MLSB and MLSBi phenotype) confer multiple-resistance to many antibiotic classes (i.e. macrolides, lincosamides, and streptogramines B) (Lewis & Jorgensen, 2005) and such phenotypes have been already reported worldwide including in developing countries (Siberry et al., 2003; Ahmed et al., 2010b). Clindamycin is useful therapeutic option for MRSA infections however there have been cases of antibiotic treatment failures in patients with MRSA infections caused by inducible clindamycin resistance (MRSA-MLSBi) strains (Lewis & Jorgensen, 2005; Siberry et al., 2003). MRSA-MLSBi strains cannot be detected by standard susceptibility tests however such resistance can be detected using a designed test called the D-test (CLS 2006; Ahmed et al., 2010b). Other important phenotypes such as vancomycin resistant S.aureus (VRSA) has been also described and reported which confer further resistance to important antibiotic drugs such as vancomycin, one of the drug of choice to treat MRSA infections (Brown et al., 2005; Martins & Cunha, 2007).

Many risk factors were identified to be associated with acquiring MRSA infection such as prolonged
hospitalization, and antimicrobial therapy. Nasal colonization has also been identified as a risk factor for infection and carriage of MRSA in various healthcare settings (von et al., 2005). MRSA colonization also occurs at sites other than the nose (e.g. pharynx, axilla, rectum, perineum) (Eveillard et al., 2006) which might play an important role in development and transmission of infection. Until recently MRSA is primarily considered a nosocomial infection, acquired in hospital settings and mainly affects healthcare workers (Zorgani et al., 2009b; unpublished data from Libya). Recently, MRSA colonization has been identified in people who have had no association with hospitals or the other risk factors. These have been identified as community acquired (CA-MRSA), as opposed to hospital-acquired (HA-MRSA) (Martins & Cunha, 2007). The first report of clinical CA-MRSA was in the 1980s (Saravolatz et al., 1993) and since after reports of CA-MRSA have increased (Fey et al., 2003). Studies have shown that many hospital MRSA infections were actually acquired before admission (Layton et al., 1995).

CA-MRSA is bacteriologically, clinically, and epidemiologically, distinct from HA-MRSA (CDC, 1999) and isolates tend to be resistant to fewer antimicrobial drugs and carry different virulent genes. CA-MRSA isolates commonly carry genes for the Panton-Valentine leukocidin (PVL) toxin and a different type of the gene complex system called staphylococcal cassette chromosome mec (SCCmec) (Naimi et al., 2003). Methicillin resistance in staphylococcus species is mediated by the staphylococcal cassette chromosome mec (SCCmec) cassette which contains mobile genetic elements (e.g. mec genes) and characterized into five different types (I to V) (Martins & Cunha, 2007).

Animals can be a source and a reservoir of MRSA (Weese et al., 2010; Garcia-Alvarez et al., 2011). The first isolation of clinical MRSA from animals was reported from cow (Devriese et al., 1972). Animals could be a source of zoonotic MRSA and people in-contact with animals are most likely to be colonized with MRSA. Different animals have been reported to be a zoonotic source of MRSA (Pak et al., 1999; Lee, 2003; Baptiste et al., 2005; Weese et al., 2006) which subsequently can infect their owners (Scott et al., 1988; Cefai et al., 1994; Seguin et al., 1999; Baptiste et al., 2005). There is evidence for veterinarians that MRSA could be an occupational infection in domestic animals (Baptiste et al., 2005). Therefore animals can carry and be colonized with MRSA and pose a zoonotic threat to other animals, veterinarians and to the public (Baptiste et al., 2005; Voss et al., 2005; Bens et al., 2006; Khanna et al., 2008). Moreover humans have been implicated in the passage of MRSA to companion animals and few studies have reported such possibility of transmission (Seguin et al., 1999).

MRSA can also be considered a food-borne pathogen, causing and responsible for MRSA food-poisoning (Jones et al., 2002; Weese et al., 2010; Garcia-Alvarez et al., 2011). MRSA food-poisoning is a rare however the incidence level is increasing (Chiou et al., 2000). According to our knowledge no-fatal report has been documented due to MRSA.

Although, only in humans, studies have tackled the MRSA situation in Libya (El-Bouri, 2009; Zorgani et al., 2009a,b; Ghenghesh et al., 2009; Rahuma et al., 2005; Belgasim et al., 2010; Ahmed et al., 2010a,b) and fewer documented the prevalence of MRSA among health care workers (Zorgani et al., 2009b; Belgasim et al., 2010; unpublished data from Libya). More data are needed in order to fully understand the epidemiology, and microbiology of MRSA and other nosocomial organisms. Although transmission of such organisms is most frequently documented in health care facilities, other sources such as animals might play a role in the emergence and transmission of antimicrobial-resistant microbes (Seguin et al., 1999; Garcia-Alvarez et al., 2011). Increasing experience with these organisms will improve the understanding of the routes of transmission and effective preventive measures.

Dedication:
This mini-review is dedicated for Libyan motivated researchers and clinicians in different medical disciplines.

References


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