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Community-associated Methicillin-Resistant *Staphylococcus aureus* (CA-MRSA)

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Methicillin resistance in staphylococci is conferred by the *mec* gene, which codes for a penicillin-binding protein with little affinity for current marketed beta-lactam antibiotics – the cornerstone of antibacterial therapy. Previously limited to strains of *S. aureus* (MRSA) circulating in hospitals, the appearance of MRSA in the community (CA-MRSA) in the 1980's, followed by its explosive spread in US and other parts of the world this decade, marked a critical evolutionary milestone for the organism and signaled the need for paradigm shifts in the perception and management of staphylococcal infections worldwide. Whereas different infection control measures exist for preventing the spread of MRSA in hospitals and other institutional facilities (i.e. handwashing, isolation and quarantine of colonized and infected patients, donning of protective gear like gloves/aprons, etc), these are not measures that can be easily translated into the community.

Relevant points that have emerged from the molecular studies of CA-MRSA are:

- CA-MRSA strains are different at the genetic level from hospital strains of MRSA (HA-MRSA) – these are not closely related strains of *S. aureus*.
- While multiple different strains (ST's) of CA-MRSA exist, there are generally 1 or 2 predominant strains for each geographic region.
- Some strains of CA-MRSA are epidemic, and are found in multiple countries, although it is unclear at present if these are local methicillin-susceptible strains that have independently acquired the *mec* gene, or if this represents the spread of very successful CA-MRSA clones. It is likely that both phenomena exist.

CA-MRSA infections also present differently from HA-MRSA infections. Other than affecting a different patient demographic, they are also associated with spectacular and lethal infections such as necrotizing fasciitis, necrotizing pneumonia, and Waterhouse-Friderichsen syndrome (previously seen only in severe meningococcal infection). These are attributed to the fact that CA-MRSA strains in general carry far more virulence genes in its genome than HA-MRSA, as well as perhaps a function of their portal of entry into the host and host's immune system – healthcare-acquired CA-MRSA in US hospitals present little differently from other HA-MRSA.

The reason(s) for the success of some *S. aureus* strains (above the others) is not clear, despite the many studies performed. It is also unclear how *S. aureus* strains/lineages have evolved over the decades since the first description of this organism, although experts suggest that the transfer of genetic elements from other more benign staphylococci play a major role, perhaps far more than mutation within the organism's genome itself. This is best exemplified by the finding of ACME (arginine catabolic mobile element) – a genetic element common in other skin staphylococci – in the hyper-endemic USA300 CA-MRSA; this element is speculated to be at least partially responsible for the hyper-transmissibility of USA300.

To date, the predominant approach to the problem of CA-MRSA (and *S. aureus* in general) has been that of a biomedical model. Further work is required to elucidate the reasons for the success of certain *S. aureus* sequence types, and to identify factors that may result in useful strategies for the containment of further spread of CA-MRSA in the open community.