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## INTRODUCTION TO THIS ISSUE

### Epidemiology of methicillin-resistant *Staphylococcus aureus* with emphasis on veterinary and community settings

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Although first described in 1961, methicillin-resistant *Staphylococcus aureus* (MRSA) strains continue to pose a significant problem in healthcare settings and more recently in the general community. The escalating volume of literature on the subject with over 450 review articles listed on PubMed on epidemiological aspects of MRSA since 1979 reflects not only the burden of disease associated with this organism and the interest of the scientific community in defining strain populations and their evolution as well as the detection of carriage, but also indicates the continuing need for efficient treatment, and control of outbreaks. The strain types, and patient risk factors for infection with hospital-acquired (HA)-MRSA are well documented in the literature, but the emergence and dissemination of community-acquired (CA)-MRSA in otherwise healthy individuals such as children, sportsmen and military personnel, have presented significant new problems for the diagnosis, definition of epidemiological patterns of spread and management of these strains [1].

CA-MRSA infections are increasingly prevalent in the USA but are, as yet, generally less frequent in Europe and other parts of the world. They are most often isolated from skin and soft tissue infections but less commonly cause serious systemic infection such as necrotizing pneumonia. The presence of the bacteriophage-encoded Panton–Valentine leucocidin (PVL) is closely associated with CA-MRSA strains in the USA and Europe but the role of this and other secreted toxins in different presentations of infection remains to be clarified. CA-MRSA strains are associated with the presence of staphylococcal chromosome *mec* (SCC*mec*) element types IV, V and VII and are more often of genetic lineages distinct from HA-MRSA. However, the epidemiological picture is becoming more complex as hospital strain lineages appear in non-hospital community settings and outbreaks with CA-MRSA in hospitals are being reported [2].

This themed issue comprises a collection of papers documenting local experience of various aspects of the epidemiology of MRSA, and less so methicillin-susceptible (MSSA) strains, in the hospital, general community including military trainees and care

homes, and food-producing and companion animals. In addition, some articles are included because they describe unique observations of specific risk factors and carriage or present data from geographical areas not widely represented in the international literature. Some notable highlights include the paper by Miller *et al.* (pp. 655–665) which proposes a novel term of ‘feral’ MRSA to describe HA-MRSA strains that persist in individuals in the community who have regular healthcare contacts. These strains are genetically distinct from other non-hospital epidemic strains isolated from persons with recent contact with healthcare services. Cutaneous injection wound infections with *S. aureus* is common in injecting drug users (IDU). The study by Lloyd-Smith *et al.* (pp. 713–720) found *S. aureus* in 25 of 59 wounds in a cohort of IDU subjects in the community and 16 of 18 MRSA recovered were classified as CA-MRSA by the presence of PVL. Although susceptible to therapeutically relevant antimicrobials the majority of CA-MRSA were resistant to clindamycin which has implications for empirical treatment of these infections. The impact of CA-MRSA infection in a large cohort of military trainees is well illustrated by the study of Morrison-Rodriguez *et al.* (pp. 721–729) who found a peak rate of 42 cases per 1000 soldiers totalling over 3500 infections in the 5-year surveillance period. MRSA in care homes for the elderly has been the subject of a number of investigations but the contribution of dementia to colonization rates has not been hitherto reported. Infection control measures are difficult in this population and thus one might assume that they are at higher risk for colonization by *S. aureus* including MRSA. However, this hypothesis was not supported by the report of Lasseter *et al.* (pp. 686–696) who studied 751 residents in 51 care homes and found that dementia was not a significant risk factor for acquisition of either MRSA or MSSA and, perhaps counter-intuitively, that MRSA colonization decreased with increasing age of subjects. *S. aureus* is a rare cause of community-onset pneumonia (COP) in children following influenza but Kallen *et al.* (pp. 666–672) report 30 episodes of COP, 12 of which were due to MRSA. About one-third of patients were treated as outpatients prior to hospital admission and

only three received antimicrobials. Further, about half of the patients were not treated empirically with antimicrobials recommended for MRSA pneumonia on admission, including several who eventually grew MRSA. These findings reflect a failure to recognize MRSA as a potential cause of illness in these patients. There are relatively few studies on the genetic lineages of *S. aureus* prevalent in the Middle East. However data from Lebanon (Tokajian *et al.* pp. 707–712) suggests that while there is considerable heterogeneity in *spa* gene types in MRSA; a PVL-positive clone (ST80-MRSA-IVc) is widespread in Beirut. Although strictly outside the theme of the issue we have included a paper on the distribution of the SCCmec element in coagulase-negative staphylococci (Garza-Gonzalez *et al.* pp. 645–654) as these species may represent a source of these genes which are acquired by MRSA through horizontal transfer between species.

MRSA in animal populations has gained increasing attention over the last few years. On the one hand, animals kept as pets such as dogs or horses, living in close contact with their owners may carry MRSA strains and become reservoirs or vectors. Loeffler *et al.* (pp. 595–605) review the epidemiological, clinical and genetic differences and similarities that exist between CA-MRSA in humans and MRSA strains isolated from companion animals. In food animals, MRSA ST398 has recently triggered major debate as – unlike most other CA-MRSA strains – it appears to be fully adapted to an animal host, namely the pig, but possibly also other species such as cattle or poultry (Vanderhaeghen *et al.* pp. 606–625). The occurrence of MRSA in food animals is of concern as transmission to consumers is a possibility although the risk is currently considered to be negligible [3]. The European Food Safety Authority (EFSA) nevertheless asked all EU Member States to collect data on MRSA in pigs [4]. Whether the geographical patterns documented in this report are due to epidemiological factors or differences in sampling design requires further investigation. Biosecurity and minimizing selection pressure by applying principles of prudent antimicrobial prescription will be key strategies to limit the spread of MRSA in meat production systems across farms and country borders.

Based on the current evidence, it is not yet possible to assess the public health significance of MRSA isolated from either food or companion animals. Occupational exposure in professions such as veterinarians (Abbott *et al.* pp. 764–771) and also farmers or slaughterhouse workers (Mulders *et al.* pp. 743–755; van Cleef *et al.* pp. 756–763) deserves particular attention as these groups appear to be at increased risk

of carriage. Catry *et al.* (pp. 626–644) review possible options to prevent animal-to-human transmission and also emphasize the need for increased awareness and improved communication between veterinary and public health specialists.

Major research projects are currently under way to further elucidate the epidemiology of MRSA in animal and human populations. In particular, countries with significant pig production industries have made funding available to investigate the emergence of MRSA from pigs. So has the European Commission in its Framework 7 Programme (see [www.fp7-pilgrim.eu](http://www.fp7-pilgrim.eu) and [www.concord-mrsa.eu](http://www.concord-mrsa.eu)). The outcomes of these studies will help improve our understanding of the epidemiology of MRSA at the human–animal interface. This knowledge may also help explain and manage the emergence of resistant bacteria from animals and their public health impact in general.

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