

Microbiology Congress 2018: The influence of livestock on human infections with LA-MRSA - Matjaz Ocepek - Institute of Microbiology and Parasitology

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Infections caused by the methicillin resistant *Staphylococcus aureus* (MRSA) are traditionally nosocomial, but recent reports have indicated an increased frequency of community acquired infections. Livestock associated MRSA (LA-MRSA) is often present in domestic animals, especially in pigs. Although LA-MRSA strains usually do not cause the disease in animals, they could serve as potential source for human infections. In Slovenia, the number of people colonized with LA-MRSA is increasing. Both human and animal samples in addition to environmental samples were collected from 16 farms in Slovenia, where at least one case of LA-MRSA was previously confirmed per family. All the obtained isolates were tested for their antimicrobial susceptibility with the micro dilution method for the minimal inhibitory concentration (MIC). In addition, they were confirmed by the multiplex PCR for 16S rRNA, nuc, mecA, mecC and PVL genes.

Spa typing was also performed, using the Ridom StaphType software. All the human isolates of LA-MRSA were resistant to Cefoxitin, Tetracycline and Penicillin, some of them also to Ciprofloxacin and Clindamycin. In animals, similar susceptibility patterns were found, but none of the animal isolates were resistant to Ciprofloxacin. The human isolates mostly belonged to spa types t011 and t034, but t1451, t10765 and t1344 were also present. The evidence of LA-MRSA in animals was confirmed for five farms and all of those isolates belonged to the spa type t011. It can be assumed that pigs are a likely source of human infection, but it can also be concluded that LA-MRSA strains are already spreading within the human population. Namely, LA-MRSA was isolated from humans at farms, where both the animal samples and dust samples collected from the stables were negative.

During the past 25 years an increase in the prevalence of methicillin-resistant *Staphylococcus aureus* (HA-MRSA) was recorded worldwide. Additionally, MRSA infections may occur outside and independent of hospitals, caused by community associated MRSA (CA-MRSA). In Germany, we found that at least 10% of these sporadic infections are due to livestock-associated MRSA (LA-MRSA), which is initially associated with livestock.

The majority of these MRSA cases are attributed to clonal complex CC398. LA-MRSA CC398 colonizes the animals asymptotically in about half of conventional pig farms. For about 77%–86% of humans with occupational exposure to pigs, nasal carriage has been reported; it can be lost when exposure is interrupted. Among family members living at the same farms, only 4%–5% are colonized. Spread beyond this

group of people is less frequent. The prevalence of LA-MRSA in livestock seems to be influenced by farm size, farming systems, usage of disinfectants, and in-feed zinc. LA-MRSA CC398 is able to cause the same kind of infections in humans as *S. aureus* and MRSA in general. It can be introduced to hospitals and cause nosocomial infections such as postoperative surgical site infections, ventilator associated pneumonia, septicemia, and infections after joint replacement. For this reason, screening for MRSA colonization at hospital admittance is recommended for farmers and veterinarians with livestock contacts. Intrahospital dissemination, typical for HA-MRSA in the absence of sufficient hygiene, has only rarely been observed for LA-MRSA to date.

The proportion of LA-MRSA among all MRSA from nosocomial infections is about 3% across Germany. In geographical areas with a comparatively high density of conventional farms, LA-MRSA accounts for up to 10% of MRSA from septicemia and 15% of MRSA from wound infections. As known from comparative genome analysis, LA-MRSA has evolved from human-adapted methicillin-susceptible *S. aureus*, and the jump to livestock was obviously associated with several genetic changes. Reversion of the genetic changes and readaptation to humans bears a potential health risk and requires tight surveillance.

Although most LA-MRSA (>80%) is resistant to several antibiotics, there are still sufficient treatment options. docking, exclusively for CXCR4. The results obtained for CCR5 suggest the likelihood that different active scaffolds bind in several ways within the CCR5 pocket. Ligand based virtual screening approaches utilize structure-activity data from a set of known actives molecules in order to identify likelihood drug candidates for experimental confirmation.⁵² Quantitative structure-activity relationships (QSAR), pharmacophore modeling, similarity or substructure searching and three-dimensional shape matching are a number of the strategies that are utilized in LBSV method. Quantitative Structure Activity Relationship (QSAR) is one among the frequently used approach in ligand based virtual screening.