

## OCCURRENCE AND CHARACTERIZATION OF LIVESTOCK-ASSOCIATED METHICILLIN-RESISTANT *STAPHYLOCOCCUS AUREUS*

Modestas Ružauskas<sup>1</sup>, Natacha Couto<sup>2</sup>, Rita Šiugždinienė<sup>1</sup>, Adriana Belas<sup>2</sup>, Irena Klimienė<sup>1</sup>, Marius Virgailis<sup>1</sup>, Constanca Pomba<sup>2</sup>

<sup>1</sup>*Veterinary Academy, Lithuanian University of Health Sciences  
Mickevičiaus 9, LT-44307, Kaunas, Lithuania; Tel: +37061515240; E-mail: ruzauskas@lva.lt*

<sup>2</sup>*Laboratory of Antimicrobial and Biocide Resistance, Faculty of Veterinary Medicine  
Technical University of Lisbon  
Av. da Universidade Técnica, 1300-477 Lisboa, Portugal; Tel: +351919207336; E-mail: cpomba@fmv.utl.pt*

**Abstract.** Methicillin resistant *Staphylococcus aureus* causes a wide range of severe and economically-important diseases in humans and animals. Different types of MRSA are associated with different hosts but the transmission occurs between them. The aim of this study was to investigate possible spread of MRSA among livestock in Lithuania and to determine their types and antimicrobial resistance. Cattle (n=120), horses (n=120) pigs (n=160) and poultry (pooled samples, n=120) were tested for MRSA prevalence. From a total of 520 samples tested, 4 isolates of methicillin resistant *Staphylococcus aureus* (0.8 %) were identified. All isolates were obtained from the finisher pigs delivered from the same farm complex. Multiplex PCR demonstrated presence of *mecA*, *nuc* and 16S genes in all tested cultures. All MRSA isolates were identified as ST398. Sequencing of *spa* genes and *SCCmec* typing revealed that all strains belonged to the *spa* type t011 and *SCCmec* V. PFGE revealed two different clones among the isolates. Susceptibility testing revealed resistance to tetracycline in all MRSA isolates attributed to *tetK* and *tetM* genes. All tested isolates were resistant to erythromycin owing to the presence of *ermB* gene as well as resistances to azithromycin, clindamycin and quinupristin/dalfopristin. One isolate was resistant to trimethoprim/sulfamethoxazole and carried the resistance gene *dfpK* while the other isolate was resistant to the combination of amoxicillin and clavulanic acid. All of the isolates were susceptible to fluoroquinolones, cefotaxime, chloramphenicol, fosfomicin, fusidic acid, gentamicin, linezolid, vancomycin, mupirocin and teicoplanin.

**Keywords:** MRSA; ST398; livestock; antimicrobial resistance.