

INVESTIGATION OF MRSA ISOLATES FROM PIG ORIGIN, ENVIRONMENT AND STUFF BY *SPA* TYPING, ANTIMICROBIAL RESISTANCE AND *SE* GENE DETECTION

Meldra Ivbule¹, Edvīns Miklaševičs², Liene Čupāne², Laima Bērziņa³, Andris Bālinš⁴, Anda Valdovska^{4,5}

¹Food and Veterinary Service, Dienvidzemgale administration, 10 K. Helmaņa street, Jelgava, LV-3004, Latvia

²Riga Stradins University, Institute of Oncology, 13 Pilsoņu street, Riga, LV-1002, Latvia

³Latvia University of Agriculture, Faculty of Information Technology, 1 Lielā street, Jelgava, LV-3001, Latvia

⁴Latvia University of Agriculture, Biotechnology Research Laboratory, 8 K. Helmaņa street, Jelgava, LV 3004, Latvia

⁵Latvia University of Agriculture Faculty of Veterinary Medicine, 8 K. Helmaņa street, Jelgava, LV 3004, Latvia

Correspondence to: M. Ivbule, e-mail: Meldra.Ivbule@pvd.gov.lv, tel.: 371 28700311

Abstract. MRSA (methicillin resistant *Staphylococcus aureus*) is hard curable and highly resistant zoonotic soft tissue pathogen which is also capable to produce enterotoxins and cause food toxiconfections. The aim of the study was the characterization of MRSA isolates from different pig farms and slaughterhouses based on interaction of antimicrobial resistance, *spa* type, *SE* genes and source of MRSA isolates. In total 405 pigs, 105 carcasses, 34 workers as well as 46 samples from environment from several farms and slaughterhouses were examined by conventional microbial and molecular methods. In total 155 (14.6%) MRSA isolates were detected from 1064 samples tested and included 11 positive pigs (27.4%) from all tested pigs, 2 isolates (4.3%) from environment, 3 isolates (4.3%) from milk, 7 isolates (6.7%) from pig carcasses and 7 isolates (20.6%) from workers.

From all MRSA isolates 48.4% contained *sea*, 1.3% *seb*, 5.9% *sec* and 9.7% *seh*. Study showed that *sea* mostly appears alone (70.4%) in MRSA isolates or together with *seh* (14.8%), but *seh* trends to be together in isolate genome with other genes that are coding *SE*. In the same time in these MRSA isolates *sec* appears alone or together with *sea*. Contrary to other investigations, our study indicated high *sea* distribution in MRSA isolates and only some isolates with *sec*, moreover among MRSA *spa* types with high *sea* distribution antimicrobial resistance was lower.

Keywords: methicillin resistant *Staphylococcus aureus*, pigs, zoonosis, enterotoxins genes