A Livestock-Associated, Multidrug-Resistant, Methicillin-Resistant Staphylococcus aureus Clonal Complex 97 Lineage Spreading in Dairy Cattle and Pigs in Italy

Pandemic methicillin-resistant Staphylococcus aureus (MRSA) clonal complex 97 (CC97) lineages originated from livestock-to-human host jumps. In recent years, CC97 has become one of the major MRSA lineages detected in Italian farmed animals. The aim of this study was to characterize and analyze differences in MRSA and methicillin-susceptible S. aureus (MSSA) mainly of swine and bovine origins. Forty-seven CC97 isolates, 35 MRSA isolates, and 6 MSSA isolates from different Italian pig and cattle holdings; 5 pig MRSA isolates from Germany; and 1 human MSSA isolate from Spain were characterized by macrorestriction pulsed-field gel electrophoresis (PFGE) analysis, multilocus sequence typing (MLST), spa typing, staphylococcal cassette chromosome mec (SCCmec) typing, and antimicrobial resistance pattern analysis. Virulence and resistance genes were investigated by PCR and microarray analysis. Most of the isolates were of SCCmec type V (SCCmec V), except for two German MRSA isolates (SCCmec III). Five main clusters were identified by PFGE, with the German isolates (clusters I and II) showing 60.5% similarity with the Italian isolates, most of which (68.1%) grouped into cluster V. All CC97 isolates were Panton-Valentine leukocidin (PVL) negative, and a few (n = 7) tested positive for sak or scn. All MRSA isolates were multidrug resistant (MDR), and the main features were erm(B)- or erm(C)-mediated (n = 18) macrolide-lincosamide-streptogramin B resistance, vga(A)-mediated (n = 37) pleuromutilin resistance, fluoroquinolone resistance (n = 33), tet(K) in 32/37 tet(M)-positive isolates, and blaZ in almost all MRSA isolates. Few host-associated differences were detected among CC97 MRSA isolates: their extensive MDR nature in both pigs and dairy cattle may be a consequence of a spillback from pigs of a MRSA lineage that originated in cattle as MSSA and needs further investigation. Measures should be implemented at the farm level to prevent spillover to humans in intensive farming areas.

General information
State: Published
Organisations: National Food Institute, Research Group for Genomic Epidemiology, Instituto Zooprofilattico Sperimentale delle Venezie, Federal Institute for Risk Assessment, Complutense University, Ghent University, Universite Libre de Bruxelles
Number of pages: 6
Pages: 816-821
Publication date: 2016
Peer-reviewed: Yes

Publication information
Journal: Applied and Environmental Microbiology
Volume: 82
Issue number: 3
ISSN (Print): 0099-2240
Ratings:
BFI (2018): BFI-level 2
Web of Science (2018): Indexed yes
BFI (2017): BFI-level 2
Scopus rating (2017): CiteScore 3.99
Web of Science (2017): Impact factor 3.633
Web of Science (2017): Indexed yes
BFI (2016): BFI-level 2
Scopus rating (2016): CiteScore 4.08
Web of Science (2016): Impact factor 3.807
Web of Science (2016): Indexed yes
BFI (2015): BFI-level 2
Scopus rating (2015): CiteScore 4.14 SJR 1.891 SNIP 1.308
Web of Science (2015): Indexed yes
BFI (2014): BFI-level 2
Scopus rating (2014): CiteScore 4.02 SJR 1.857 SNIP 1.384
Web of Science (2014): Impact factor 3.668
Web of Science (2014): Indexed yes